



Assessing matrilineal genetic diversity in Mexico through the analysis of ancient mitogenomes spanning 2,300-500 YBP

Izarraras-Gomez, Alan; Villa-Islas, Viridiana; Bravo-Lopez, Miriam; Sandoval-Velasco, Marcela; Perez-Campos, Elizabeth M.; Herrera-Munoz, Alberto; Villanueva-Medina, Eugenia; Aguayo-Haro, Ramiro; Valdiosera, Cristina; Avila-Arcos, Maria C.

DOI:
[10.1002/ajpa.24023](https://doi.org/10.1002/ajpa.24023)

Publication date:
2020

Document version
Publisher's PDF, also known as Version of record

Document license:
[CC BY](https://creativecommons.org/licenses/by/4.0/)

Citation for published version (APA):
Izarraras-Gomez, A., Villa-Islas, V., Bravo-Lopez, M., Sandoval-Velasco, M., Perez-Campos, E. M., Herrera-Munoz, A., ... Avila-Arcos, M. C. (2020). *Assessing matrilineal genetic diversity in Mexico through the analysis of ancient mitogenomes spanning 2,300-500 YBP*. 129-129. <https://doi.org/10.1002/ajpa.24023>



PROGRAM OF THE
**89TH ANNUAL MEETING OF THE
 AMERICAN ASSOCIATION OF PHYSICAL
 ANTHROPOLOGISTS**
 APRIL 15 – 18, 2020

To be held at the
JW Marriott LA Live
 900 West Olympic Boulevard • Los Angeles, CA 90015

AAPA Scientific Program Committee

Steven R. Leigh, Chair

Amanda Agnew	Rebecca Gilmour	Kent Johnson	Sean Prall
Kari Allen	C. Eduardo Guerra Amorim	Erin Kane	Melissa Schaefer
Ben Auerbach	Lauren Halenar-Price	Claire Kirchhoff	Elizabeth St Clair
Jonathan Bethard	Ashley Hammond	Myra Laird	Claire Terhune
Nicole Burt	Donna Harrison	Christina Nicholas	Sam Urlacher
James Calcagno	Geoff Hayes	Heather Norton	Qian Wang
Zachary Cofran	Amber Heard-Booth	Robert O'Malley	Timothy Webster
Paul Constantino	Brian Hemphill	Alejandra Ortiz	Katherine Weisensee
Lynn Copes	Nathan Holton	Nicholas Passalacqua	Julie Wieczkowski
Jennifer Cramer	Rob Hoppa	Christine Pink	Frank Williams
Andrew Deane	Jennifer Hotzman	Stephanie Poindexter	John Willman
Maureen Devlin	Rebecca Jabbour	Emma Pomeroy	
Christina Fojas	Jessica Joganic		

AAPA Meetings Director

Lori Strong, Burk & Associates, Inc.

Los Angeles Advance Team

Graciela Cabana	Christopher Kuzawa	Stephanie Meredith
Anne L. Grauer	Steven R. Leigh	Amy Rector
Edward H. Hagen	Kristi Lewton	Heide Rohland
Leslea Hlusko	W. Scott McGraw	Lori Strong

Program Assistant

Kathleen McGuire

Local Arrangements Committee

Kristi Lewton
 Stephanie Meredith

2019-2020 AAPA Executive Committee

Anne L. Grauer

President

Leslie C. Aiello

Past President

Steven R. Leigh

Vice President and Program Chair

Rachel Caspari

Treasurer

Graciela Cabana

Secretary

Trudy Turner

Editor, *American Journal of Physical Anthropology*

Lyle W. Konigsberg

Editor, *Yearbook of Physical Anthropology*

Nathaniel Dominy

Career Development

Christina Torres-Rouff

Student Affairs

Kristi Lewton

Membership

Robin Nelson

History and Honors

MESSAGE FROM THE VP & PROGRAM CHAIR

2020 Abstract Issue

This volume consists of accepted abstracts submitted for presentation at the 89th Annual Meeting of the American Association of Physical Anthropologists in Los Angeles, California. A total of 1246 abstracts were submitted by the October 16, 2019 deadline. Each abstract was subjected to peer-review by two members of the program committee, with reviews completed by December 1, 2019. The committee recommended rejection for 21 abstracts (1.7%), and three abstracts had been withdrawn by January 22, 2020. Authors of accepted abstracts were notified on December 7.

The 2020 AAPA abstract issue includes 1222 peer-reviewed scientific papers, which will be presented in either podium or poster sessions at the annual meeting in Los Angeles, California. Once again, our program is truly international, with scientists from all over the world including Africa, Asia, Australia, Europe, Latin America, and the Middle East. We are pleased to be joined in Los Angeles by our partner organizations, the Paleopathology Association (PPA), the Human Biology Association (HBA), the American Association for Anthropological Genetics (AAAG), and the Dental Anthropology Association (DAA) and the Paleoanthropology Society (PAS). Abstracts are presented alphabetically by the last name of the first author.

The abstracts illustrate the remarkable capabilities of our discipline, covering a broad range of research topics, with global reach and spanning incredible time depth. A total of 24 invited symposia (6 podium sessions and 18 poster sessions) included 314 abstracts. Contributed abstract submissions totaled 909. Broken down by subfield, these include Bioarchaeology (224), Primatology (197), Paleoanthropology (127), Human Biology (108), Functional Anatomy and Tissue Biology (93), Genetics and Genomics (82), Forensics (61) and Education in Biological Anthropology (16).

Acknowledgements and Appreciation

My sincere thanks to everyone who helped organize the 2020 meetings, including review of abstracts. We are immensely grateful to the 49 remarkable and dedicated members of our Program Committee, who conducted and completed reviews thoughtfully, thoroughly, and expeditiously. Thanks are due to our extraordinary business partners, Lori Strong and her team (from Burk & Associates), as well as Ed Hagen (our webmaster, app developer, and member of the Los Angeles Advance Team). We also thank the Los Angeles Advance Team. Our program assistant, Kathleen McGuire, has been a tremendous help, as have the Officers and other members of the Executive Committee. Special thanks to Leslie Aiello and Anne Grauer for aiding production of our annual meetings in many ways. Finally, we extend our most sincere thanks to the Local Arrangements Committee, Drs. Kristi Lewton and Stephanie Meredith.

Steve Leigh
AAPA Vice President and Program Chair

ABSTRACTS

Post-conceptive mating in wild woolly monkeys, a Neotropical primate with no evidence of infanticide

LAURA ABONDANO¹, TONI E. ZIEGLER² and ANTHONY DI FIORE¹

¹Department of Anthropology, University of Texas at Austin, ²Wisconsin National Primate Research Center, University of Wisconsin-Madison

Female fertility varies according to reproductive hormone concentrations, but females may be sexually receptive during different reproductive stages. Among many primate species, females have been observed engaging in post-conceptive copulations, which are sometimes discussed as a strategy to confuse paternity and reduce the risk of infanticide. Here, we describe post-conceptive mating behaviors in a population of wild woolly monkeys (*Lagothrix lagotricha poeppigii*) at the Tiputini Biodiversity Station in Amazonian Ecuador. Woolly monkeys live in multimale-multifemale social groups that are characterized by a promiscuous mating system with no clear dominance hierarchies among males. Genetic evidence suggests that paternity skew may be high; nonetheless, mating skew is minimal, and all males display affiliative behavior towards young infants. We investigated the temporal relationship between copulations and fecal progesterone (PdG) and estrogen (E1G) metabolites from receptive females in 2017 who gave birth to offspring in 2018 ($n = 4$). Estimated conceptions were confirmed with endocrine profiles that showed a significant increase in PdG and E1G ($W = 0$, $p < 0.05$) after conception. All females were seen copulating both before and after they conceived, with higher rates of copulations post conception ($W = 1$, $p < 0.05$). The last mating event recorded for these females averaged 35 ± 22 days after conception. Our results indicate that post-conceptive mating is not restricted to primate species with high levels of infanticide and, in woolly monkeys, might be used by females to confuse paternity among different males who may provide certain social benefits to a female and her offspring.

Funded by NSF BCS-1540403, NSF BCS-1638822, the L.S.B. Leakey Foundation, and the University of Texas at Austin.

Exploring the difference in variation in development and eruption of second and third molars in adolescence

ARIELA MARIE A. ADAME, HEATHER J. NESBITT, PHARA WHITE and LAURA E. CIRILLO
Anthropology, University of Nevada, Reno

Despite being the most highly documented teeth because of the age of development and frequent radiographic documentation, third molars (M3) have been known to complicate the understanding of both dental formation and eruption due to increased variation. Previous research has

focused on a large range of variation in the timing of initial mineralization, variation in root length, and inconsistent methods that fail to account for unique morphology as the explanation of poor dental age estimation accuracy and precision (Foti et al. 2003, Olze et al. 2004, Liversidge 2008).

To reopen the discussion into the complication of the third molar, 388 radiographs from the Craniofacial Research Instrumentation Laboratory at the AA Dugoni School of Dentistry were examined for development and eruption of the mandibular M2 and M3 of individuals between 8 and 18 years old. Development was scored using Moorrees et al. (1963) tooth development stages, and eruption was scored using the modified Bengston stages described in AlQahtani (2009). M2 had a higher Pearson's correlation coefficient for development and eruption stage (.8 and .74, respectively) compared to M3 stages (.71 and .64). While eruption timing was excessively varied, the range in age of timing for developmental stages only increased by an average of around one year in the M3 sample compared to the M2 sample. This study suggests that M3 development is not too highly variable to pursue for further research and should be reconsidered in development studies.

The Continuing Deciduous Dilemma – Investigating Early Infant Stress and Maternal Health in Neolithic Northern Vietnam

ALISHA B. ADAMS¹, SIÂN E. HALCROW¹, HIEP HOANG TRINH², NGUYEN THI MAI HUONG², TRAN THI MINH² and MARC F. OXENHAM³

¹Biological Anthropology Research Group, Department of Anatomy, University of Otago, ²Department of Archaeology, Vietnamese Institute of Archaeology, ³School of Archaeology and Anthropology, College of Arts and Social Sciences, Australian National University

Stress in early development has not been studied in detail, especially within prehistoric contexts, despite it being a sensitive indicator of overall population health. The growth of deciduous dentition covers fetal and early infant development, but there have been very few studies which have examined defects during this period. However, with the use of topographic profiling of enamel, a microscopic method of measuring changes in enamel depth to identify linear enamel hypoplasia (LEH) on human deciduous dentition, significant changes in enamel depth have been able to be quantified, allowing us to examine gestational and early infant stress, and extrapolate maternal health.

This paper presents the deciduous LEH profiles of 21 individuals (70 deciduous maxillary incisors/canines) from the site of Man Bac in Neolithic Northern Vietnam. 100% (21/21) of individuals have deciduous LEH occurring both before and after birth. We explore if there is a relationship

between age at death and deciduous LEH frequency and how this relates to maternal and population health during the Neolithic agricultural transition, while contending with osteological paradox. We also illustrate how this research can contribute to our understanding of the deciduous tooth mineralization process by examining timing and presentation of deciduous LEH.

University of Otago Doctoral Scholarship, Social Sciences and Humanities Research Council of Canada Doctoral Award

Snake-species discrimination by wild Rylands' bald-faced saki monkeys (*Pithecia rylandsi*)

DARA B. ADAMS^{1,2}, MELISSA C. PAINTER³ and THOMAS WILSON⁴

¹Anthropology, The Ohio State University, ²Anthropology, Humboldt State University, ³Psychology, University of Michigan, ⁴Anthropology, Wake Technical Community College

Given the high diversity of tropical snake species, the ability to detect and recognize dangerous from non-dangerous snakes is likely important to primate survival. Here, we conducted experiments ($n = 32$) on bald-faced saki monkeys (*Pithecia rylandsi*) in the Peruvian Amazon to assess their ability to recognize non-venomous, venomous, and predatory snakes. We presented sakis with realistic snake models including an Amazon tree boa (*Corallus hortulanus*), coral snake (*Micrurus lemniscatus*), and boa constrictor (*Boa constrictor*). Sakis detected coral snake and boa constrictor models more frequently than tree boas (Fisher's exact test, $p < 0.021$), but detection latency did not differ based on model type ($F_{1,2.467} = 1.240$, $p = 0.362$). However, once detected, snake type significantly influenced latency to move ($F_{1,6} = 16.979$, $p = 0.006$). Among snakes, boa constrictors elicited a faster reaction (mean latency \pm SE: 8.5 ± 2.9 s) than coral snakes (57.6 ± 20.3 s) and tree boas (57.0 ± 18.0 s). Snake type also significantly influenced the number of calls produced and calling duration ($F_{2,4.492} = 120.440$, $p < 0.001$), with boa constrictors eliciting significantly more alarm calls (64.0 ± 21.9) for longer durations (832.9 ± 177.6 s) compared to coral snakes (10.1 ± 7.6 calls, 17.4 ± 11.0 s). Sakis almost never alarm called to Amazon tree boas, with only one brief (4 s) alarm call produced across trials. Comparisons of snake models revealed distinct patterns of response, which suggests that sakis discriminate among snake species according to level of danger.

This research was supported by National Science Foundation (BCS-1341174), Animal Behavior Society, The Society for Integrative and Comparative Biology, Tinker Foundation, and The Ohio State University (Columbus and Mansfield)

ABSTRACTS

Biological diversity and social organization at Early Bronze Age Karataş-Semayük

DONOVAN M. ADAMS¹, KELSIE A. GOODHART¹, ALI METIN BÜYÜKKARAKAYA² and MARIN A. PILLOUD¹

¹Anthropology, University of Nevada, Reno,

²Anthropology, Hacettepe University

The Early Bronze Age (EBA) in Anatolia is marked by significant changes in social, political, and economic structures, as well as growth in trading networks, and the development of new technological styles. Bioarchaeological investigations of EBA Anatolia are limited, precluding a holistic understanding of early urbanization processes. The present study utilizes dental metric and morphological data collected on the permanent dentition of Karataş-Semayük, with comparative data collected on samples from çine-Tepecik and Laodikeia (southwestern Turkey) and gathered from the literature on Cypriot, Greek, Anatolian, and Levantine populations to assess the effect of biological (and, by proxy, cultural) diversity on community identity formation and biological relationships.

Shannon and Simpson's Diversity indices exhibit biological diversity comparable to that present at Neolithic çatalhöyük and higher than those of other EBA sites. Mean Measure of Divergence analyses exhibit Karataş-Semayük clustering with Greek and then Cypriot sites. This close relationship with the Aegean bolsters the argument of an interregional cultural sphere that encompassed Greece, southeastern Europe, and western Anatolia during the EBA. Possible migration, and subsequent gene flow, between Cyprus and southwestern Anatolia is potentially supported by preliminary results. Karataş-Semayük likely consisted of a predominantly local population with uniform mortuary and architectural practices. There may have been limited migration of non-local individuals, resulting in the greater extent of biological diversity identified compared to other EBA sites. This migration, increasing population density throughout occupation, potential seasonal transhumance, and participation on trade routes may have stimulated the emerging social stratification evident at Karataş-Semayük.

Research supported by NSF BCS#1848473, UNR GSA Research Grant, UNR International Activities Grant, and Russell J. and Dorothy S. Bilinski Fellowship

Zygomaxillary shape variation in Southern African papionin monkeys

JUSTIN W. ADAMS^{1,2}, DANIEL E. EHRLICH³ and MICHELLE SINGLETON^{3,4}

¹Anatomy and Developmental Biology, Monash University, ²Palaeo-Research Institute, University of Johannesburg, ³College of Graduate Studies, Midwestern University, ⁴Anatomy, Chicago College of Osteopathic Medicine

Extant African papionin crania exhibit facial fossae ranging from deeply excavated suborbital fossae to shallow lateral rostral fossae. In contrast, facial fossae are weak or absent in many fossil papionins. Prior quantitative analysis of fossa variation has been hampered by zygomaxillary surface (ZMS) complexity and limited homologous ZMS landmarks. This study employs surface semilandmark (SLM) analysis to investigate ZMS shape variation in fossil and extant papionins from southern African to improve understanding of fossa variation and evolution of papionin facial form. The study sample comprised 87 crania representing 8 fossil and extant species. Semilandmarks ($p=450$) were used to capture ZMS shape bilaterally. Following Procrustes superimposition with sliding, ZMS variation was explored using PCA and CVA of size-adjusted SLM coordinates. PC1 (54% variance) separates extant and some fossil *Papio* from most *Parapapio* and *Procercocebus*. Positive PC1 scores reflect *Papio*'s coronally oriented malar surfaces, sagittally oriented maxillary ridges, and excavated lateral rostrum, in contrast with receding malars, convergent maxillary ridges, and convex maxillary surfaces in *Parapapio* and *Procercocebus*. Negative PC2 (11%) scores in some *P. izodi* and *P. angusticeps* reflect reduced maxillary excavation, more receding malars, and increased dorsal rostrum breadth compared to extant *Papio*. CV1 (43%) also separates extant *Papio* from fossil species with shape trends similar to PC1, while CV2 (26%) contrasts a more baboon-like ZMS in *P. izodi*, (positive) with a slightly excavated ZMS in *Procercocebus* and *Parapapio broomi* (negative). These results support the diagnostic value of ZMS shape and phenetic distinctiveness of *P. izodi* and *Pp. broomi*.

This research was supported by the Australian Research Council (DP170100056), The Leakey Foundation, and by Midwestern University Department of Anatomy, ORSP, and Core Facility.

Geometric morphometric analysis of the adult modern human pubic symphysis and implications for fossil reconstruction

MAYOWA T. ADEGBOYEGA¹ and TIMOTHY D. WEAVER^{1,2}

¹Anthropology Department, University of California, Davis, ²Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

The pubic symphysis is a secondary cartilaginous joint – a fibrocartilage and hyaline joint usually at the midline – that connects the left and right pubic bones to complete the anterior margin of the pelvic aperture. It is also responsible for absorbing shock during the transfer of the load from the upright trunk to the hips during locomotion and other weight bearing activities. Because cartilage is not preserved in fossil remains, our understanding of the morphology of the interpubic space is reliant on studies of modern

humans. Several attempts have been made to investigate the width of the pubic symphysis in modern humans, but many of these studies have produced conflicting results on the relationship between the morphology of the pubic symphysis with factors such as age, sex, and body mass index (BMI).

This study focuses on investigating the morphology of the interpubic space between the two pubic bones in adult modern humans from 106 patients – ranging from the ages of 20 to 96 – who have undergone CT imaging in the University of California Health system by employing geometric morphometrics and multivariate linear regression analyses. Our goals are to provide clarity on the correlations between symphyseal thickness with sex, age, BMI, and history of childbirth, and to use that information to improve on the accuracy of fossil pelvic reconstructions which will provide more realistic reconstructions of the pelvic dimensions of our hominin ancestors.

How is identity reflected in the human face?

KAMAR AFRA¹, BRIDGET FB. ALGEE-HEWITT² and MICHELLE D. HAMILTON³

¹Anthropology, University of Tennessee, ²Center for Comparative Studies in Race and Ethnicity, Stanford University, ³Anthropology, Texas State University

Genotype-phenotype studies increasingly link SNPs to the dimensions of the face for presumed homogeneous populations. To fully appreciate the significance of these findings, it is important to investigate how these results differ between hard and soft tissues and among individuals within populations. In prior work, we investigated the connection between SNPs previously identified as informative of soft tissue expression and measurements of the craniofacial skeleton. Using matched genetic and skeletal information on 17 individuals from a single U.S. population (White) and of presumed common continental ancestry (European), we obtained significant Spearman correlations for 11 SNPs. In the present study, we ask if continental ancestry variation within a labeled population should be of concern when interpreting these genotype-phenotype correlations. We evaluate the homogeneity in ancestry composition for the same set of individuals by integrating our samples within a diverse dataset of 2242 modern Americans and applying an unsupervised model-based clustering routine to 13 craniometrics. Under a trihybrid admixture model, we generated a mean European ancestry estimate of 69.65% ($\pm SD = 18\%$) for the full White sample. We inferred higher quantities of European ancestry, 88.50%-93%, for our subset of 17 individuals. These elevated estimates are of interest with respect to the distribution of population-informative SNPs: we found, for example, that one of our

ABSTRACTS

sampled individuals displayed SNPs commonly associated with Latin-American populations. These results underscore the complex interrelationship between environment and genetics, and the need for a continued research into connections between ancestry, social identity, and morphogenetic expression.

Balancing the Scales of Bioarchaeology: Meaningful Studies of Health and Function in Past Populations, Communities and Individuals

SABRINA C. AGARWAL

Department of Anthropology, University of California Berkeley

While bioarchaeological practice begins with the study of one skeletal element and one individual skeleton at a time, the discipline of rigorous bioarchaeological interpretation was built on population level study. But what is the “population” in bioarchaeology, and are “past populations” a truly biologically and/or socially meaningful focal unit? Studies of health and function in past populations have long been criticized for small sample sizes and the inherent bias of selective mortality/differential frailty in samples of archaeological skeletons. At the same time, contemporary bioarchaeologists have also shifted focus to include more humanistic perspectives, focusing on individual (osteobiographical) data or “communities” of practice or identity as the unit of focus in data interpretation. This paper will present age- and sex-related patterns of long bone aging and functional geometry in a Late Medieval sample from Villamagna, Lazio, Italy (1300 AD – 1450 AD), along with comparative (pre)historic data. While temporal data on bone aging and functional morphology across human populations has been shown to pattern in predictable ways (for example, human bone morphology indicates less rigorous activity over time, or bone quantity diminishes with aging), this only the case when other relevant communities such gender, status, or labor groups are often subsumed or not included in larger “population” data sets. Multiscalar analyses (that include individual data, community subgroups, as well as population data) demonstrate the more nuanced aspects of function, health and lived experiences in the past, and provide a more evocative representation of human diversity and adaptation for public engagement.

A novel method for comparing morphometric and biomechanical data of cancellous bone structure in human hand bones to analyse bone functional adaptation

JESSYE A. AGGLETON¹ and KATHARINE ROBSON BROWN^{1,2}

¹Department of Anthropology & Archaeology, University of Bristol, ²Department of Mechanical Engineering, University of Bristol

Cancellous bone structure adapts to loading forces. It has previously been proposed that past manual behavioural activities can be derived from analysis of the cancellous bone structure. We tested the methodological hypothesis that it is possible to analyse the cancellous structure of select human hand bones morphometrically and biomechanically to infer functional bone adaptation in relation to past loading behaviours. A novel comprehensive method was developed to compare the values and spatial distributions of morphometric parameters (bone volume density, degree of anisotropy, and trabecular thickness), with the predicted magnitudes and spatial distributions of stress and strain from different manual activity loading scenarios (i.e. hand grips) resulting from validated Finite Element Analysis (FEA). The method was tested on a pilot dataset: micro-CT scans from a post-medieval archaeological human assemblage with known life histories from St Bride’s Church, London. The morphometric analysis method found significant differences in the morphometric parameters analysed between individuals with different levels of manual force activity during life, as well as between age groups. The validated FEAs found qualitative differences of high stress and strain locations and magnitudes between manual activity loading scenarios. A comparison of these results suggested that cancellous bone functional adaptation appeared to be more localised in the proximal phalanx distal epiphysis depending on manual activity, compared to the proximal epiphysis. Overall, this novel comprehensive method was able to spatially compare morphometric differences in cancellous bone structure to modelled biomechanical data, and can be used to infer bone functional adaptation.

Morphological integration and evolutionary potential of the shoulder girdle in humans and non-human primates

ELIZABETH R. AGOSTO

Anatomy, Cell Biology & Physiology, Indiana University School of Medicine

The morphology of the primate shoulder girdle is immensely variable and reflects the functional demands of the upper limb. Consequently, the observed morphological variation among extant primate taxa is hypothesized to be the result of selection for different functional demands.

Evolutionary analyses of the primate shoulder girdle often assess this anatomical region, and its traits, individually. Thus, implicitly assuming the independent evolution of the shoulder girdle. However, the shoulder girdle shares both functional and developmental relationships with the basicranium and pelvic girdle that have previously been shown to influence its evolution. Whether these relationships are similar across primate taxa, and how they may affect morphological variation among primates is unknown. This study evaluates the strength of the covariance and evolutionary potential across four anatomical regions: shoulder girdle, basicranium, pelvic girdle, and humerus. Measures of morphological integration and evolutionary flexibility are assessed among four primate genera: *Homo*, *Alouatta*, *Colobus*, and *Hylobates*. Results demonstrate that patterns of integration and evolutionary flexibility among anatomical regions differ across primate genera. Overall, humans have the highest evolutionary potential, which may contribute to their divergent morphology. These patterns reveal a nuanced relationship among primate taxa that do not strictly correspond to locomotor function. Therefore, evolutionary hypotheses of primate shoulder girdle evolution that evaluate functional demands may not account for the effect of the relationships between anatomical regions. Based on these results, I argue the observable morphological differences in the primate shoulder girdle may be a manifestation of differences in trait covariances among anatomical regions.

This research is supported by a National Science Foundation Doctoral Dissertation Improvement Grant (NSF BCS-1825995).

A staple food resource, *Leucomphalos callicarpus*, may temper fluctuating fruit availability for Bornean orangutans at Tuanan, Indonesia

WILLIAM D. AGUADO¹, TIMOTHY D. BRANSFORD², ASTRI ZULFA³ and ERIN R. VOGEL¹

¹Department of Anthropology, Rutgers University, ²Department of Anthropology, Northern Illinois University, ³Department of Biology, National University, Indonesia

Primates often face seasonal shortages of their preferred foods. When preferred foods are unavailable, primates must forage for alternative resources that enable them to meet their nutritional and energetic requirements. Understanding how primates persist through these periods of heightened risk of malnourishment has important implications for conservation and habitat management. We asked if wild Bornean orangutans (*Pongo pygmaeus wurmbii*) focus on specific food species to meet nutritional requirements during lean fruit periods. We used data derived from the 16-year dataset of forest phenology and orangutan diet at Tuanan in Central Kalimantan, Indonesia. We analyzed data from monthly

ABSTRACTS

phenology surveys, over 42,000 observation hours on orangutans from over 4,000 full day nest-to-nest follows, and calculated the nutritional composition of the most consumed orangutan plant foods. We found that the leaves, seeds, and flowers of a perennially fruiting liana, *Leucomphalos callicarpus* (Fabaceae), locally called "kamunda", were consumed year-round, and were the target of a disproportionate amount of feeding time and caloric intake when the percentage of fruiting trees—preferred orangutan foods—declined. Kamunda may be considered a "staple food resource" because of its high spatial and temporal availability, consistent use by orangutans, and high macronutrient content. We suggest that orangutans at Tuanan consume kamunda to cope with episodes of fruit scarcity and that this species, which is not found in abundance at other Bornean orangutan sites, may contribute to the high orangutan density at Tuanan.

Funding was provided by the USAID, the National Science Foundation, The Leakey Foundation, Rutgers University, and the Center for Human Evolutionary Studies, Rutgers University.

A Comparative Study of the Primate External Ear using Three-dimensional Geometric Morphometrics

ASHLEY AHONEN¹ and ROLF QUAM^{1,2,3}

¹Anthropology, Binghamton University, ²Centro UCM-ISCIII, de Evolución y Comportamiento Humanos, ³Division of Anthropology, American Museum of Natural History

The cartilaginous external ear plays a fundamental role in the physiology of audition and understanding the evolution of primate hearing can shed light on primate sensory ecology. Variation in primate external ear morphology has also been suggested to follow taxonomic lines. Nevertheless, variation of external ear morphology in primates has received little attention to date from anthropologists. In this study, three-dimensional geometric morphometrics, complemented by linear metrics, was used to analyze interspecific variation in the shape of the external ear (pinna, helix, and concha) of sixteen primate species relying on physical ear molds and 3D models derived from CT scan data. The results indicate that while the helix shows the greatest variability at the attachment sites to the head, there is not a clear taxonomic pattern to the overall shape variation of this structure. Shape variation of the concha more closely follows the major taxonomic division with the primate order. The concha of platyrrhines shows a teardrop shape, with considerable narrowing in the inferior portion. In catarrhines, the concha becomes more rounded inferiorly while the hominid concha has an irregular shape, particularly in the anterior structures. Comparing the size of the concha in relation to the pinna did not show any consistent

pattern across the primate order, suggesting that these two structures vary independently. This study demonstrates the value of geometric morphometrics as a tool which may aid further hearing studies in primatology and biological anthropology.

A potential trade-off in robbing and bartering behavior in long-tailed macaques in Uluwatu temple, Bali, Indonesia

NALINA AIEMPICHIKIJKARN¹, BRENDA MCCOWAN¹, I. NENGAH WANDIA² and JEAN-BAPTISTE LECA³

¹Animal Behavior Graduate Group, University of California, Davis, ²Primate Research Center, Universitas Udayana, Indonesia, ³Department of Psychology, University of Lethbridge, Canada

Free-ranging long-tailed macaques (*Macaca fascicularis*) in Uluwatu temple rob valuable objects as tokens to barter for food. These interactions are reminiscent of the token exchange paradigm whereby animals learn the referential meaning of inedible objects. The objective of our study was to determine the best variables to predict robbing and bartering behavior (hereafter RB). We predicted that low-ranking and peripheral monkeys would exhibit more RB to compensate for their more limited food access (food constraint hypothesis). We conducted 110 observation blocks (totaling 55 hours) using all-occurrence sampling and recorded 114 robbing attempts. We also sampled 17 out of 27 adult individuals using a case-control method to conduct focal observations in order to calculate the attribute of ranks, group position, proximity centrality, and grooming centrality. Our analytical model indicated the frequency of robbing attempts was marginally higher among high-ranking animals ($p = 0.054$), which consisted mostly of males, and proximity betweenness centrality (within 3 m) showed a significant negative relationship with robbing attempts ($p = 0.044$). Our results partially supported the food constraint hypothesis in that there may be a trade-off between seeking opportunity to perform RB and being in the central position of socio-spatial network. RB may impose time constraints on some monkeys, as high-ranking individuals who engage in RB more frequently have less time to devote social opportunities and be in proximity to conspecifics (where proximity may not drive grooming opportunities), whereas low-ranking individuals may not be able to afford this constraint (where proximity may drive grooming opportunities).

Local Practice Between Empires: Physical Activity and Osseous Response in Colonial Mexico

EDGAR ALARCÓN TINAJERO¹ and JORGE A. GÓMEZ-VALDÉS²

¹Anthropology, University of Georgia, ²Laboratorio de Bioarqueología, Posgrado en Antropología Física, Escuela Nacional de Antropología e Historia, INAH

Bone cells remodel and redistribute mass over the course of years in response to strain from repetitive mechanical activity. Over time, bone remodeling produces cross-sectional properties in diaphyses that vary according to activity patterns. Tasks associated with non-mechanized agriculture strains bone in patterned ways leaving a record in skeletal remains. Interpretations of agricultural tasks in San Gregorio Atlapulco, a Colonial Mexican town, are offered based on calculated cross-sectional properties of a sample of adults (ages 19-57, n=44) from cemetery burials (N=411). Body mass was estimated from femoral head breadth and terminal adult stature from maximum femur lengths using population-appropriate regression formulas. Cross-sectional properties were calculated from periosteal measurements of key points in the humeri and femora. In this sample of adults, Cross-sectional Mobility Indices show no statistically significant difference among sexes. Statistically significant differences in humeral bilateral asymmetry is observed among males only. Sex-based division of labor is inferred from significant differences in overall cross-sectional properties which are potentially affected by statistically significant sexual dimorphism in estimated body mass and stature. Historical documents and the archaeological record attest to deep transformations of Mesoamerican communities following Spanish contact including demographic loss, settlement coalescence, changes in land use, land tenure, and agriculture. While capitalizing on historical sources this study highlights the strategies of one community – agriculture at the exclusion of more mobile subsistence practices and individual task specialization. This study also highlights the gendered labor dynamics in an intensive agricultural context.

Supported by UGA: Graduate School, Summer Research Travel Grant and Innovative and Interdisciplinary Research Grant; CAIS, Norman Herz Award for Student Research; Department of Anthropology, Janis Faith Steingruber Travel Award.

Evolutionary changes in neurocranial structure do not correlate with cortical reorganization in humans

JOSÉ LUIS ALATORRE WARREN¹, MARCIA PONCE DE LEÓN¹, WILLIAM D. HOPKINS^{2,3} and CHRISTOPH P.E. ZOLLIKOFER¹

¹Department of Anthropology, University of Zurich, ²Neuroscience Institute, Georgia State University,

ABSTRACTS

³Division of Developmental and Cognitive Neuroscience, Yerkes National Primate Research Center

The human brain is approximately three times as large as that of our closest living relatives, the great apes, and exhibits autapomorphic sulcal patterns in several regions. Fossil neurocrania are regularly examined—both qualitatively and quantitatively—to document when and how these differences emerged during hominin evolution. Using MRI and same-individual CT/MRI data of 41 humans and 24 chimpanzees, we quantify the topographical relationships between brain sulci and internal and external neurocranial features, as well as the associated patterns of variation in and covariation between brain and neurocranial features. Our results show a posterior shift of the pre- and postcentral gyri in human relative to chimpanzee brains, reflecting reorganization of the frontal opercular region (Broca's area in our species). Likewise, human neurocrania differ from those of chimpanzees in having relatively larger parietal bones and a more anterior position of the cerebellar fossa. Modularity/integration analysis suggests that changes in neurocranial and brain morphologies occurred largely independently during human evolution.

Funded by Swiss NSF grant #31003A_135470 to CPEZ.

Skeletal morphological adaptation of the modern human ankle and forefoot: a study of plasticity in response to cultural pressures

MALORIE E. ALBEE

Department of Anthropology, The Ohio State University

Although prior anthropological research has established that our skeletal biology is influenced by our cultural background, the interplay between growth and development and cultural practices is not well understood. This study aims to contribute to this topic by testing the relative influence of biodemographic variables and cultural pressures on the adult morphology of the skeletal foot. To test this hypothesis, three aspects of skeletal tarsals and metatarsals, robusticity, osteoarthritis (OA), and enthesal changes (EC), were contrasted with biodemographic and habitual activity patterns for recent modern humans. The sample consists of 32 adult white males born on or after 1950 from the William M. Bass Donated Skeletal Collection at the University of Tennessee-Knoxville Forensic Anthropology Center. The effects of age, stature, body mass, and occupation on the pedal skeleton were determined via linear regression. The results indicate that there is a statistically significant positive correlation between age and metatarsal robusticity, but only for the second ($r_s=0.5318$; $p=0.0017$) and third metatarsals ($r_s=0.4892$; $p=0.0045$). There is also a significant positive correlation ($r_s=0.4373$; $p=0.0123$) between age

and EC of the insertion point of *Peroneus brevis m*. The relationships between stature and second metatarsal robusticity, stature and first metatarsal EC, age and third metatarsal OA, and occupation and first metatarsal robusticity approach significance ($p<0.1$) and suggest avenues for further research given a larger sample. No significant correlations including the talus or calcaneus were found. These findings indicate that the influence of environmental pressures on the skeletal foot is concentrated in greatest magnitude on the metatarsals.

The rainforest vervet: Locomotor behavior, habitat preference, and pelage variation in *Cercopithecus dryas*

DANIEL ALEMPIJEVIC¹, EPHREM M. BOLIABO³, TERESE B. HART³, JOHN A. HART³ and KATE M. DETWILER^{1,2}

¹Biological Sciences, Florida Atlantic University, ²Anthropology, Florida Atlantic University, ³TL2 Project, Frankfurt Zoological Society

Cercopithecus dryas has been known to science for 87 years, yet few studies have investigated their ecology and taxonomy. Pelage variation among the few specimens available has led to taxonomic confusion. New genomic evidence confirms *C. dryas* is a sister lineage to *Chlorocebus*. As the only rainforest representative of this savanna-woodland clade, field studies of *C. dryas* are essential to understand its unique ecology, document pelage patterns, and determine affinities to *Chlorocebus*. Due to the difficulty of observing *C. dryas*, we developed a multi-stratum (0-30 m) camera trap technique to determine *C. dryas*' locomotor behavior, habitat preference, and pelage variation. Using local ecological knowledge to locate *C. dryas*, we placed camera trap "columns" at Camp Bartho (CB) in the Lomami National Park and in the Bafundo Village Forest (BVF) in the park's buffer zone. We found no significant difference in *C. dryas* detection height across surveys ($p=0.996$) with 96.97% of detections occurring in the understory-mid canopy range (2-10 m). We found a highly significant association between *C. dryas* and anthropogenic clearings ($c^2=10.322$, $p=0.0013$). Anthropogenic clearings dominated the BVF site where the *C. dryas* detection frequency was greatest (BVF = 2.03; CB = 0.72). We confirmed an ontogenetic shift in pelage color, and discovered mature males exhibit a remarkably vibrant anogenital region when compared to the "red, white and blue" display of *Chlorocebus*. These results suggest *C. dryas* shares a tolerance to disturbance with *Chlorocebus* but is adapted to their rainforest habitat with arboreal tendencies and richer coloration.

Funding for this study was generously provided by the Margot Marsh Biodiversity Foundation, Muhammed Bin Zayed Species Conservation Fund, Primate Conservation Inc., and the International Primatology Society.

Dietary isotopic analysis as an investigative tool for identifying unknown human remains in New York City

HELEN S. ALESBURY¹, RHONDA QUINN², LIGIA CEJA¹, ANGELA SOLER³, ALEXANDR TRIFONOV² and LINDA GODFREY⁴

¹Forensic Operations, New York City Office of Chief Medical Examiner, ²Department of Sociology, Anthropology, and Social Work, Seton Hall University, ³Forensic Anthropology, New York City Office of Chief Medical Examiner, ⁴Department of Earth and Planetary Sciences, Rutgers University

Incorporating stable isotopic analyses into forensic biological profiles has been used to help guide investigations of unidentified human remains. Dietary isotopes ($\delta^{13}C$, $\delta^{15}N$) have been employed to indicate geographic regions and dietary trends of unidentified human remains; however, culturally influenced food traditions pose interpretative complications especially in multicultural metropolitan regions such as New York City. This study investigates the utility of and variation in $\delta^{13}C$ and $\delta^{15}N$ values of human bone collagen samples representing 34 forensic cases of unknown identities from the past 30 years in the custody of the New York City Office of Chief Medical Examiner (OCME). NYC residents and the OCME cases have relatively lower $\delta^{13}C$ and $\delta^{15}N$ values than other US residents, indicating protein diets comprised of less animal products and less corn/sugarcane. The OCME cases have significantly higher $\delta^{13}C$ and $\delta^{15}N$ values than NYC residents but show comparable variances. We frame our OCME results within geolocation isotopic data from the same samples acquired from IsoForensics, Inc. and discuss various influences of dietary isotopes including geography, food traditions, health, and socioeconomic status. One identified case is explored with dietary and geolocation isotopic data given the context of the NYC residents and other OCME cases to demonstrate the utility of dietary isotopic data. This research shows the potential for integrative isotopic analyses of unidentified human remains as well as the importance of a holistic anthropological approach to interpretation of forensic casework in multicultural contexts.

Funding provided to RLQ by the National Science Foundation (NSF BCS-1455274).

A computational framework for estimating ancestry and adult age-at-death from shape measures of the pubic symphysis

BRIDGET FB. ALGEE-HEWITT¹ and JIEUN KIM²

¹Center for Comparative Studies in Race and Ethnicity, Stanford University, ²DeBusk College of Osteopathic Medicine, Lincoln Memorial University

Conventional adult age estimation methods rely upon population-specific standards to determine chronological age. While such a targeted approach is said to provide a more accurate approximation of chronological age, it requires the prior

ABSTRACTS

assessment of ancestry. A fully computational shape-based method is proposed here to identify the major population of origin and generate probabilistic estimates of continental ancestry without advance knowledge of sex for 333 pubic symphyses representing Black, Hispanic, and White males and females. Continuous shape measures were obtained by subjecting laser scan-derived coordinate data from the pubic symphysis to three shape algorithms already published for their use in estimating age. These shape measures were subjected to unsupervised model-based clustering to produce proportions of continental ancestry, as well as traditional single ancestry classifications. Analyses produce a three-cluster solution, corresponding to some fraction of African, Indigenous-American, European ancestry, irrespective of sex. Correct classification into a single ancestry is high (76-91%) and inferred ancestry proportions agree with prior genetic and craniometric admixture estimates. Results indicate that shape differences in the pubic symphysis among the three sampled populations are informative of ancestry. It is possible, therefore, to create a two-step pipeline for age-at-death estimation: calculate shape measures and infer ancestry; choose the most appropriate population-specific data to estimate age-at-death from the shape measures of the pubic symphysis using regression models. As morphology may be affected by life history factors that are shared among the sampled individuals representing the same identity group, further work is needed to tease apart ancestry from environmental effects.

This research is supported by National Institute of Justice (2015-DN-BX-K010) and Wenner-Gren Foundation (CONF-772) grants awarded to Algee-Hewitt & Slice and Algee-Hewitt & Kim respectively.

Seasonal workload, reproductive effort, and testosterone levels among Qom men

LOUIS C. ALVARADO¹, PETER T. ELLISON², CAITLIN LEWARCH³ and CLAUDIA R. VALEGGIA⁴

¹Anthropology, University of Pittsburgh, ²Human Evolutionary Biology, Harvard University, ³Molecular and Cellular Biology, Harvard University, ⁴Anthropology, Yale University

Testosterone is integral to men's life history strategies, although separate adaptive mechanisms are proposed for determining testosterone variation: H1) behavioral investment in mating effort versus paternal involvement; H2) energetic regulation of somatic investment toward mating effort; and H3) physiological support of physical activity. Here, we report hormone data from Western Qom men, a rural indigenous population of transitional foragers. The wet season, or Wo'e, for Western Qom is characterized by increased food availability, decreased workload, and a culturally-ascribed time of mateship formation. This contrasts with the dry season, nakabia'ga, with greater work demands and nutritional constraint.

Anthropometric, demographic, and life history data along with saliva samples were collected during Wo'e and nakabia'ga for 47 Qom men, 17-67 years. We examine seasonal variation in reproductive effort, testosterone levels, and workload to parse competing predictions. Morning and evening testosterone were significantly higher, 33% and 40%, respectively, during Wo'e, a period when nutritional constraint and workload is attenuated but mating effort intensified. And although seasonal energy availability was increased generally across the study sample, testosterone elevation was more specific and significantly higher among single/childless men than pair-bonded fathers for morning testosterone, 89% versus 19% increase, but with no statistical difference in evening values. Moreover, testosterone elevation was age-dependent only to the extent that younger ages had more single/childless men; older single/childless men exhibited testosterone seasonality analogous to their younger single/childless counterparts. Among Western Qom men, the overall patterned variation of fluctuating testosterone is most consistent with behavioral partitioning of mating and parenting effort.

Ethnicity, fertility, and tobacco use: a biocultural test of the fetal protection model of female smoking

TIFFANY A. ALVAREZ and EDWARD HAGEN
Anthropology, Washington State University

Currently, cross-country variation in gender equality is thought to be the primary factor producing global tobacco use sex differences, with gender inequality, especially in low-to-middle-income countries, preventing women from obtaining and using tobacco. Our alternative hypothesis draws on the "fetal protection" theory from evolutionary anthropology which emphasizes that reproductively-aged women protect their fetuses and nursing infants via an evolved a network of toxin defenses, characterized by upregulated detoxification of- and/or strong aversions to- teratogenic substances (e.g. tobacco)—individual-level defenses that are furthermore reinforced by culture-level proscriptions aimed at safeguarding fetal/offspring health. Although support for the fetal protection model has been found (Hagen et al. 2016), prior research has used data aggregated at the nation-level and has neither examined individual-level variation nor considered that cultural norms may also influence tobacco use. Using individual-level data from a high fertility, tobacco-growing, ethnically and socioeconomically diverse province in the South Central Andes (Jujuy, Argentina), we explore the relationship various fertility indices and sociocultural tobacco norms have on nulliparous and multiparous women's tobacco use outcomes (N=108), while controlling for demographic features and considering ethnic differences as main effects. Smoker status was determined via salivary

cotinine and cross-validated with questionnaire data. Our analyses reveal ethnic differences in tobacco use attitudes and behaviors and suggest fertility characteristics are important factors in female smoking decisions. Consistent with fetal protection model predictions, these findings suggest smoking vulnerabilities intersect with sex and socio-cultural variables in an additive manner and open the door to future areas of research.

This investigation was supported in part by funds provided for medical and biological research by the State of Washington Initiative Measure No. 171.

The Human *NF1* Locus: A Unique Hominin Genotype with Potential Evolutionary Significance

ANDREA J. ALVESHERE¹ and VINCENT M. RICCARDI²

¹Sociology and Anthropology, Western Illinois University, ²Director, The Neurofibromatosis Institute

The autosomal dominant genetic disorder, Neurofibromatosis Type 1 (NF1), derives from the human *NF1* gene, which influences many of the physical, cognitive, and behavioral traits that distinguish *Homo sapiens* from other fossil and extant primate taxa. The ordinary, non-mosaic NF1 disorder results from a germline pathogenic mutation in the ~300,000 bp *NF1* supergene and is characterized by behavioral elements, benign tumors of the nerve sheath (e.g., neurofibromas), macrocephaly, short stature, heat intolerance, learning disabilities (involving speech, spatial reasoning, executive functioning, and musicality), and resistance to obesity, diabetes, alcoholism, and opiate addiction. The disorder is fully penetrant, but heterozygosity allows for unaffected offspring and the morbid phenotype requires additional changes, such as somatic mutation of the normal allele. It is thus progressive, and the ultimate phenotype is highly variable, moderating the disorder's impact on reproductive success.

New research reveals that both the wild-type human *NF1* allele and resulting neurofibromin protein are unique compared to those of other extant primates, yet the modern human *NF1* coding sequence is identical to those from Neanderthal, Denisovan, and early modern human specimens. DNA sequences that would replicate the chimpanzee (ancestral) neurofibromin amino acid sequence have never been documented among modern humans, aside from a somatic mutation in tumor tissue. No non-human primate has been documented to have the NF1 syndrome, but it is the likely diagnosis for the Cro-Magnon 1 specimen. These data suggest a complete and functionally-significant replacement of the ancestral *NF1* allele prior to the emergence of *Homo sapiens* in the hominin lineage.

ABSTRACTS

Demographic Factors Influencing Glucocorticoid Variation in Wild Hamadryas Baboons

ALEXIS L. AMANN, SHAHRINA CHOWDHURY, JACINTA BEEHNER and LARISSA SWEDDELL

New York Consortium in Evolutionary Primatology, City University of New York

Variation in fecal glucocorticoids (GCs) in primates has been linked to numerous factors, including psychosocial or metabolic 'stressors' as well as individual traits related to life history and reproduction. Any study aiming to assess the effects of acute stressors on GCs must begin with an understanding of the factors shaping baseline GC levels. Here we explore three possible factors underlying such variation in wild hamadryas baboons. Hamadryas are characterized by a unique multi-level social system comprising one-male units (OMUs) that form successively larger social units. Leader males within OMUs have apparent exclusive reproductive access to females, whereas non-leader males do not. Using fecal samples collected in 2014-2018 at Filoha, Ethiopia, we assess how fecal GC concentrations vary across age, female reproductive state, and male reproductive status (leader or non-leader). Fecal hormones were extracted in the field followed by radioimmunoassay at the University of Michigan. Our results suggest that GCs are higher in older individuals for both males (repeated measures ANOVA, $p = 0.008$) and females (a non-significant trend; $p = 0.074$), and that pregnant females have higher values than lactating females ($p = 0.025$). Contrary to expectations, we found no differences between cycling females and females in other reproductive states nor between leader and bachelor (follower and solitary) males ($p = 0.122$). We conclude that two of the main factors underlying GC variation in wild hamadryas baboons are age and female reproductive state, highlighting the need to control for such factors when using GCs as a proxy for environmental challenges.

Early life environments predict gut microbiome composition of adult women in Cebu, Philippines

KATHERINE R. AMATO¹, SAHANA KUTHYAR¹, PRIYANKA PRADHAN², DELIA CARBA³, JUDITH BORJA³, THOMAS W. MCDADE¹ and CHRISTOPHER W. KUZAWA¹

¹Anthropology, Northwestern University, ²Feinberg School of Medicine, Northwestern University, ³Office of Population Studies, University of San Carlos

Early life environments shape future health outcomes, with factors such as nutrition and microbial exposure influencing the development and subsequent phenotypes of metabolism and immune function. However, gaps exist in our understanding of the mechanisms responsible for these patterns. Gut microbes represent one

potential pathway through which early life environments can influence physiology and health in infancy and beyond. Infants are born mostly sterile and acquire microbes from contact with caregivers and the environment during the first three years of life. Many of the microbiome traits obtained during this period may be retained into adulthood, and gut microbes have been shown to affect host metabolism, immune function, and even behavior across the lifecourse. Here, we use a long-term birth cohort, the Cebu Longitudinal Health and Nutrition Survey (CLHNS) in the Philippines, to examine the association between early life environments and the subsequent composition of the gut microbiome. We characterized gut microbiome composition in 89 women and related it to survey data collected for them at birth in 1982-1983. We found significant associations between microbiome composition and proxies for early life nutrition (maternal height: PERMANOVA $F_{1,84} = 1.4$, $p = 0.02$; household assets: PERMANOVA $F_{1,84} = 1.5$, $p = 0.007$) as well as early life microbial exposures (PERMANOVA $F_{1,84} = 4.3$, $p = 0.009$). These findings suggest that early life environments can be embodied via impacts on the gut microbiome and that these impacts can persist until adulthood. Implications for physiology and health must be further explored.

This work was funded by the Weinberg College of Arts and Sciences at Northwestern University. KRA and TM are supported as CIFAR Fellows.

Ostrich eggshell diagenesis experiments and observations: Implications for isotope analyses

STANLEY H. AMBROSE and ANDREW M. ZIPKIN
Anthropology, University of Illinois

Ostrich and other large ratite eggshell (OES) is widely used for environmental reconstruction with carbon, oxygen and nitrogen isotopes, and radiocarbon dating. Strontium isotopes of OES artifacts can be used to reconstruct provenience, human mobility, and interaction networks. OES can provide an isotopic baseline for reconstructing past environments and provenience of artifacts if diagenetic contamination in archaeological shell can be excluded.

OES has two main structural layers with different diagenetic potentials. The palisade (outer) layer, ~1500 μ m thick, is micritic calcite with 1-2% organic matter. It absorbs tissue stain solutions, and large amounts of uranium after burial (Sharp et al. Quaternary Science Reviews 2019). It becomes dark brown to black when heated to >250°C, and oxygen and carbon isotope ratios decrease systematically above 350°C. The mamillary/cone (inner) layer is ~600 μ m thick, comprising translucent columnar calcite crystals, ~200 μ m wide. It does not absorb organic staining solutions, absorbs ~100X less uranium,

and does not shift carbon and oxygen isotope ratios up to 450°C. It remains white/translucent when heated to ~450°C, except for the rounded cone tops, which blacken. Porous micritic calcite that absorbs stains covers the cone layer. This layer and cone tops should be removed before sampling.

Strontium isotope ratios of inner and outer layers of surface-collected modern OES from Kenya and archaeological OES from northern Malawi differ substantially, likely due to absorption of soil Sr in the palisade layer. Separation of the cone layer crystals and decontamination by acid-etching can insure accurate elemental and isotopic analyses of modern and archaeological OES.

Research in Malawi is funded by NSF grant BCS-1725123 to Ambrose and Zipkin, titled: Testing models of ancient forager social and territorial organization with a strontium isoscape

Introducing Hominins and Building Bridges: The Origins Community Art Project

KATHRYN L. ANDERSON^{1,2}, OSCAR SANTOYO³, ANDREW MONTGOMERY¹ and BECCA PEIXOTTO^{1,4}

¹Center for the Exploration of the Human Journey, Perot Museum of Nature and Science, ²School of Art and Humanities, University of Texas at Dallas, ³Community Engagement, Perot Museum of Nature and Science, ⁴Evolutionary Studies Institute, University of the Witwatersrand

The Perot Museum of Nature and Science introduced a community art project in 2019 to complement a temporary exhibition, *Origins: Fossils from the Cradle of Humankind*, which featured original fossils of *Australopithecus sediba* and *Homo naledi*. Drawing on an interest in STEAM-centered educational programming and the museum's mission to make the science of evolution accessible to a general audience, local schools, civic partners, and non-profit organizations were invited to help welcome the fossils to Dallas through an art project. Participants were provided a 3D replica of the skull of one of two hominins visiting from South Africa along with information about each species and their significance to paleoanthropology. Groups were asked to reflect on their own role within the community and our common human origins to create an artistic design on the model. The decorated models were incorporated into a special display outside of the exhibit, bringing a new level of community participation and engagement with human evolution to the museum. The first call for participants resulted in 35 contributed pieces of artwork. Thirty of those included summaries detailing motivations behind the design. These anecdotes point toward common themes and motivations among the artists, including the importance of diversity, an interest in African culture, and reflections on the history of our common human origins. These results demonstrate community interest in both

ABSTRACTS

human origins and participating in the life of the museum and will inform the development and implementation of future community outreach initiatives.

Infant mortality risk associated with decreased male commitment and shorter interbirth intervals among American births

KERMYT G. ANDERSON

Anthropology, University of Oklahoma

Infant mortality (death before first birthday) is predicted to be influenced by male investment (greater investment reducing risk of infant death) and interbirth interval (IBI) (risk of mortality decreasing as duration since previous live birth increases). This study uses 2014-2015 merged natality and mortality files for 3,946,963 U.S. births (second birth or greater). Infant mortality rate is 5 deaths/1000 births. Mean IBI is 50.0 months. Male commitment is measured by maternal marital status: married (63.2% of births), unmarried with paternity acknowledged (26.0%), and unmarried with paternity not acknowledged (i.e., no father on birth certificate) (10.8%). Male commitment is expected to be highest for married women and lowest for unmarried women without paternity acknowledgment. Logistic regression models that control for maternal sociodemographic factors (age, ethnicity, education, income, BMI) and birth factors (caesarian, premature, birthweight, sex) show higher infant mortality for unmarried women both with (OR=1.08, $p<0.001$) and without (OR=1.37, $p<0.001$) paternity acknowledged, relative to married women. IBI has a weak linear relationship with infant mortality (OR=0.998, $p<0.001$), but a stronger nonlinear relationship when divided into thirds; compared with long IBI (>53 months), increased odds of infant death are associated with short IBI (≤ 28 months) (OR=1.28, $p<0.001$) and medium IBI (28 to 53 months) (OR=1.07, $p<0.001$). Interactions between marital status and IBI were nonsignificant. Infant mortality risk is greater when the father does not acknowledge paternity or when IBI is short. These results advance life history theory by supporting predictions regarding parental investment and tradeoffs between current and future reproduction.

An analysis of the postcranial skeleton of the large-bodied colobine specimen L895-1 from Shungura, Omo Valley, Ethiopia

MONYA ANDERSON

Anthropology, Texas A&M University

L895-1 is a partial skeleton of a large-bodied cercopithecoid from Upper Member G of the Shungura Formation putting its age between 2.05-2.07 Ma. It is the most complete colobine skeleton known from the Turkana Basin and despite its discovery

in 1973, has never been described. Based on the large size of the postcranial elements, it was tentatively assigned to *Paracolobus mutiwa*, but the lack of associated craniodental complicates its taxonomic affiliation. Other large-bodied cercopithecoids known from temporally overlapping deposits include *Cercopithecoides kimeui*, *C. williamsi*, *Rhinocolobus turkanensis*, *Theropithecus oswaldi*, *T. brumpti*, and *Soromandrillus quadratirostris*. L895-1 preserves bones of the fore and hindlimb with functionally relevant features useful for eliminating certain taxa.

The limbs show morphologies more consistent with the colobine morphotype such as a weak trochlear flange on the humerus, symmetrical coronoid process on the ulna, medially curved greater trochanter on the femur, and in its middle cuneiform morphology. It is also distinct from the arboreal *R. turkanensis* and lacks the more extreme terrestrial features seen in *C. williamsi*. Of its contemporaries, L895-1 most closely resembles the controversially assigned *P. mutiwa* specimen KNM-WT 16827 with its relatively short/robust long bones and its mix of seemingly more terrestrially adapted features. If L895-1 is indeed the same species as KNM-WT 16827, the two specimens are separated in age so their morphological differences could be explained by temporal variation. Whatever its taxonomic affiliation, L895-1 highlights the diversity of locomotor modes and size in the fossil colobines relative to their modern counterparts.

This research was supported by the University of Oregon and the National Science Foundation (Proposal No. 1650923).

The transcriptome provides a window into SIV tolerance in a wild primate

TANNER J. ANDERSON¹, NOAH D. SIMONS², NELSON TING^{1,3} and KIRSTIN N. STERNER¹

¹Anthropology, University of Oregon, ²Evolutionary Anthropology, Duke University, ³Institute of Ecology and Evolution, University of Oregon

Unlike HIV in humans, simian immunodeficiency virus (SIV) infection in natural nonhuman primate hosts is generally considered nonpathogenic. To understand the relationship between SIV infection and host immune responses at the molecular level, we have generated transcriptomic data from whole blood samples from 29 red colobus representing 12 SIV-infected (2 female and 10 male) and 17 noninfected (6 female and 11 male) individuals. RNA-seq data were generated from libraries prepared from globin-depleted whole blood and sequenced on an Illumina NextSeq 500 with single end 150bp reads. Gene expression was then quantified using the Ugandan red colobus genome as a reference (GCF_002776525.2). We found that SIV infected Ugandan red colobus monkeys show no evidence of immune activation during chronic infection at the transcriptome level, despite maintaining high viral loads. In addition to

this dataset, we used ~138M paired end reads from the same 29 samples to generate blood transcriptomes for each individual. We then used GATK to call SNPs from these data and PLINK 1.9 to infer relatedness. We are currently testing the effect of viral infection on gene expression using linear mixed-effects models to control for relatedness and dominance rank. This expanded analysis will provide a more nuanced understanding of the relationship between infection status, viral load and gene expression in an important wild primate model. Importantly, this research has identified molecular mechanisms that may enable many nonhuman primates to tolerate SIV infection and offers greater insight into the coevolution between nonhuman primates and immunodeficiency viruses more generally.

Funding by NIH grant TW009237 and NSF BCS1540459

Curating, researching and exhibiting human remains from around the world, a British Museum perspective

DANIEL ANTOINE

Egypt and Sudan, The British Museum

The British Museum holds and cares for human remains from around the world. Representing diverse cultures over thousands of years, this important collection is a unique record of the varied ways different societies have conceived of death. Their study also helps advance important research in fields such as archaeology, anthropology, biology, palaeopathology and bioarchaeology. The information and insight gained through the archaeological and scientific analysis of human remains is ever increasing, particularly as scientific methods improve and develop, all of which continues to inform our understanding of past societies and can be shared with museum visitors. Their display and study provides one of the most direct and insightful sources of information on past lives, human biology, different cultural approaches to death, burials practices and belief systems. The British Museum is committed to curating the human remains in its collection with care, respect and dignity, and has developed a policy that outlines the principles governing the respectful and lawful holding, display, study and care of human remains in the Museum's collection. Within this ethical framework, the important role human remains play in our understanding of the past is discussed using recent examples of British Museum Nile valley gallery displays and exhibitions that feature new bioarchaeological research.

Supported by the Institute for Bioarchaeology

ABSTRACTS

An fMRI investigation into the neurocognitive bases of stone tool manufacture

ZARA ANWARZA^{1,2,3}, SHELBY S.J. PUTT^{3,5}, LANA RUCK^{1,3,4} and P. THOMAS SCHOENEMANN^{1,3,4}

¹Cognitive Science Program, Indiana University, ²Department of Philosophy, Indiana University, ³Stone Age Institute, ⁴Department of Anthropology, Indiana University, ⁵Department of Sociology and Anthropology, Illinois State University

Recent investigations into lithic technology have considered whether activation of language networks in the brain during stone tool manufacture supports hypotheses about the possible co-evolution of language and stone tool technology. Our team launched a naturalistic fMRI study in order to investigate the cognitive underpinnings of Oldowan, Acheulean, and Levallois technologies, focusing on their activation of language networks. Our subjects, including expert stone toolmakers and naïve participants with no prior stone tool training, watched naturalistic videos of three Paleolithic technologies being made by an expert toolmaker while being scanned. Subjects were asked to imagine themselves performing the same actions as the toolmaker in the video. We performed event-related GLM analyses on the subjects' fMRI data, focusing on activation during observation and flaking events. Across all technologies, our team found activation in networks involved in language production and comprehension, including BA 44/45/47 (IFG), BA 6 (vPMC and dPMC), BA 7 (SPL), BA 40 (IPL), and BA 22 (PMTG). Flaking events engaged language networks more reliably than observation. Previous neurocognitive work on toolmaking suggested that increased stone tool complexity yields increased activation. While this pattern applied to a comparison between the Oldowan and Acheulean technologies, we found greater activation for the Acheulean than the Levallois. Once subject expertise was factored in, however, we found the expected increases in activation from Oldowan (lowest), through Acheulean (intermediate), to Levallois toolmaking. This study is the first neuroimaging analysis of the Levallois technology, providing insight into the extent to which Levallois comprehension requires expertise.

This research was supported in part by grant 52935 from the Templeton Foundation titled: "What Drives Human Cognitive Evolution?"

Population-genetic and functional investigation of high altitude adaptation in the Himalayan populations

ELENA ARCIERO¹, MARC HABER^{1,2}, THIRSA KRAAIJENBRINK², ASAN³, MICHAŁ SZPAK^{1,10}, PILLE HALLAST^{1,11}, NIKOLAOS PANOUSIS¹, YUAN CHEN¹, SHANE MCCARTHY¹, IRENE GALLEGU ROMERO⁹, HUANMING YANG³, MARK JOBLING⁴,

GEORGE VAN DRIEM⁵, PETER DE KNIJFF², QASIM AYUB^{6,7}, YALI XUE¹ and CHRIS TYLER-SMITH¹

¹Human Genetics, The Wellcome Sanger Institute, Wellcome Genome Campus, Hinxton, United Kingdom, ²MGC Department of Human and Clinical Genetics, Leiden University Medical Centre, Leiden, the Netherlands, ³BGI-Shenzhen, Shenzhen 518083, China, ⁴Department of Genetics, University of Leicester, United Kingdom, ⁵Himalayan Languages Project, Institut für Sprachwissenschaft, University of Bern, Bern, Switzerland, ⁶Monash University Malaysia Genomics Facility, Tropical Medicine and Biology Multidisciplinary Platform, 47500 Bandar Sunway, Selangor Darul Ehsan, Malaysia, ⁷School of Science, Monash University Malaysia, 47500 Bandar Sunway, Selangor Darul Ehsan, Malaysia, ⁸Institute of Cancer and Genomic Sciences, University of Birmingham, Birmingham, B15 2TT, United Kingdom, ⁹Melbourne Integrative Genomics, University of Melbourne, Parkville, VIC, 3013, Australia, ¹⁰EMBL-European Bioinformatics Institute, Wellcome Genome Campus, Hinxton, United Kingdom, ¹¹Institute of Biomedicine and Translational Medicine, University of Tartu, Tartu, Estonia

The Himalayas provide a diversity of environments for humans, some of which have required substantial genetic adaptation. We have used a combination of SNP-chip data, genome sequences and functional studies to explore the demographic history, genetic structure and signatures of adaptation in the Himalayan populations. We previously genotyped ~600,000 genome-wide SNPs in 883 Himalayan individuals from 49 different autochthonous groups from Nepal, Bhutan, North India and the Tibetan Plateau in China, and have now generated whole-genome sequences of 100 individuals from a subset of these populations plus four additional ones. We find that the Himalayan populations share a genetic component derived from a common ancestral population, followed by the development of local fine structure correlating with language and geographical distribution, with variable gene flow from neighbouring populations. High-altitude adaptation seems to have originated in a single ancestral population and spread widely across the Himalayas: We find a major demographic expansion taking place only 3,000-4,000 years ago, coinciding with the archaeological evidence of permanent settlements above 2,500 m. We find signatures of adaptation to high altitude in *EPAS1* and other genes involved in the hypoxic response. We performed *in vitro* functional validation of variants in the *EPAS1* region that have been previously reported to result from introgression of DNA from the Denisovans using cell lines with and without the adaptive haplotype. We find that *EPAS1* expression in normoxia or hypoxia remains constant in cultured cells with the Denisovan introgressed haplotype, unlike cells with the lowland haplotype where it increases in hypoxia.

Our work was funded by Wellcome (grant 098051).

Phylogenetic analysis of extant colobine monkeys using craniodental data

JULIA L. ARENSON

PhD Program in Anthropology, The Graduate Center, CUNY, New York Consortium in Evolutionary Primatology (NYCEP)

The colobines are a widespread and successful radiation represented by two extant groups, the Asian Presbytina and the African Colobina, and a relatively diverse fossil record across Africa and Eurasia. However, traditional views hold that little phylogenetic signal is contained in their craniodental morphology, and few published studies have used morphological data to estimate colobine phylogeny. This study uses craniodental characters and updated methodology to estimate phylogenetic relationships among extant colobines. 270 (127 qualitative, 143 quantitative) characters were coded for males and females separately in 19 colobine species representing all ten colobine genera, plus three outgroups (*Victoriapithecus macinnesi*, *Allenopithecus nigroviridis*, and *Macaca fascicularis*). Size-adjusted quantitative characters were corrected for allometry when highly correlated with size ($r > 0.5$), and otherwise coded using gap-weighted coding. The matrix was analyzed using parsimony in TNT, and recovered a single most parsimonious tree. The Colobina form a monophyletic group with well-supported genus arrangements congruent with molecular analyses, and multiple well-supported molecular clades are recovered among the Presbytina as well. However, Presbytina are recovered as paraphyletic, with the odd-nosed colobine clade diverging first, followed by *Semnopithecus*, then a clade with *Trachypithecus* and *Presbytis* sister to the African colobines. Mapping synapomorphies on the tree demonstrates Asian colobines are generally primitive relative to African colobines, consistent with previous studies of colobine comparative morphology. These results demonstrate a phylogenetic signal in the craniodental morphology of the Colobinae, and future inclusion of fossil taxa may provide better polarity for extant species and allow exploration of their potential evolutionary relationships.

This study was funded by a Doctoral Student Research Grant, The Graduate Center, CUNY; Provost's Office Pre-Dissertation Research Funding, The Graduate Center, CUNY; and NSF GRFP Grant No. 40F79-02 04.

Genomic insights into the human population history of Northwestern Amazonia

LEONARDO ARIAS^{1,2}, GUILLERMO BARRETO², BRIGITTE PAKENDORF³ and MARK STONEKING¹

¹Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, ²Laboratorio de Genética Molecular Humana, Departamento de Biología, Universidad del Valle, Cali, Colombia, ³Dynamique du Langage, UMR5596, CNRS & Université de Lyon, Lyon, France

ABSTRACTS

Northwestern Amazonia (NWA) contains tremendous linguistic and cultural diversity, but has remained underrepresented in most molecular anthropological studies to date. Previous studies have primarily relied on sampling few individuals from widespread populations across the continent and investigating low-resolution markers. These studies found that Amazonians harbor less genetic diversity than Andean populations, as consequence of isolation and drift. In this study, we investigate patterns of genetic diversity in a comprehensive sample covering the extant ethnolinguistic diversity of NWA, consisting of ~300 individuals from 25 Native-American groups, with different subsistence and cultural practices. We generated genome-wide data from the Human Origins SNP array and compared these to published SNP data from the Americas, as well as published complete mtDNA sequences and 2.3 Mb of the male-specific-region of the Y-chromosome from the same populations.

Admixture analyses show a west to east decline of non-Native ancestry among populations: ~17% and ~3% of the ancestry of groups living on the Andean foothills is of European and African origin, respectively, while groups in the east show 100% Native-American ancestry. However, this Native-American ancestry is heterogeneous; we identified several ancestry components not present among other populations in the Americas for which genome-wide data are available. Hunter-gatherers show higher frequencies of these components, while horticulturalists show variable frequencies. Genetic similarities inferred by outgroup-f3-statistics are consistent with uniparental markers results; the latter in addition show sex-specific demographics: female-biased migration among groups and larger female effective population sizes. Our study provides new fine-scale insights into the population history of NWA.

Inter-population differences in enamel secretion rates: a comparison between modern and ancient populations

CHRISTOPHER ARIS¹, PATRICK MAHONEY¹, MACKIE C. O'HARA² and CHRIS DETER¹

¹Human Osteology Laboratory, Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, ²Department of Anthropology, The Ohio State University, Columbus, OH 43210, USA

Human enamel growth occurs as ameloblast cells secrete and mineralize protein matrix. Studies of enamel daily secretion rates (DSRs) have yielded significant insights into the evolution of permanent tooth enamel across hominin species. However, inter-population variation of modern human permanent enamel DSRs has received less attention, particularly for anterior tooth types. This study utilizes dental histological thin sections to examine DSRs calculated for lateral and cuspal enamel regions for permanent molar, canine,

and incisor crowns from five British populations. These samples date from the Roman (70-400AD), Early-Anglo Saxon (500-600AD), Late Anglo-Saxon (800-1200AD), Medieval (1100-1500AD), and modern day period. A total of 338 teeth were analyzed: molar ($n=89$), canine ($n=69$), incisor ($n=80$). Results display consistent and significant trends towards decreasing DSRs from the ancient to modern populations. This was observed in all molar cuspal ($p<0.00$), lateral mid ($p<0.01$) and outer ($p<0.00$) regions, in all incisor cuspal and lateral regions (all $p<0.00$), and in all canine cuspal and lateral regions (all $p<0.00$). These data provide the first evidence for a change in the daily rate of enamel growth in human permanent dentition, in multiple permanent tooth types, over a 2000 year period. This alludes to a previously unidentified plasticity in modern human enamel growth. Ongoing research will investigate whether similar variation has occurred in other enamel variables over this period of time in these populations.

Referential data sets of cut marks from the Theodore Roosevelt Expedition to East Africa (1909-1910)

MIRANDA ARMOUR-CHELU

No department, Unaffiliated

The basis for identifying the function of cut marks created during the scavenging or butchery of large mammals derived from prehistoric contexts is largely informed by three data sets, namely, ethnographic and experimentally produced assemblages and the fossil evidence or archaeofaunas. Long standing concerns regarding the objectivity and accuracy of experimental studies have necessitated the development of independent and referential data sets for the interpretation of ancient cut marks.

This study documents the cut marks observed from a series of large mammal skeletons collected by the Theodore Roosevelt Expedition to East Africa (1909-1910). The animals were butchered by members of the Wakamba tribe who were trained and directed by Edmund Heller of the Smithsonian Institution. The value of this sample of cut marks is that they constitute an independent or referential data set for comparison with fossil and experimentally produced cut marks and indications of their purpose.

One conclusion of the study is that removal of a single muscle mass, such as the quadriceps, is a two-step process which results in separate sets of cut marks. The initial cut mark is incurred with the severing of the quadriceps tendon, close to its point of attachment (a transverse cut). The second entails the separation of the body of the muscle from the shaft of the femur, comprising longer, obliquely oriented marks. While this finding

raises issues with the interpretation of cutmark frequencies expressed by individual element it also may provide insights as to the quantity of flesh remaining on the bone.

Pleiotropic effects on the recent evolution of human hip circumference and infant body size

AUDREY M. ARNER¹, HUGO REYES-CENTENO², GEORGE PERRY^{1,2} and MARK GRABOWSKI^{2,3}

¹Departments of Anthropology and Biology, Pennsylvania State University, ²DFG Center for Advanced Studies "Words, Bones, Genes, Tools", University of Tübingen, ³Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

Bipedalism is hypothesized to have had an evolutionary impact on human parturition. Specifically, the morphology of the human pelvis that permits habitual bipedalism may also constrain fetal brain and body size, a phenomenon known as the obstetric dilemma. Some of the assumptions behind this model have been questioned by recent work, but the genetic mechanisms underlying the potential coevolution of these traits remain largely unknown. Here we use a GWAS approach and the UKBiobank dataset to test whether two proxies for the obstetric dilemma (female hip circumference and first child birth weight) are associated with the same genetic variants in a pleiotropic manner. Using genotype-phenotype data, we identified 148 single nucleotide polymorphisms (SNPs) significantly associated with female hip circumference and 49 SNPs significantly associated ($P<5\times 10^{-8}$) with first child birth weight. Of these SNPs, 9 influence both women's hip circumference and first child birth weight, suggesting pleiotropic impacts on the traits. We further found that SNPs significantly associated with female hip circumference causally affect first child birth weight ($P=3.88\times 10^{-5}$), but not vice versa ($P=0.449$). Using the singleton density score statistic, which evaluates polygenic trait-associated allele frequency changes, we observe tentative evidence of recent (past ~3000 years) positive selection on SNP alleles associated with increased women's hip circumference ($P=0.0381$), but no evidence of selection on first child birth weight ($P=0.3516$). Overall, these results suggest that increased female hip circumference may have been a target of recent positive selection in the UK population, potentially resulting in a pleiotropic increase in offspring birth weight.

The Penn State University Erickson Discovery, Presidential Leadership Academy Enrichment, and Liberal Arts Enrichment Grants (all to A.M.A.); NIH grant R01-GM115656 (to G.P.); and DFG grant FOR-2237.

ABSTRACTS

Stable Carbon Isotopes of Mammalian Tooth Enamel and Paleoenvironments of the Early Miocene Locality Buluk, Kenya

IRISA D. ARNEY¹, ELLEN R. MILLER², ISIAH O. NENGO³, ELLIS M. LOCKE^{4,5} and WILLIAM J. SANDERS^{1,6}

¹Department of Anthropology, University of Michigan, ²Department of Anthropology, Wake Forest University, ³Turkana Basin Institute, Stony Brook University, ⁴Institute of Human Origins, Arizona State University, ⁵School of Human Evolution and Social Change, Arizona State University, ⁶Museum of Paleontology, University of Michigan

Buluk, a late Early Miocene (16 Ma) fossil locality in northern Kenya, has yielded a rich fauna with ~30 mammalian species. This includes at least three species of catarrhine primates: the stem cercopithecoid *Noropithecus bulukensis*, the stem hominoid *Afropithecus turkanensis*, and a small-bodied stem catarrhine that has been previously attributed to *Micropithecus* or *Simiolus*. These primates are crucial for understanding the evolution and diversification of modern catarrhine lineages, and knowledge of their associated paleoenvironments is critical to that understanding. Here we present stable carbon isotope compositions ($\delta^{13}\text{C}$) of herbivore tooth enamel (N=67) from artiodactyls, proboscideans, rhinocerotids, and hyracoids from Buluk. $\delta^{13}\text{C}$ values were used to characterize dietary ecology and reconstruct the habitat of these faunal communities.

$\delta^{13}\text{C}$ values from Buluk range from -11.6 to -8.4‰, indicating paleohabitats dominated by C_3 dietary resources. These $\delta^{13}\text{C}$ values are higher than values typical of herbivores foraging in modern closed canopied forests and are more consistent with diets associated with broken canopy or woodland habitats. Lower $\delta^{13}\text{C}$ values found in hyracoids, rhinocerotids, large suids, and deinothères suggest these taxa likely foraged in more covered areas, while higher $\delta^{13}\text{C}$ values in sanithères, anthracotheres, elephantoids, and tragulids imply a preference for more open habitats. These results are consistent with prior geochemical analyses, which have suggested a seasonal, subhumid woodland paleoenvironment. $\delta^{13}\text{C}$ values from Buluk overlap considerably with $\delta^{13}\text{C}$ values from other Early Miocene localities from East Africa and suggests extensive variability among C_3 dominated broken canopy/woodland habitats for early Miocene catarrhine sites.

Funding for this project was provided by the Leakey Foundation, The Turkana Basin Institute, National Geographic, The University of Michigan and Foothill De Anza Foundation

Evaluating a “field-friendly” approach to cell culture: Can capillary blood replace venous?

JACOB E. ARONOFF¹ and THOMAS W. MCDADE^{1,2}

¹Anthropology, Northwestern University, ²Institute for Policy Research, Northwestern University

Chronic inflammation is linked to degenerative diseases of aging such as cardiovascular disease (CVD), prompting studies investigating the developmental, ecological, and behavioral predictors of elevated inflammation. However, these studies have relied on basal measures of inflammatory biomarkers, which present limited information on the dynamics of the regulation of inflammation. In contrast, cell culture is routinely used in laboratory settings, in which blood samples are incubated under controlled conditions with ligands that activate inflammatory processes, providing insight into individual differences in sensitivity to pro- and anti-inflammatory signals. These methods require large volumes of venous blood and infrastructure for transferring, incubating, centrifuging, and freezing samples, making implementation difficult in field-based settings. Here we present results from a miniaturized cell culture method in which we culture capillary blood from the finger in a portable incubator, and then transfer the sample to filter paper as a dried blood spot (DBS) post-incubation for storage and transport. Using 30 μL capillary blood from two individuals, we found substantial production of IL-6 after a 4-hour incubation with 80 ng/mL lipopolysaccharide (LPS) (Mean = 585.4, SD = 89.1 pg/mL). In addition, we exposed a sample from one individual to varying concentrations of hydrocortisone in addition to LPS ($10^{5.5}$, 10^6 , 10^7 mol/mL hydrocortisone) to initiate a down-regulatory response and found cytokine values of IL-6 were higher with lower concentrations of hydrocortisone (33.2, 90.4, 326.1 pg/mL respectively). Our results suggest the feasibility of conducting cell cultures across a wide range of settings.

Testing the First Assumption of Trivers-Willard Hypothesis: Maternal condition (social status) is associated with offspring sex-ratio and male offspring postnatal growth in *Macaca mulatta*

JUAN PABLO. ARROYO and LORENA MADRIGAL
Applied Anthropology, University of South Florida

The three assumptions of Trivers-Willard hypothesis (TWH) are: 1) maternal condition is associated with offspring condition, 2) offspring condition differences remain until adulthood, and 3) offspring condition influences fitness differently by sex. TWH proposes that offspring sex-ratio can shift if it increases fitness and predicts lower proportions of male offspring under poor conditions. Attempts at testing TWH on macaques have yielded varied results. Here we test the first TWH assumption, that maternal condition is

associated with offspring condition, by assessing relationships between maternal-dominance-rank (MDR) and male-offspring-growth. We also test TWH's prediction of lower male offspring proportions in poor conditions, by comparing offspring sex-ratios among and between high-ranking and low-ranking mothers. Low MDR was associated with receiving more aggression ($r_s = -0.512$, $p = 0.000$), and with producing male offspring with lower weight ($r_s = 0.600$, $p = 0.024$) and lower BMI ($r_s = 0.613$, $p = 0.020$). Low-ranking mothers produced a lower proportion of male offspring ($n=9$) than female offspring ($n=22$) ($X^2 = 5.452$, $p = 0.020$); and a lower proportion of male offspring (29%), in comparison with medium-high ranking mothers (52.1%) ($X^2 = 4.643$, $p = 0.031$). Findings suggest that low MDR in macaques: 1) is associated with compromised male offspring growth, and 2) results in a lower proportion of male offspring. Relationships between MDR and offspring sex-ratio appear to become significant at the lowest third of the dominance-hierarchy, suggesting a stress-mediated biological threshold for shifting offspring sex-ratios. Results show that maternal stress during pregnancy disproportionately affects male offspring wellbeing.

A relatively conserved oral microbiome in non-human primates

ABIGAIL E. ASANGBA^{1,2}, LAWRENCE MUGISHA^{3,4}, JOSHUA RUKUNDO⁵, REBECCA J. LEWIS⁶, ALI HALAJIAN⁷, LILIAN CORTÉS-ORTIZ⁸, RANDALL E. JUNGE⁹, MITCHELL T. IRWIN¹⁰, JOHAN KARLSON¹¹, ANDREW PERKIN¹¹, KAREN L. BALES¹², STEVEN R. LEIGH^{13,2} and REBECCA M. STUMPF¹²

¹Department of Anthropology, University of Illinois at Urbana-Champaign, ²Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, IL, USA, ³Ecohealth Research Group, Conservation & Ecosystem Health Alliance (CEHA), Uganda, ⁴Department of Wildlife & Aquatic Animal Resources, College of Veterinary Medicine, Animal Resources & Biosecurity (COVAB), Makerere University, Uganda, ⁵Chimpanzee Sanctuary and Wildlife Conservation (Chimpanzee Trust), Ngamba Island, Uganda, ⁶Department of Anthropology, University of Texas at Austin, TX, USA, ⁷Department of Biodiversity, University of Limpopo, South Africa, ⁸Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI, USA, ⁹Columbus Zoo and Aquarium, Columbus, OH, USA, ¹⁰Department of Anthropology, Northern Illinois University, DeKalb, IL, USA, ¹¹Tanzania Forest Conservation Group and Nocturnal Primate Research Group, Dar es Salaam, Tanzania, ¹²Department of Psychology, University of California, Davis, CA, USA, ¹³Department of Anthropology, University of Colorado-Boulder, Boulder, CO, USA

Multiple factors are known to shape the primate microbiome, resulting in variations in the microbiome both within and between individuals. Here we extend the scope of these studies across eight body sites and 17 non-human primate

ABSTRACTS

(NHP) species to elucidate relative variation in the various microbiomes due to factors including host species, host phylogeny and diet using 16S rRNA data. Our meta-analysis revealed a wholly distinct and possibly conserved NHP oral microbiota characterized by low alpha and beta diversities compared to other body sites. Focused analyses within the NHP oral microbiome revealed differences due to host species, host phylogeny and dietary differences. For instance, the analysis of composition of the microbiome (ANCOM) showed several differentially abundant microbial taxa (Ruminococcaceae, Streptococcaceae, Lachnospiraceae, Peptostreptococcaceae, Actinomycetaceae, Nocardiaceae, Atopobiaceae, Porphyromonadaceae, Prevotellaceae, Fusobacteriaceae, Pasteurellaceae, Neisseriaceae, Enterobacteriaceae, Spirochaetaceae) among host species, host phylogenetic groups and diets. Our alpha and beta analyses also revealed statistically significant effects of host species, host phylogeny and diet on the oral microbiome, with host phylogeny explaining most (~40%) of the variation. However, the linear discriminant analysis of effect size (LEfSe) revealed four significant discriminative biomarkers only among host species including two taxa in the Pasteurellaceae family (*Hooilock leuconedys*) and two taxa in the Gamaproteobacteria order (*Propithecus diadema*). This is consistent with the results of the multivariate association with linear models (MaAsLin) which also showed associations only between host species and microbial community abundance and function. These results are indicative of a distinct, conserved NHP oral microbiome containing certain host specific differences.

Funding: NSF BCS 0820709, NSF BCS 0935347, NIH OD 011107.

Beyond dimorphism: sexual polymorphism and human skeletal variation

CLAUDIA M. ASTORINO

Department of Anthropology, The Graduate Center, City University of New York, NYCEP, The New York Consortium in Evolutionary Primatology, Department of Integrative Biology, University of California, Berkeley, Human Evolutionary Research Center, University of California, Berkeley

Sexual dimorphism in the human skeleton has long been recognized as an important area of research in biological anthropology. Although sex is considered to be a binary variable, approx. 1.7% of people globally are born with a combination of biological traits that do not conform to definitions of male or female: intersex people. Intersex people may possess karyotypes, alleles, external sex traits, internal sex traits, hormone types, and/or hormone levels that are typical for males, typical for females, and/or atypical for either, all in the same body. Since population genetics define "rare" traits as being present in < 1% of a given population, intersex traits – and thus, intersex people

– are not rare. For this reason, sex differences in humans may be more accurately characterized as sexually polymorphic than sexually dimorphic. Studies on sex differences in human skeletal traits are numerous, but almost nothing is known about skeletal variation and patterns of sex differences in intersex people. It is predicted that – controlling for ancestry, geography, and environmental factors – people with certain forms of intersex should exhibit skeletal sex indicator morphology that does not significantly differ from typical males (e.g., hypospadias) or typical females (e.g., complete androgen insensitivity), while people with other forms of intersex may differ substantially in skeletal sex indicator expression. Shifting paradigms from sexual dimorphism to sexual polymorphism will allow biological anthropologists to more accurately and comprehensively characterize sex variation and patterns of sex differences in the human skeleton.

The fuzzy nature of paleopopulations defies typology

SHEELA G. ATHREYA¹ and REBECCA R. ACKERMANN²

¹Anthropology, Texas A&M University, ²Archaeology, Human Evolution Research Institute, University of Cape Town

Paleoanthropology is rooted in intellectual and conceptual traditions of describing, classifying, and arbitrarily defining units. Hominin phylogenies are typically constructed based on assumptions about taxonomic discreteness at the species level despite a lack of consensus over how to identify species in the fossil record. The issue of where to draw the boundaries of a paleopopulation is similarly unclear but more insidious because it is tied to historical efforts to validate racial categories and argue that regional groups are separate species with deeply distinct evolutionary roots. The Modern Human Origins debate that began in the 1980s has been a venue for paleoanthropologists to try to construct a post-racial narrative for our species. "Out of Africa" and related models are seen as inclusive because they emphasize humanity's single (recent) origin and shared genetic material. Ironically, although growing evidence contradicts this narrative, researchers continue to treat paleopopulations as discrete evolutionary units while minimizing the reality that continuous variation has created fuzzy boundaries in nature. This approach perpetuates the idea of regional groups as evolutionarily separate units. The recent discourse around human/Neanderthal/Denisovan discreteness in the face of hybridization is an example of this. We are still, as Caspari points out, framing our study of past human variation around typological and essentialist constructs. Here we argue that there is no unifying concept for paleopopulation that is not

circular and typological, and that referring to them as discrete units has inadvertently but significantly reproduced support for the concept of race in the study of human evolution.

Habitual activity induced musculoskeletal stress markers among prehistoric rice farmers: A case study from Japan

ASHLEY M. ATKINS¹, CHRISTOPHER J. BAE¹ and ROBERT W. MANN²

¹Anthropology, University of Hawaii at Manoa, ²Anatomy, John A. Burns School of Medicine, University of Hawaii

The transition from fishing, hunting, and gathering to full time agriculture occurred at different times in different places throughout the world. Here, we argue that different habitual activities performed by hunter-gatherer-fishers and farmers can be identified in the postcranial skeleton. This hypothesis was tested by studying known Holocene human skeletal collections from four sites (Koura, Doigahama, Kanenokuma, and Ichinotani) that dates to the Yayoi (Bronze Age) period in Japan, long considered to represent a large scale rice agricultural society. This collection is currently curated in the Kyushu University Museum. An investigation into musculoskeletal stress markers (MSM) of the Yayoi people can inform on the stresses of the different activities these people participated in. This study modifies the Hawkey and Merbs (1995) method to score three morphological traits (robusticity, stress lesions, and ossification exostosis) with intermediate scores with the goal of creating a more reliable MSM system. A total of 72 muscle attachments (36 per side) from the upper and lower limbs were used to assess the MSMs of 104 individuals. The general pattern shows that MSMs of those who participated mostly in rice farming had higher total scores than those that relied more on fishing, hunting and gathering. Of the four sites used in this study, we found that the individuals from Koura and Doigahama participated in a combination of deep sea fishing, hunting and gathering, as well as some rice farming, while those from Kanenokuma and Ichinotani relied almost exclusively on rice farming for subsistence.

Funding was given from the Department of Anthropology at the University of Hawaii at Manoa.

Performance of adaptive boosting classifier based on incomplete dataset in biological sex prediction using postcranial bones

MENNATTALLAH H. ATTIA¹ and MOHAMMED H. ATTIA^{2,3}

¹Forensic medicine and clinical toxicology, Faculty of medicine, Alexandria University, ²Department of Biomedical Engineering, Medical research institute, Alexandria University-Egypt, ³Institute for Intelligent

ABSTRACTS

Systems Research and Innovation., Deakin University, Australia

In forensic anthropology, group and period specific methods are crucial for reliable sex estimation. However, variations in discriminating efficiencies from training to validation datasets in the same region were reported. Cross-population testing showed more fluctuations due to unacceptable sex bias. Data science provides alternatives to classical classifiers e.g., neural networking (NN), support vector machine (SVM), and quadratic discriminant analysis (QDA) classifiers. Flawed outputs may occur because of modeling techniques and poor quality of data e.g., missing values, multicollinearity, and overfitting. Therefore, researchers draw confusing conclusions about interpopulation differences or the need to renew standards. Adaptive boosting (Adaboost) combines multiple models to improve the performance by focusing on incorrectly classified observations. Challenging sex estimation task was designed to compare the performance of adaboost to other machine learning algorithms using training sample of ancient native Americans from Goldman's dataset (n=539) and validated on modern Thai (n=104) and Hong Kong (n=77) populations which were donated by Christopher King; based on the shared historical Asian ancestry. 13 standard measurements from left humerus, femur, and tibia were the input variables. Despite extensive missing data in the training sample, the accuracy ranged from 68% (QDA) to 86% (adaboost). In the test populations, the average accuracy in Thai sample ranged from 54% (SVM) to 89% (adaboost) and in Hong Kong sample ranged from 54% (SVM) to 88% (adaboost). Adaboost is a powerful classifier which outperformed other classifiers in both datasets and showed notable stability despite the interpopulation differences and temporal separation.

Variance in the primate axial skeleton and selection regimes: assessing models of trait evolution using a phylogenetic comparative approach

BENJAMIN M. AUERBACH¹ and ELIZABETH R. AGOSTO²

¹Anthropology, The University of Tennessee,
²Anatomy, Cell Biology & Physiology, Indiana University School of Medicine

Primate shoulder girdle morphological variation is often modeled as occurring from adaptive responses to different locomotor functions driven by diet or habitat. We recently demonstrated that the morphology of the primate shoulder girdle evolves through correlated responses to directional selection with functionally and developmentally related traits, namely the basicranium, pelvic girdle, humerus and vertebral column. Differences in the strength of the underlying correlations influences how traits can respond

to directional selection, yielding morphological variation among primates. However, while our analyses of evolvability among these traits show the potential for correlated responses to evolution, we have not assessed how variation in the direction of selection differentially affected trait evolution.

In this study, we test three hypotheses of primate diversification (n=49 species) across traits of the axial and appendicular skeleton using phylogenetic comparative methods. Results indicate an Ornstein-Uhlenbeck process models primate evolution better than Brownian Motion. Of the hypotheses tested, a model for locomotion-related selection best fits the data, however, the model produced by a Bayesian analysis most accurately describes the variation among primate taxa. This model suggests selective pressures that motivate changes in the primate bauplan manifest at higher taxonomic levels. Morphological distinctions at the genus and species level may be the result of how groups of organisms are able to respond to the selective pressure to modify the bauplan, but not evolve new bauplans. Combined with previous results, we argue that primate morphological diversity is manifest through trait covariance across the skeleton, along with taxonomic hierarchically structured responses to selection.

This research is supported by a National Science Foundation Doctoral Dissertation Improvement Grant (NSF BCS-1825995).

Curating Biomolecules: Molecular Legacies and Untold Stories from the Smithsonian's Biological Anthropology Collections

RITA M. AUSTIN^{1,2}, COURTNEY A. HOFMAN^{1,2} and SABRINA B. SHOLTS²

¹Anthropology, University of Oklahoma,
²Anthropology, National Museum of Natural History

Museums hold a unique position in society as repositories and disseminators of knowledge for the public. Since the high-throughput sequencing revolution of the last decade, museum collections are being accessed for destructive sampling now more than ever. Anthropology collections are being used as a ready source of curated and contextualized human remains for biomolecular analyses to reveal the human past. However, researchers and museums have yet to fully consider and incorporate the distinct histories of museum collections: namely, how the excavation/ recovery and museum stewardship may affect the biomolecular signals being recovered and subsequently the narratives being put forth. While museum collections are more heavily documented and analyzed, they have been removed from their original contexts and handled, forcing reliance on the documentation about the source populations and museum methodologies.

Post-deposition, -excavation, and -recovery histories of remains has not been widely integrated into current biomolecular analyses as affecting studied individuals' and population stories.

Here, we discuss intra- and inter-collection shotgun metagenomic results and archival research being conducted on the Smithsonian Institution's Biological Anthropology collections. Extracted dental calculus DNA from six skeletal collections revealed individual and collection molecular trends, with extraction DNA quantification ranging from 0-38.2ng/mg across collections. As the primary collector for several of the collections, Aleš Hrdlička's archival travel accounts and departmental communications reveal first-hand documentation of acquisition, shipping, and treatment contexts and previously unknown factors in biomolecular preservation.

Funding was provided by the Smithsonian Institution's National Museum of Natural History and the National Science Foundation's Doctoral Dissertation Improvement Grant #1920152.

Convergence of innominate morphology in suspensory primates: a 3D geometric morphometrics approach

MONICA V. AVILEZ^{1,2}, JENNIFER EYRE^{1,2} and SCOTT A. WILLIAMS^{1,2}

¹Center for the Study of Human Origins,
Department of Anthropology, New York University,
²New York Consortium in Evolutionary Primatology

The bony pelvis is perhaps one of the most complicated structures in the body. Considering its complex structure, using three-dimensional (3D) geometric morphometrics in analyzing shape variation between primate groups is important as it maintains the 3D shape of the innominate. Locomotor modes can vary within and between species, and primates are not restricted to a single style. Platyrrhines are mainly arboreal quadrupeds that also display leaping behaviors. The exception are the atelines, a group of species who use suspensory and climbing behaviors while locomoting and feeding similar to apes, albeit with prehensile tails. The aim of this study is to investigate if there is convergence in shape of the pelvis in suspensory primates, and to elucidate what factors (such as function, phylogeny, and/or allometry) might be driving variation in shape. Following Lewton (2015), 3D landmarks were collected from a range of anthropoid primates (n=133) with a focus on atelids and hominoids. Results show that the first axis of Procrustes-adjusted variance (accounting for 52% of total shape variation) correlates strongly with centroid size and is therefore driven by allometry. Subsequent axes demonstrate clear separation of locomotor groups. A phylomorphospace analysis shows that *Ateles*, hylobatids, and some colobines pull away from their respective outgroups in similar directions. Future analyses will include

ABSTRACTS

semi-landmarks to better capture the complex shape of the pelvis and the inclusion of fossil pelvises to test hypotheses of locomotor behavior in extinct primates.

This material is based upon work supported by the NSF-GRFP under Grant No. 1839302 to MVA, NSF GRFP-1650895 to JE, and a Leakey Foundation Grant to SAW.

A Regional Comparative Analysis of External Auditory Exostosis in Pre-Hispanic Peru

MIA K. AYER¹, RITA M. AUSTIN^{2,3}, ANDREA R. ELLER³ and SABRINA B. SHOLTS³

¹Anthropology, University of Notre Dame, ²Anthropology, University of Oklahoma, ³Biological Anthropology, Smithsonian Institution's National Museum of Natural History

External auditory exostosis (EAE) is a pathology characterized by bony growths in the ear canal, commonly known as "surfer's ear" due to its association with prolonged cold water exposure. However, EAE is geographically widespread, and its etiological factors are poorly understood. To test whether EAE is specifically characterized by water temperature or specific cultural behaviors, this study compares the presence of EAE across Peruvian populations with previously published data from Panamanian populations. Using the Smithsonian's National Museum of Natural History human skeletal collections, Pre-Hispanic Peruvian crania (n=1407, 1300-1500CE) were assessed for provenance, sex, and EAE presence/absence. Chi-square analyses indicated that there was a significant correlation of EAE frequency with both location ($p=0.015$, $\phi^2=0.05$) and sex ($p=0.000$, $\phi^2=0.05$). In both Panama and Peru, the vast majority of the individuals exhibiting ear exostosis were male (87% and 85%, respectively) possibly indicating a division in EAE-associated labor and/or behavior based on sex. Due to the similarities in water temperature between Panama and Peru, in conjunction with the observed sex bias towards males, culturally determined behavior likely impacts who and where EAE occurs. More generally, high frequencies of EAE in coastal populations suggest a reliance on marine resource exploitation, and perhaps non subsistence-based shell collection. Procuring the Spondylus shell, which is well known to have economic and cultural significance across Peru, may have influenced the frequency of EAE observed. Further research and comparative analyses will explore other potential biological, cultural, and environmental factors in the expression of this pathology.

Funding for this project was provided by the University of Notre Dame and the National Museum of Natural History.

Contributions of high dimensional shape analysis to paleoanthropology

KAREN L. BAAB^{1,2}, SARAH E. FREIDLIN^{2,3} and KATERINA HARVATI^{2,4,5}

¹Anatomy, Midwestern University, ²NYCEP Morphometrics Group, ³Human Evolution, Max Planck Institute for Evolutionary Anthropology, ⁴Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoenvironment, Eberhard Karls University of Tübingen, ⁵2DFG Centre of Advanced Studies 'Words, Bones, Genes, Tools', Eberhard Karls University of Tübingen

High dimensional shape analysis now occupies a central place in paleoanthropology. Researchers use geometric morphometric data to address important questions related to systematics and evolutionary history, ontogenetic development and covariation between shape and other factors. The NYCEP Morphometrics Group (NMG), spearheaded by Eric Delson and Leslie Marcus, represents one important hub in the development and application of high dimensional shape analysis within paleoanthropology and biological anthropology more broadly. This review highlights how shape analyses influence paleoanthropological thinking, with a focus on contributions of the NMG.

Early applications focused on systematics, including assessing the taxonomic affinities of individual fossils, comparing patterns of intra- and inter-specific variation and characterizing allometric, geographic and temporal structure within species. These include the 2001 comparative analysis of the midsagittal contour of early *Homo* fossils to assess the evolutionary position of Sumbungmacan 3. Shape analyses have been instrumental in establishing that population-level differences in facial anatomy are present early in ontogeny. These analyses have identified both marked and more subtle differences among craniofacial ontogenetic trajectories between hominoid species and even populations within species. Sophisticated analyses of morphological integration and modularity provide important insights into craniofacial, dental and postcranial integration with implications for hominin evolution. Moreover, the increasing assimilation of shape data into quantitative genetic methods provides a deeper understanding of how the demographic processes that generate neutral genetic evolution also produce morphological variation among human populations and how variation within populations constrains macroevolution in hominins.

Reliability of facial identification methods in optimal photographs and suboptimal CCTV footage

NICHOLAS BACCI, MARYNA STEYN and NANETTE BRIERS

Human Variation and Identification Research Unit, School of Anatomical Sciences, University of the Witwatersrand

Facial comparison (FC) is routinely utilized in the medicolegal context through holistic review and morphological analysis. These methods have, to date, not been systematically validated, particularly when involving CCTV recordings. Increased global availability of video surveillance data emphasizes the need for accurate facial comparison methods. This study aimed to test current FC methodologies on a photographic and video recording sample.

Face pools (FP) of 175 African males of facial photographs in multiple views were compiled. Each face pool included one target photograph or CCTV recording and 10 potential matching photos. Photos of the first 75 participants were taken in standardized settings and compared to other suboptimal photos in a photo-to-photo cohort. The remaining FP (n=100) included CCTV recordings of participants compared to standardized photographs. FP were firstly analyzed via holistic review to identify potential matches. Potentially corresponding faces were then tested via morphological analysis. Method accuracy was determined through hit-rate, sensitivity and specificity calculation.

Higher accuracy for morphological analysis ($\kappa=0.96$, $p<0.01$) compared to holistic review ($\kappa=0.76$, $p<0.01$) was found within the photo-to-photo cohort. High sensitivity was identified for both methods (1.00 and 0.97), while a slightly higher specificity was identified for morphological analysis (0.99) over holistic review (0.95). Preliminary CCTV results show decreased accuracies for holistic ($\kappa=0.65$, $p<0.01$) and morphological ($\kappa=0.88$, $p<0.01$) analyses.

In conclusion, morphological analysis, although subjective, yielded better results. Overall higher accuracies were observed within the photo-to-photo cohort compared to CCTV recordings as it involves higher quality, controlled images.

The National Research Foundation of South Africa sponsored this research. Any information expressed in this study is the authors' and therefore the NRF does not accept any liability in regards.

Fission-fusion sociality shapes the gut microbiome in black-and-white ruffed lemurs (*Varecia variegata*)

ANDREA L. BADEN^{1,2} and TIMOTHY H. WEBSTER³

¹Anthropology, Hunter College - CUNY, ²The New York Consortium in Evolutionary Primatology, (NYCEP), ³Anthropology, University of Utah

ABSTRACTS

Host organisms exhibit remarkable variation in the abundance and composition of microorganisms in their guts, diversity that is shaped by a complex combination of factors. Some of these factors are heritable, such as aspects of the host's genome and vertical transmission from mother to offspring. Others stem from their physical and social environments. Here, we investigate the role that fission-fusion social dynamics (FFD) plays in gut microbiome variation in 18 individuals (12 adults and 6 juveniles) belonging to one community of black-and-white ruffed lemurs (*Varecia variegata*). We combined twelve-months (September 2017 – August 2018) of climatic, dietary, social, and microbiome (n=194 samples) data to ask whether and how sociality modulates microbiome variation. Dietary diversity (H') within the community was low (H'=1.547), and did not differ significantly across individuals or by season. By contrast, sociality (Association Indices, Als) varied significantly across dyads (Als, mean=0.04±0.11SD, p<0.001). In the microbiome, alpha diversity varied both within and among individuals over time. Beta diversity also varied, with significant differences corresponding to seasonal changes in FFD (PERMANOVA pseudo-F = 5.77, p = 0.001, permutations = 999). Using longitudinal linear mixed effects models, we will further explore the relative impacts that H' and Als play in modulating microbial diversity. Taken together, our results suggest that the dynamic nature of fission-fusion social dynamics shapes the microbiome, potentially through myriad factors including dietary diversity and social transmission.

Funding was provided by The Leakey Foundation, PSC-CUNY, and Hunter College.

Early modern humans in China: A view from Guangxi

CHRISTOPHER J. BAE¹, WEI WANG² and WEI LIAO³
¹Department of Anthropology, University of Hawai'i of Manoa, ²Institute of Cultural Heritage, Shandong University, ³Center for Paleoanthropology Research, Anthropology Museum of Guangxi

The origins of modern humans continues to be of great interest with Asia's role becoming increasingly prominent in these discussions. With the increasing number of modern human fossils dating to the late Middle Pleistocene and early Late Pleistocene being reported from different regions of Eurasia it is clear that the traditional Out of Africa at 60 ka BP model does not work. Here, we report on an increasing number of modern human fossil localities from Guangxi, southern China that date to this critical time period when modern humans appeared in the region. In particular, modern humans from the Chongzuo (Zhirendong, Yanlidong) and Bubing (Lunadong) regions of Guangxi indicate not only that modern humans appeared early in the region, but may not have been isolated early occurrences. In fact, modern humans may have been in the

region more or less continuously beginning by the late Middle Pleistocene. It would appear that modern humans arrived initially in southern China and then spread north to central China. A later second major dispersal wave of modern humans across the northern corridor arrived in Mongolia and northern China during the latter half of the Late Pleistocene and spread southwards into central China, eventually reaching Korea, Japan, and eastern Siberia. What happened when these different groups of modern humans met in places like central China remains a major question in paleoanthropology. Contributions from genetics and archaeology will be discussed in light of the hominin fossil and geochronological datasets.

Absence of suspensory foraging postures in *Pygathrix nemaeus*: using Ladan's kinesphere as a proxy for below branch locomotion

KATIE E. BAILEY
Anthropology, University of North Carolina Wilmington

The douc langurs (genus *Pygathrix*) are well known for using high proportions of arm-swinging behavior in captivity and in the wild. This derived behavior (relative to other colobines) is poorly understood in its evolutionary origin. One potential explanation is that this behavior evolved in conjunction with foraging on the terminal ends of branches via a suspensory feeding posture, increasing the feeding sphere. This sphere, known as Ladan's kinesphere, is limited by the distance an individual can reach. It has been suggested that primates can increase their feeding sphere from above the branch to below the branch by adopting a suspensory feeding posture. A suspensory feeding posture is particularly useful for larger bodied primates that would otherwise be unstable on terminal branches. Here, I test whether a suspensory feeding posture is used by the red-shanked douc, and if it may explain their proclivity for below branch locomotion. I filmed these monkeys in the Son Tra Nature Reserve, Vietnam between October 2016 and April 2017. Data were extracted continuously from the footage and analyzed in R. Preliminary results show that red-shanked doucs in this study did not use a suspensory feeding posture at all (n=0/830). Sitting accounts for 90% of their feeding posture, followed by three-limb support reach (6.14%), flexed bipedal stand (1.81%), extended bipedal stand, forelimb suspend-stand (>1%). These results indicate that a suspensory feeding posture did not likely contribute to the evolution of arm-swinging in this Endangered primate.

This research was supported in part by the Department of Anthropology, Texas A&M University and Primate Conservation Inc.

New human remains from Ksar Akil and their relevance to circum-Mediterranean dispersals of early *Homo sapiens*

SHARA E. BAILEY^{1,2} and CHRISTIAN A. TRYON^{3,4}
¹Department of Anthropology, Center for the Study of Human Origins, New York University, ²New York Consortium in Evolutionary Primatology, ³Department of Anthropology, University of Connecticut, ⁴Department of Anthropology, Harvard University

New archival research at Harvard University's Peabody Museum revealed photographs and radiographs of a previously undescribed individual from the Early Upper Paleolithic (early Ahmarian) levels of Ksar Akil (Lebanon), one of the few circum-Mediterranean archaeological sites that documents early dispersals of *Homo sapiens*. Few human fossils exist from this area and time period, and the skull and associated post-crania of the juvenile known as 'Egbert' from Ksar Akil are now lost. We provide a dental analysis of first-generation casts of Egbert and the first description of the "new" fourth individual, the latter found adjacent to Egbert during the 1938 excavations and only noted briefly in initial publications. The "new" individual consists of dental/mandibular material only, and, like Egbert is from level XVII or XVIII, conservatively dated from ~39-43 ka. Archival photographs suggest a juvenile of 7-9 years, similar to that estimated for Egbert. Compared to other fossil *H. sapiens* individuals, the teeth of Egbert and the new individual are remarkably modern. The upper and lower deciduous first molars are bicuspid; the upper deciduous second and permanent first molars possess quite reduced hypocones and square occlusal outlines. The lower first permanent molars are four-cusped, a rare trait even among recent *H. sapiens*. Its presence in two contemporaneous individuals at Ksar Akil suggest a possible locally distinctive population marker for groups in the Levant at this time, and thus one possible line of evidence useful for studies seeking to understand the geographic origins of early *H. sapiens* groups in Europe and elsewhere.

This research was funded through the Radcliffe Institute for Advanced Study and the American School of Prehistoric Research.

The Morphology of Ballistic Trauma

STEPHANIE A. BAKER¹ and JENNIFER R. KIELY²
¹Biological Science, Sam Houston State University, ²Forensic Science, Sam Houston State University

In forensic anthropology, bone fracture morphology provides potential evidence in the mechanism of injury or death. Specifically, the type of weapon used, the trajectory of impact, and the direction of fire can also be interpreted from internal and external bone morphology. Morphological characteristics, such as buttresses and sutures, are also applicable when analyzing

ABSTRACTS

ballistic trauma. This study analyzed fracture morphology of sagittal and coronal plane crano-maxillofacial gunshot wounds of five specimens from the Applied Anatomical Research Center's (AARC) skeletal collection. Methodologies include enumerating and describing the etiology of ectocranial fractures, any missing bony segments, and the macroscopic fractures for each specimen. Sliding calipers were used to measure the distance (mm) of the entrance and exit wounds in relation to identifiable bony landmarks. The distribution of fractures and fracture locations on the crano-maxillofacial region were analyzed and assessed to determine similarities and differences among the sagittal and coronal plane gunshot wound specimens. Results indicate that radiating fractures run parallel to buttressed areas of the cranial vault in both sagittal and coronal plane gunshot wounds but run perpendicular to buttressed areas of the face in sagittal plane specimens only. The value of this research could provide additional evidence to reconstruct death histories of relatively incomplete skulls with suspected ballistic trauma. The ultimate goal is to provide the medicolegal community with a larger, more refined data set to better understand ballistic trauma by examining fracture morphologies of sagittal and coronal gunshot wounds in skeletonized human remains.

Prehistoric health on the Southern coast of Brazil related to worldwide subsistence practices

SYDNEY M. BAKER¹ and MARK HUBBE^{1,2}

¹Department of Anthropology, Ohio State University, ²Instituto de Arqueología y Antropología, Universidad Católica del Norte, Chile

Between ~ 6000 and 1000 years BP, the Southern Coast of Brazil was occupied by populations that built shellmounds, locally known as sambaquis, as residential and funerary sites. Sambaqui populations are described as fisher-hunter-gatherers. Around 1000 BP, ceramics were introduced to the area, associated to top layers of sambaquis as well as to new shallow sites. Usually, the introduction of ceramics is considered an indication of agricultural practices, but previous studies have found minimal differences in health between sambaqui and coastal ceramic populations. Here, we expand on this discussion by comparing the prevalence of health and life-style skeletal markers among sambaqui and coastal ceramic populations to prevalences observed among hunter-gatherer and agricultural populations worldwide. Prevalence data for several traditional osteological markers was collected from published data for 23 sambaqui and 9 coastal ceramic sites, and compared to Hunter-Gatherers and Agriculturists using Kruskal-Wallis and post-hoc pairwise tests. For caries, agriculturists show higher prevalence than all other groups (hunter-gatherers, sambaquis, coastal ceramic

sites; $p < 0.001$ for all). For AMTL, sambaquis show lower prevalence than agriculturists and hunter-gatherers ($p < 0.05$ for both). For hyperostosis porotica, sambaquis show higher prevalence than hunter-gatherers ($p = 0.004$). For cribra orbitalia, these are no significant differences in the pairwise comparisons. LEH and abscesses show no statistical difference among groups ($p = 0.404$ and $p = 0.148$, respectively). For all markers, there are no significant differences between sambaquis and coastal ceramic sites. These results show that health and lifestyle among coastal Brazilians sites present patterns that are not directly comparable to either hunter-gatherer or agriculturist lifestyles.

Impact of anthropogenic factors on affiliative behaviors among wild bonnet macaques

KRISHNA BALASUBRAMANIAM¹, PASCAL MARTY¹, MALGORZATA ARLET², BRIANNE BEISNER¹, STEFANO KABURU³, ELIZA BLISS-MOREAU⁴, ULLASA KODANDARAMAJAH⁵ and BRENDA MCCOWAN¹

¹Population Health and Reproduction, University of California at Davis, ²Department of Human Evolutionary Biology, Adam Mickiewicz University, ³Department of Biomedical Science and Physiology, University of Wolverhampton, ⁴Department of Psychology, University of California at Davis, ⁵Centre for Research and Education in Ecology and Evolution, Indian Institute of Science Education and Research

In nonhuman primates, allogrooming confers many benefits, and may be influenced by many socioecological factors. Despite increasing conflict between humans and wild primates, the impact of anthropogenic factors on grooming remains understudied. We tested two contrasting hypotheses regarding how anthropogenic factors may influence macaques' grooming and other affiliative interactions. We asked whether interactions with humans decreased macaques' affiliative behaviors by imposing time-constraints, or increased affiliation on account of macaques' consumption of anthropogenic foods culminating in more free-time. We collected data (11 months) on human-macaque and macaque-macaque interactions using focal-animal sampling on two groups of wild bonnet macaques (*Macaca radiata*) in Southern India. For each macaque, we calculated frequencies of human-macaque interactions, rates of foraging on natural/anthropogenic food, rates of monitoring humans, dominance ranks, grooming duration, grooming partner diversity, and frequencies of short-duration affiliative interactions (e.g., coalitionary-support, lip-smacking). We found strong evidence for time-constraints - macaques that monitored humans more groomed for shorter durations, and groomed fewer partners. These effects were independent of group ID, sex, dominance rank, and climatic season. However, monitoring humans had no impact

on frequencies of short-duration affiliation. We found no evidence for the free-time hypothesis - foraging on anthropogenic food predicted neither grooming nor affiliation. Our results are consistent with recent findings on other macaque species/populations in human-impacted environments. Macaques in urban environments may rely more on short-duration affiliative behaviors for maintaining social bonds. More broadly, conservation research should evaluate inter-individual differences in primate/wildlife behavior.

This work was supported by the American National Science Foundation Coupled Natural and Human Systems grant (NSF-CNH #1518555) awarded to the PI Dr. Brenda McCowan.

Characterizing migration waves into Chilean Patagonia and Tierra del Fuego using ancient DNA

CHRISTINA M. BALENTINE^{1,2}, MIGUEL VILAR³, FLAVIA MORELLO⁴, MANUEL SAN ROMÁN⁴, LAUREN C. SPRINGS⁵, SAMANTHA M. ARCHER², JAIME MATA-MÁGUEZ⁵, RICK W. A. SMITH^{6,7}, NATALIE WING⁸, MARTA ALFONSO-DURRUTY⁹ and DEBORAH A. BOLNICK^{10,2}

¹Department of Integrative Biology, University of Texas at Austin, ²Department of Anthropology, University of Connecticut, ³National Geographic Society, ⁴Instituto de la Patagonia, Centro de Estudios del Hombre Austral, Universidad de Magallanes, ⁵Department of Anthropology, University of Texas at Austin, ⁶Neukom Institute for Computational Science, Dartmouth College, ⁷Department of Anthropology, Dartmouth College, ⁸Glastonbury High School, Glastonbury, CT, ⁹Department of Sociology, Anthropology, and Social Work, Kansas State University, ¹⁰Institute for Systems Genomics, University of Connecticut

While numerous studies have investigated the broad-scale peopling of the Americas, comparatively few have focused on the settlement of the southernmost region of these continents. In Patagonia and Tierra del Fuego (Fuego-Patagonia), archaeological evidence points to two major waves of migration into the region: an initial wave of terrestrial hunter-gatherers and a later wave of specialized marine hunter-gatherers. Previous analyses of mitochondrial DNA (mtDNA) from 27 ancient Fuego-Patagonians (ca. 3,500-390 BP) supported this hypothesis, suggesting that the groups exhibited distinct haplogroups. Terrestrial and Mixed diet hunter-gatherers exhibited mainly the C1b and D1 mtDNA haplogroups whereas Marine hunter-gatherers exhibited mainly D4h3a. Based on these data, we hypothesized that individuals belonging to the D4h3a haplogroup migrated into the region at a different time than those belonging to C1b and D1.

To test this hypothesis, we combined our previous sample with 22 additional individuals (ca. 6,000-780 BP) from Fuego-Patagonia, for a total $N = 49$. Ancient DNA was extracted and preliminary analyses indicated high endogenous DNA

ABSTRACTS

preservation. The mtDNA hypervariable regions (HVR1 and HVR2) were PCR-amplified and Sanger sequenced. Indices of molecular diversity, haplotype networks, and demographic simulations were analyzed to characterize genetic variation in ancient Fuegian-Patagonians. Haplogroup diversity was greater for Terrestrial hunter-gatherers than either Marine or Mixed diet hunter-gatherers. Further, pairwise F_{ST} comparisons indicated statistically significant differentiation between Marine and Terrestrial groups and between Marine and Mixed diet groups, but not between Terrestrial and Mixed diet groups. We discuss the implications of these results for the early population history of southern South America.

This study was funded by the National Geographic Society and FONDECYT (Chile). C. M. Balentine is supported by an NSF Graduate Research Fellowship.

Maturation and stabilization of the infant gut microbiome in wild geladas

ALICE BANIÉL¹, JACINTA C. BEEHNER^{2,3}, THORE J. BERGMAN^{2,4}, ARIANNE MERCER⁵, LAUREN PETRULLO⁶, LAURIE REITSEMA⁷, SIERRA SAMS⁵, NOAH SNYDER-MACKLER⁵ and AMY LU¹

¹Anthropology, Stony Brook University, ²Psychology, University of Michigan, ³Anthropology, University of Michigan, ⁴Ecology and Evolutionary Biology, University of Michigan, ⁵Psychology, University of Washington, ⁶Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, ⁷Anthropology, University of Georgia

The development of the gut microbiome during infancy affects metabolic programming, immune function, and nervous system development and has been linked to important health outcomes later in life. However, how and why the trajectory of gut maturation varies from one infant to another remains poorly understood in nonhuman primates, which represent ideal models to examine how early life conditions impact the gut microbiome, and ultimately, developmental and fitness outcomes. Here, we analyzed the gut microbiome composition of wild infant geladas (*Theropithecus gelada*), using 16s rRNA amplicon sequencing of 504 fecal samples from 111 individuals between 0-4 years old. We investigated age-associated changes in the composition and function of infant gut microbiome, while controlling for infant sex and seasonal variation. As predicted, age was the strongest structuring factor of the gut microbiome community (beta diversity) ($R^2=9\%$, $P<0.001$). Microbial richness (alpha diversity) increased rapidly and linearly during the first 10 months of life, plateauing later in infancy. Comparisons of beta diversity between 378 mother-infant pairs suggests that infants reach an adult-like microbiota configuration around 18 months; however, interindividual variation in the timing of this transition appears high. Young infants had more bacterial taxa associated with the metabolism of oligosaccharides found in breast milk (Bifidobacteriaceae,

Streptococcaceae, Lactobacillaceae), while older infants displayed an increase in fiber-degrading bacteria, associated with the introduction of grasses in their diet. Our findings highlight the dynamic nature and individuality of the gut colonization process in early life. Future studies should aimed at unraveling the socioecological determinants generating such variation.

Early twentieth-century dissection methods: A case study from the early years of the University of Utah's School of Medicine.

MEGHAN E. BANTON and DERINNA V. KOPP

Antiquities Section, Utah Division of State History

Construction on the George Thomas Building (GTB) at the University of Utah in 2016 resulted in the discovery of commingled human remains. Evidence of craniotomies, medical laboratory glassware (ca. 1900 to 1930), and historic research suggest the remains are anatomical specimens from the University of Utah's School of Medicine (UUSM), likely from the period between the school's establishment (1905) and completed construction of the GTB (1935). Research was undertaken to determine how perimortem alterations observed in the skeletal assemblage compare to documentation of early twentieth-century dissection standards, as well as UUSM specific practices. Standard osteological methods of recording and analysis were applied to GTB skeletal assemblage. The results of this analysis were then compared to historic documentation relevant to dissection and the UUSM. These comparisons produced interesting results. Marks (cuts, sawing, chiseling) displayed in the skeletal remains are locationally and directionally identical to those described for craniotomies, laminectomies, and shoulder dissections in anatomy texts from the time. Course catalogs (1906-07 and 1918-19) indicate the UUSM taught six or seven anatomy courses focused on dissection of particular body regions; this is reflected in the assemblage - there is a varied number of skeletal elements, suggesting they were buried as bodily portions as opposed to whole cadavers. The GTB remains provide direct evidence of dissection consistent with methodology common to the period, while the nature of the assemblage affirms the regional anatomy pedagogy implemented by the early UUSM. Such findings provide valuable insight into early twentieth-century medical school practices.

The analysis of the skeletal remains was funded by the University of Utah Campus Planning Department.

Quantifying regional variations of secondary osteons' size from white-tailed deer proximal humeri as a tool to predict compressive vs. tensile loading

MEIR M. BARAK¹ and JACK NGUYEN²

¹College of Veterinary Medicine, Department of Veterinary Biomedical Sciences, Long Island University, ²Department of Biology, Winthrop University

A fundamental question related to human evolution is when hominins became bipeds and what was the locomotor behavior of humans and chimpanzees' last common ancestor. Previous research demonstrated that external and internal bone morphology can serve as a source of functional information. The aim of this study was to find whether the size and morphology of secondary osteons, the product of intracortical remodeling, can differentiate between cortical bone regions loaded in compression vs. tension. To this end, we used cross-sections from the proximal diaphysis of seven white tailed deer humeri, a bone that is loaded in bending, as a test case. In each cross-section we quantified the extent of intracortical remodeling and secondary osteon, and central canal size and morphology (circularity). Altogether, 865 and 604 osteons were analyzed in the cranial (loaded in tension) and caudal (loaded in compression) cortices respectively. Our results revealed that except for small periosteal and endosteal areas that contained primary bone tissue, both the cranial and caudal cortices were fully remodeled. While secondary osteon and central canal circularity did not differ significantly between cortices, both were significantly smaller in the caudal (compressive) cortex. Secondary osteonal area was 8,233 μm^2 and 14,106 μm^2 , and central canal area was 354 μm^2 and 454 μm^2 in the caudal and cranial cortices respectively. These results demonstrate that intracortical remodeling in the compressive cortex forms significantly smaller secondary osteons and central canals, a fact that may help us to infer the locomotion behavior of extinct species.

Study was supported by grants from the National Center for Research Resources and the National Institute of General Medical Sciences from the National Institutes of Health.

Genetic relationships and linguistic diversity in present-day populations of South America

CHIARA BARBIERI^{1,2}, RODRIGO BARQUERA³, LEONARDO ARIAS⁴, JOSÉ R. SANDOVAL⁵, OSCAR ACOSTA⁵, CAMILO ZURITA^{6,7}, ABRAHAM AGUILAR-CAMPOS⁸, ANA M. TITO-ÁLVAREZ⁹, RICARDO SERRANO-OSUNA⁹, RUSSELL D. GRAY², FABRIZIO MAFESSONI⁴, PAUL HEGGARTY², KENTARO K. SHIMIZU¹, RICARDO FUJITA⁵, MARK STONEKING⁴, IRINA PUGACH⁴ and LARS FEHREN-SCHMITZ^{10,11}

¹Department of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland, ²Department of Linguistic and Cultural

ABSTRACTS

Evolution, Max Planck Institute for the Science of Human History, Jena, Germany, ³Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Jena, Germany, ⁴Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, ⁵Centro de Investigación de Genética y Biología Molecular (CIGBM), Universidad de San Martín de Porres, Lima, Peru, ⁶Cátedra de Inmunología, Facultad de Medicina, Universidad Central del Ecuador, Quito, Ecuador, ⁷Unidad de Investigaciones en Biomedicina, Zurita&Zurita Laboratorios, Quito, Ecuador, ⁸Clinical Laboratory, Unidad Médica de Alta Especialidad (UMAE) # 2, Instituto Mexicano del Seguro Social (IMSS), Ciudad Obregón, Sonora, Mexico, ⁹Carrera de Enfermería, Facultad de Ciencias de la Salud, Universidad de Las Américas, Quito, Ecuador, ¹⁰UCSC Paleogenomics, Department of Anthropology, University of California, Santa Cruz, USA, ¹¹Genomics Institute, University of California, Santa Cruz, USA

Studies of Native South American genetic diversity have been crucial to elucidating early migrations and broad continental structure. In recent years, high-throughput genomic data and denser sampling coverage have provided new opportunities to disentangle complex historical scenarios, also at a regional scale. Here, we analyze the genetic structure of populations living in western South America, with a focus on their linguistic histories, by generating Y chromosome and autosomal data (Affymetrix Human Origins SNP array). We search for connections between the Andes, home to expansive complex societies and to Quechua – a widely spoken indigenous language family – and Amazonia, with its understudied population structure, scattered language family distribution and rich cultural diversity. Our results compare the ancient genetic structure of the region against more recent layers of haplotype exchange. A contrasting pattern emerges between the two kinds of data analyzed: in the paternal line, we describe a north-south divide between Quechua speakers, while in the autosomal data we detect recent demographic connections between the two groups, and across the Andes-Amazonia divide. Long-distance genetic connections between speakers of Tupí languages (a widespread Amazonian family) suggest that here too, indigenous languages were spread not by cultural contact alone. This parallel between genetic and linguistic history highlights how language acts as a preferential tracer of population mobility within and across ecogeographic domains.

Wenner-Gren postdoctoral grant (Gr. 9395), University Research Priority Program of Evolution in Action of the University of Zurich.

Human brain evolution and language development: gene expression variation between human brain language structures and their homologues in chimpanzees

NICOLE L. BARGER¹, JILLIAN WEBBER¹, AUSTIN K. BEHEL¹, WILLIAM D. HOPKINS², BRENDA J. BRADLEY¹ and CHET C. SHERWOOD¹

¹Anthropology, The George Washington University, ²Comparative Medicine, University of Texas, MD Anderson Cancer Center

Language is central to human social and cultural behavior. Although this behavioral specialization is subserved by evolutionary modification of brain circuits, its molecular correlates in the language cortices of the ventral frontal (VFC) and superior temporal (STC) cortex are poorly understood. However, these structures are not functionally discrete and participate in additional networks, e.g., STC participates in the social brain circuit. We hypothesized that VFC and STC would share a large set of differentially expressed (DE) genes characterized by increased expression in human brains and distinct from the social brain network. EdgeR was used to identify DE genes from RNAseq data comparing human brain language regions (VFC, STC) and social brain structures (STC, orbital FC, medial FC, and amygdala) with their homologues in chimpanzees (5 humans and 5 chimpanzees; FC>1 or <-1; FDR p<0.05). Contrary to our hypothesis, compared to other regions, STC and VFC contained more genes expressed lower (LE) in humans, although STC contained the second largest number of genes expressed higher (HE). Of the 1306 and 1049 DE genes in the STC and VFC, respectively, these regions shared 48 LE but only 17 HE genes, while most DE genes overlapped across all regions analyzed (258 HE; 145 LE). These data suggest that canonical brain language regions may be characterized by coordinated downregulation of gene expression in human evolution. Increases in regulatory mechanisms like noncoding RNAs or DNA methylation could drive this variation, especially given the prolonged period of human juvenile development and social nature of language acquisition.

This research is supported by NSF INSPIRE grant (SMA-1542848).

Faunal turnover at Mille-Logya (Plio-Pleistocene, Ethiopia) reflects in situ environmental change: implications for the origins of *Homo*

W. ANDREW BARR¹, DENIS GERAADS², DENNÉ REED³, RENÉ BOBE^{4,5,6}, JONATHAN WYNN⁷ and ZERESEYEN ALEMSEGED⁸

¹Department of Anthropology, Center for the Advanced Study of Human Paleobiology, George Washington University, ²CR2P, Sorbonne Universités, MNHN, CNRS, UPMC, ³Department of Anthropology, University of Texas at Austin, ⁴Primate Models for Behavioural Evolution Lab, Institute of Cognitive & Evolutionary

Anthropology, School of Anthropology, University of Oxford, ⁵Gorongosa National Park, Mozambique, ⁶Interdisciplinary Center for Archaeology and Evolution of Human Behavior (ICArEHB), Universidade do Algarve, ⁷Division of Earth Sciences, National Science Foundation, ⁸Department of Organismal Biology and Anatomy, University of Chicago

The lower Awash Valley of Ethiopia preserves a significant record of *Australopithecus afarensis* at Hadar and Dikika in addition to the earliest fossil yet attributed to *Homo* from Ledi-Geraru at 2.8 Ma. However, understanding the context of the extinction of *A. afarensis* and the origin of *Homo* is hampered by the limited preservation of sediments between 2.9 – 2.3 Ma in the region. The Mille-Logya Project (MLP) preserves fossiliferous sediments post-dating 2.9 Ma. Here we present a quantitative analysis of the MLP mammalian fauna and explore implications of MLP faunal change for the origin of *Homo*.

We collected and identified vertebrate fossils from each of three MLP time-successive fossil zones: Gafura (NISP=218), the Seraitu Lake beds (NISP=1100), and Uraitele (NISP=410). We computed Sørensen dissimilarity indices at genus-level for each pairwise zonal comparison. The younger faunal zones (Seraitu and Uraitele) are more similar to one another (Sørensen = 0.31) than either is to the older Gafura zone (Gafura-Seraitu Sørensen = 0.4, Gafura-Uraitele Sørensen = 0.44). A correspondence analysis of faunal abundances revealed that Gafura is compositionally more similar to the Hadar Formation faunas (especially the Denen Dora Member), while Seraitu and Uraitele are distinct from the Hadar Formation faunas in having high abundances of open-habitat alcelaphin and antilopin bovids.

Quantitative analysis of the newly collected MLP fauna provides evidence for an in situ faunal turnover consistent with an environmental shift towards more open habitats, which is broadly temporally coincident with the first evidence for genus *Homo* in the Afar.

Funding to conduct fieldwork was provided by Margaret and Will Hearst.

Innovations, social learning and traditions in white-faced capuchins: experimental and observational approaches

BRENDAN J. BARRETT^{1,2} and SUSAN E. PERRY^{3,4}

¹Cognitive and Cultural Ecology Group, Max Planck Institute of Animal Behavior, ²Department of Human Behavior, Ecology and Culture, Max Planck Institute for Evolutionary Anthropology, ³Department of Anthropology, University of California, Los Angeles, ⁴Center for Behavior, Evolution, and Culture, University of California, Los Angeles

We show how longitudinal research increases our understanding of innovation and cultural transmission. Using observational and experimental

ABSTRACTS

data collected since 1990 at Lomas Barbudal Biological Reserve, Costa Rica, we show how individual differences and behavioral context affect innovation rates, social learning strategies, and cultural change in white-faced capuchin monkeys, *C. capucinus*. Using a 72,710-hr observational data set and hierarchical mixture models, we illustrate how age and sociality predict individual-level innovation rates across behavioral domains. We experimentally examine what social learning strategies capuchins used to learn to open *Sterculia* fruits. Naïve individuals were exposed to knowledgeable tutors who differed in 7 processing techniques varying in efficacy. Using experience-weighted attraction models, we found that individuals exhibited a payoff-biased learning strategy and were likely to copy techniques of older individuals (but unlikely to copy the techniques of maternal kin). In a 10-year study of 248 individuals, we used EWA models to examine if social learning of *Sloanea* processing changes with age: Individuals primarily copied older tutors, but males were more likely to copy age-mates. Reliance on social information decreased within an individual's lifetime, and social learning strategies employed also changed. In a longitudinal observational study of 21 females, engaged in an easier foraging task in which the two options were equally profitable, young females preferentially used the mother's technique. These studies taken together, suggest that, younger capuchins are more likely to seek and incorporate social information about foraging tasks, and to do so from older individuals.

Funding: MPI-EVAN, UCLA; grants: NSF (1638428, 0613226, 848360), NGS (7968-06, 8671-09, 20113909, 9795-15; GRF #1650042), TWCF (0208), Leakey Foundation (20152777, 20112644, 20082262, 20060592), Wenner-Gren, ASP, ARCS Foundation.

The Diet and the Menu: Temporal and Regional Variation in Human Paleodiet in the Prehistoric San Francisco Bay Area

ERIC J. BARTELINK¹ and MELANIE M. BEASLEY²

¹Anthropology, California State University, Chico,

²Anthropology, Purdue University

The late Holocene hunter-gatherer societies of the San Francisco Bay Area of central California consumed a wide range of protein resources, including high trophic level marine fish, anadromous fish, marine mammals, terrestrial herbivores, and shellfish. In addition, wild plant resources were key dietary staples, especially acorns, small seeds, and root foods. Stable isotope analysis on 134 burials from the Bay Area has revealed significant regional and temporal variation in human paleodiets (4000-200 BP). In the northeastern Bay Area (n=35), mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values are $-15.1 \pm 1.7\text{‰}$ and $14.1 \pm 2.9\text{‰}$, respectively, reflecting the dietary importance of high trophic-level marine resources. In comparison, mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values for the

southeastern Bay Area (n=20) are $-18.1 \pm 0.9\text{‰}$ and $9.6 \pm 1.2\text{‰}$, indicating a greater dietary contribution from terrestrial C_3 resources. In the south Bay Area (n=79), mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values are even lower, at $-19.3 \pm 0.9\text{‰}$ and $7.8 \pm 1.2\text{‰}$, respectively. These values reflect the dietary importance of C_3 plant resources, and suggest very little input from marine or terrestrial fauna. $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ are significantly different between regions ($p < .001$, Kruskal-Wallis), reflecting latitudinal differences in the relative importance of marine versus terrestrial foods among different bayshore communities. A significant decrease through time in $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values ($p < .001$, Kruskal-Wallis) reflects greater intensification of terrestrial resources from C_3 ecosystems, including low-ranked plant resources such as acorns and small seeds. The data provide support for Late Holocene resource intensification models posited for prehistoric central California.

Funding for this research was provided in part by the National Science Foundation (No. 0424292).

Build-A-Calculus: Experimental dietary research on *in vitro* dental calculus

BJØRN PEARE BARTHOLDY, FEMKE H. REIDSMAN and AMANDA G. HENRY

Faculty of Archaeology, Leiden University

This study presents a model calculus system, which will allow experimental research to be conducted on *in vitro* dental calculus. We grow oral multispecies biofilms on plastic pegs, which are inoculated with whole saliva and suspended in artificial saliva for 25 days. The mineral composition of the *in vitro* calculus was verified using FTIR spectroscopy and archaeological and modern reference calculus.

The biofilms were submerged in solutions (0.5% w/v) containing wheat and potato starches twice daily for six minutes. Over the course of the experiment the biofilms were exposed to a large quantity of wheat (ca. 45.43×10^6) and potato (ca. 3.583×10^6) starch grains, of which only a minor proportion was visible, microscopically, in the calculus (0.0021% and 0.0018%, respectively). The proportion of small (<20 μm) grains recovered from the calculus for both wheat (0.0034%) and potato (0.0032%), was greater than for large (>20 μm) grains (0.0003% and 0.0007%, respectively). These results suggest that only a minor portion of an individual's diet is retained in the dental calculus and that there is a size bias in the incorporation of starches, such that larger grains may be underrepresented.

This model calculus system can provide the framework to perform controlled experiments addressing fundamental questions and issues concerning dental calculus, which have yet to be

explored. These include validation of sampling and extraction methods, the incorporation of dietary and other markers into the calculus matrix, and the effects of taphonomy.

This project was funded by the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation program [grant number STG-677576 ("HARVEST")].

What can we learn from the study of macroscopic and microscopic dental wear during childhood?

MARLON BAS^{1,2}, FABIAN KANZ² and KATHARINA REBAY-SALISBURY¹

¹Institute for Oriental and European Archaeology, Austrian Academy of Sciences, ²Unit of Forensic Anthropology, Medical University of Vienna

The dental system is subject to many physiological and morphological changes throughout childhood. Processes occurring in the oral environment begin to affect the teeth as soon as they erupt. Some of these processes are collectively referred to as dental wear, a complex chemo-tribological system that modifies first the microscopic surface of teeth, and then over time as more matter is removed, its entire macroscopic morphology. Decades of research have demonstrated that the physical properties of food and its preparation influence how these processes act upon teeth during mastication resulting in differences in tooth wear. Children in industrialized societies today can in fact be distinguished from most other children in the history of our species by their very slow rates of dental wear. Despite this, there have been few studies into the formation of dental wear throughout childhood in non-industrialized societies, its influence on the development of the dental system, and the information it may contain about children's diet and environment.

Here, we discuss why it is interesting to study dental wear during childhood, and what information relevant to childhood development and diet is contained in both macroscopic dental wear and the microscopic enamel surface. To illustrate we present an analysis of macroscopic and microscopic dental wear in 84 Bronze Age and 92 Medieval individuals from lower Austria. Significant differences in enamel microscopic texture (anisotropy) and occlusal surface curvature are detected between samples. We demonstrate how specific aspects of culture and technology are reflected in childhood dental wear.

The project 'The value of mothers to society: responses to motherhood and child rearing practices in prehistoric Europe' has received funding from the European Research Council (grant agreement No 676828).

ABSTRACTS

The evolution of the human torso: 3D geometric morphometrics of thorax-pelvis integration and their applications to body shape reconstruction

MARKUS BASTIR and NICOLE TORRES-TAMAYO
Paleobiology, Museo Nacional de Ciencias Naturales CSIC

The skeletal torso is a complex structure of outstanding importance to understand the evolution of human body shape, and its reconstruction allows us to approach the body plan of extinct hominin species. In the last years, 3D geometric morphometric (3DGM) techniques of sliding semilandmarks have been increasingly used and have improved considerably the estimation of missing data. Among the 3DGM approaches, Two-blocks Partial Least Squares analysis has shown a great potential for predicting missing elements by exploiting the covariation between two structures. The aim of this work is to predict the thorax morphology of the Kebara 2 Neandertal (Israel, ~60ka) from different pelvis reconstructions based on thoraco-pelvic covariation models of N=64 living *H. sapiens*. Preliminary results show a Kebara 2 thorax prediction with a wider lower ribcage than upper ribcage, as well as an invaginated thoracic spine. This prediction is very similar to a manual virtual thorax reconstruction made by other authors, with two minor differences: Kebara 2 thorax prediction is more symmetrical and seems to have a slightly more kyphotic thoracic spine than the published manual reconstruction. Despite these differences, when we projected several Kebara 2 reconstructions in PC1-PC2-PC3 subspace they all fell very close to each other, confirming the similarities between these morphologies. The method proposed here aims to complement other techniques through the calculation of a mathematical model that works as a 'scaffold' to articulate the individual fossil elements. Thus, this work extends the potential of missing data estimation beyond the methods proposed in reference works.

This research is funded by CGL-2015-63648-P (Ministry of Economy, Industry and Competitiveness, Spain).

Examining Bone Collagen and Carbonate Stable Isotope Ratio Homogeneity via Different Homogenization Methods

CHELSEA BATCHELDER¹, SAMMANTHA HOLDER¹, THOMAS MADDOX², LAURIE J. REITSEMA¹, TOSHA DUPRAS³ and RIMANTAS JANKAUSKAS⁴

¹Department of Anthropology, University of Georgia, ²Center for Applied Isotope Studies, University of Georgia, ³Department of Anthropology, University of Central Florida, ⁴Department of Anatomy, Histology, and Anthropology, Vilnius University

As the sensitivity of isotope ratio mass spectrometers (IRMS) increases and smaller amounts of sample are required for analysis, the need for homogenous samples increases. Here we

compare bone collagen and carbonate sample replicate homogeneity prepared by mortar and pestle with and without liquid nitrogen, glass rod, and nothing. We compared stable isotope ratio variance and mean among preparation methods of collagen replicates from a single individual, which were analyzed on an EA-IRMS (n=12). Carbonate from a second individual was analyzed on a Gas Bench-IRMS with preconcentration (Precon, n=12) and Gas Bench-IRMS (n=6). There were no significant differences in carbon or nitrogen isotope ratio variance (p=0.28 and p=0.38), but there were significant differences in carbon and nitrogen isotope ratio means (p=5.25e-5 and p=6.68e-4) for EA-IRMS. There were no significant differences in carbon variance for Precon or Gas Bench-IRMS (p=0.24 and p=0.28), but there were significant differences in carbon ratio means (p=8.57e-8 and p=1.25e-4). There were significant differences in stable oxygen isotope ratio variance for Precon and Gas Bench-IRMS (p=2.2e-16 and p=6.22e-10). Although there were significant differences in mean carbon and nitrogen ratios for all IRMS in this study, these differences fall within the range of error for the machine and may not be caused by preparation method. Differences in oxygen isotope ratio variance indicate that replicates where nothing was done were not homogenous. These results suggest that any method of homogenization is sufficient for isotopic analysis of bone.

Preliminary analysis of wild ruffed lemur (*Varecia variegata*) vocalizations in Ranomafana National Park, Madagascar

CARLY H. BATISTI^{1,2}, MENDRIKA N. RAZAFINDRABE³, FRANCOIS RANDRIAMANANTENA⁴ and ANDREA L. BADEN^{1,2,5}
¹Department of Anthropology, CUNY Graduate Center, ²New York Consortium in Evolutionary Primatology, New York, NY, ³Department of Animal Biology, University of Antananarivo, ⁴Centre ValBio, Ranomafana, Madagascar, ⁵Department of Anthropology, CUNY Hunter College

With recent advances in acoustic technology and software, bioacousticians now have a toolkit with which to study acoustic structure, function, and variation. Black-and-white ruffed lemurs (*Varecia variegata*) routinely exhibit distinct, contagious roar-shriek choruses, one of the ~12 calls in their vocal repertoire. Surprisingly however, there are only four published studies on *Varecia* vocalizations, the majority of which were conducted in captivity in the 1980s. We conducted a preliminary study of *Varecia* vocal communication in 38 individuals from May-August 2019 at Mangevo, Ranomafana National Park, Madagascar. We recorded ~1200 calls representing 11 call types, including two only given by males during mating (*squeal*, *quack*). There were significant differences in the frequency of call types; this ranged from the *wail* (every 52hrs) to the *hum* (every 18min). *Wails*,

barks, and *roar-shrieks* were only given by groups, whereas >90% of *mus*, *hums*, *chatters* and *growls* were given by single individuals. Females emitted significantly more *hums* than males, while males emitted more *mus*. *Roar-shrieks* (mean=14.07s) and *quacks* (mean=12s) were the longest calls and *growls* (mean=1.29s) and *mus* (mean=1.69s) were the shortest. *Chatters* were given mostly in aggressive contexts, *hums* in travel contexts, and *pulsed-grunts* following *roar-shrieks* (though not always). While our results are largely descriptive, these fundamental variables have never been published. With further quantitative analyses, we can assess if there are acoustic signatures of individual, sex, etc. in any of the calls, as well as infer function based on behaviors prior to and following different call types.

Funding generously provided by the CUNY Graduate Center (GC) Provost's Digital Innovations Grant & CUNY GC Provost's Pre-dissertation Research Fellowship

Early 20th century polio mortality among non-Māori in New Zealand reflects flattened SES gradient

HEATHER T. BATTLES

Anthropology, School of Social Sciences, University of Auckland

New Zealand in the late 19th and early 20th centuries had a reputation as a 'working man's paradise' for Pākehā (non-Māori, settlers), with extensive social mixing, low industrialization, relatively low population densities, and high home ownership rates. However, some degree of social gradient remained. The traditional polio model depicts a positive relationship between the disease and socioeconomic status (SES), with higher SES associated with exposure to the poliovirus beyond infancy/early childhood and consequent higher mortality rates. The research question addressed here is whether New Zealand's SES gradient was strong enough, and linked closely enough to living conditions (and thus differential virus exposure), to produce differential polio mortality.

This study uses occupation data from the New Zealand Census and non-Māori death registrations for the polio epidemics of 1916, 1924–25, and 1936–37. Polio deaths were classified by father's occupation using the Caversham Project scheme, which includes nine collapsible urban occupational strata and codes rural occupations separately. Non-parametric tests showed limited evidence of either differential mortality or differences in age at death among collapsed urban strata. For 1916 only, the rural group had a higher proportion of deaths ($X^2(1, n = 95) = 8.341, p = .0039, \Phi = .30$) and higher age at death (Mann-Whitney $U = 828.00, p = .026, r = -0.23$), indicating that rural Pākehā were more isolated

ABSTRACTS

from poliovirus infection prior to 1916 but faced similar risk afterwards. These results suggest that polio mortality reflected the flatter SES gradient of Pākehā New Zealand society.

This research was funded by a 2016-2018 New Staff Faculty Research Development Fund (FRDF) grant from the University of Auckland Faculty of Arts.

Biomechanical Correlates of Mandibular Premolar Root Variation in Robust and Gracile Australopithecines

SARAH E. BAUMGARTEN, SHUBHAM TAYAL and DAVID S. STRAIT

Anthropology, Washington University in St. Louis

Mandibular premolar root morphology in early hominins displays a wide range of variation, and it has been proposed that root form in primates is functionally related to diet and feeding mechanics. This project uses finite element analysis to test whether differences in premolar root morphology in two hominin species thought to differ in diet are associated with stress differences in the enamel cap, root, and periodontal ligament. Finite element models (FEMs) were constructed from microCT scans of mandibular second premolars of one *Paranthropus robustus* and one *Australopithecus africanus*. The periodontal ligament (PDL) was modeled as a solid volume between the surfaces of the root and alveolus, and was capped below the tooth cervix. The crown, root and ligament were assigned the appropriate material properties of enamel, dentin and PDL. The models were constrained along the surface of the alveolus and each subjected to a vertical bite force. The magnitude of the force in the *A. africanus* FEM was estimated as the maximum force capable of being produced by that species. The force applied to the *P. robustus* model was equal to the *A. africanus* force scaled to the two-thirds power of model volume, ensuring that any stress differences between the two models reflected differences in shape but not size. Resulting stresses in the roots of the models differed in magnitude but not distribution. Additionally, root area had a substantial effect on stresses in the PDL, suggesting that variation in root morphology may be constrained by PDL mechanics.

Multimodal communication in captive bonobos (*Pan paniscus*)

KATIE E. BEACHEM

Integrative & Evolutionary Biology, University of Southern California

Multimodal communication signals occur when one signaling method is produced, simultaneously or sequentially, with a different signaling modality. Humans use multimodal communication across languages and thus it is seen as a possible basis for language. It is hypothesized that multimodal communication is produced to facilitate the

transfer of complex signals or to clarify an incorrectly received signal. Bonobos (*Pan paniscus*) are closely related to humans and provide an analog for examining the emergence of multimodal communication. This study assessed bonobo multimodal communication to test the following predictions: that multimodal signals would be used less often than unimodal communication, that the rate of multimodal signaling increased with group size, and that bonobos would employ multimodal signals more when communicating with humans rather than conspecifics. To test these predictions, quasi-randomized all-occurrence focal observations were collected on captive bonobos during June-August 2018. Focal follows were conducted daily on the colony of 5 animals at the Ape Cognition and Conservation Initiative (ACCI) in Des Moines, Iowa. A total of 1,086 communication signals were collected. In support of the first prediction, 844 signals were produced unimodally with multimodal signals occurring less frequently or 242 times. Group size did not influence the rate of multimodal signals. Of the multimodal signals produced, 73% were directed toward humans while 26.8% were toward conspecifics ($p < 2.2e-16$). I propose that bonobo multimodal signaling may help clarify communication across species but require a higher cognitive and energetic output resulting in a preference of unimodal signals when communicating within species.

Funded through the department of Graduate Studies & the Human Biology department at the University of Southern California.

You are what you eat, but are humans too complicated for dietary mixing models?: A critique of human paleodiet reconstructions

MELANIE M. BEASLEY

Department of Anthropology, Purdue University

Stable carbon and nitrogen isotopes are used to determine relative contributions of protein resources from the paleo-menu consumed in past human diets. In ecological research, methods of interpretation have changed over the years from graphical methods (simple bivariate plots) to geometric procedures of three food sources to linear mixing models to Bayesian mixing models, which provide probability distributions for the proportional contribution of each food resource to a consumer's diet. These models were developed on non-human species. Humans are complicated. Cultural practices for processing food resources, such as cooking, fermentation, and entomophagy are an added behavioral layer of complexity to account for in dietary mixing models. Recent research on $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ meat values due to cooking, 1.8‰ and 3.5‰, respectively (Royer et al, AJPA. 2017;163:759-771) and $\delta^{15}\text{N}$ values from fermentation of muscle tissue with associated maggots, 4.5‰ and 35.8‰, respectively

(Beasley et al AJPA. 2019;168(S68):14) indicate food processing practices need to be considered in mixing models. This paper adds new data of $\delta^{13}\text{C}$ values from fermentation of muscle tissue ($n = 225$) with associated maggots ($n = 304$), 3.3‰ and 5.4‰, respectively, to critique the use of dietary mixing models for human paleodiet reconstructions. Considering isotope values of bone collagen represent average protein consumption during bone growth, approximately a decade of life depending on the bone, are human paleomenus and associated food processing practices too complex to yield meaningful interpretive value from mixing model methods applied to understanding protein food resources in the past? I argue, yes.

Species Identification Provides Information on Trade of Bear Paws in Chinese Diaspora Communities of the 19th Century

KRISTINE G. BEATY^{1,2}, BRITTANY BINGHAM^{1,2}, MARY FAITH FLORES^{1,2,3}, CARA MONROE^{1,2}, J. RYAN KENNEDY³ and BRIAN M. KEMP^{1,2}

¹Department of Anthropology, University of Oklahoma, ²Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, ³Department of Anthropology, University of New Orleans

By the late 1800s, 400,000 Chinese immigrants came to the American West Coast in response to the promise of a land with abundant resources and opportunity. The large influx of immigrants led to the development of large-scale trade networks, not only within North America, but also connecting the communities to resources from China. These networks provided access to goods such as bear paws commonly used in Chinese feasting and medicinal practices. Archaeological excavations routinely uncover bear paw remains in Chinese diaspora sites, but it is unclear from where these specimens originated. Here, aDNA techniques are used to identify the species of bear paw remains and determine whether trade networks or local sources were utilized by Chinese immigrant communities. Eighteen bear paw samples were obtained from the 19th century sites in California ($n=11$) and Oregon ($n=7$). Mitochondrial DNA was amplified and included a short region containing a 16 bp deletion that differentiates brown (*Ursus arctos*) and black bears (*U. americana*). Thirteen (~72%) of the samples amplified and indicated different sources were utilized depending on available resources. Paws from brown bears were most common in Market Street in California and were either imported from the northern part of the continent or harvested from the few brown bears still found nearby until the early 1920s. Black bear paws were represented in the Oregon sites and

ABSTRACTS

were probably locally harvested. These results show that aDNA methods can be used to better understand how early migrant communities obtained resources.

Early hominin brain evolution: what can fossil endocasts tell us?

AMELIE BEAUDET

School of Geography, Archaeology and Environmental Studies, University of the Witwatersrand

Because of its crucial role in the organism-environment interactions, the brain represents a key-element for understanding human evolution. Despite substantial developments in paleogenetics and crucial discoveries in paleo-anthropology, a number of questions about the mode and the chronology of the emergence of developmental, structural and functional traits in the human brain remain to be resolved. The endocast represents the only direct evidence of the cerebral condition in fossil hominins. In this context, a number of methodological barriers limit our understanding of the evolution of brain shape and organization in the hominin lineage. Here we develop a comprehensive approach that integrates extant human variation and fossil evidence from the well-preserved southern African early hominin record, as well as newly developed methods in imaging techniques (e.g., surface-based comparisons, automatic recognition of neocortical features), for providing new insights into the evolutionary history of the human brain. By quantifying the degree of similarities between the brain and the endocast and mapping the variation pattern in extant humans, we demonstrate that the frontal and temporal areas of the endocast could be considered as reliable proxies for the corresponding cerebral regions. Moreover, our study of the fossil record reveals that the overall shape and organization of the endocasts of Plio-Pleistocene *Australopithecus* (e.g., StW 573, Sts 5, MH 1) were closer to extant chimpanzees than to extant humans. Future investigations of the poorly known *Paranthropus* and early *Homo* cerebral condition would be of particular interest for assessing and contextualizing the emergence of the derived human-like neuroanatomical features.

Funding support provided by Claude Leon Foundation, CoE in Palaeosciences, IFAS, NRF, PAST. I thank the CHPC for access to the supercomputing center.

Life at the crossroads: Isotopic investigations of diet and mobility in late prehistoric Transylvania

JESS BECK¹, HORIA I. CIUGUDEAN², COLIN P. QUINN³, CLAES UHNÉR⁴, CHRISTOPHER F. PARE⁵, GABRIEL BĂLAN², RALUCA BURLACU-TIMOFTE² and TAMSIN C. O'CONNELL⁶

¹McDonald Institute for Archaeological Research, University of Cambridge, ²Department of

Archaeology and Conservation, Muzeul Național al Unirii, Alba Iulia, ³Anthropology Department, Hamilton College, ⁴Römisch-Germanische Kommission, Deutschen Archäologischen Instituts, ⁵Institut für Vor- und Frühgeschichte, Johannes Gutenberg-Universität Mainz, ⁶Department of Archaeology, University of Cambridge

The Apuseni Mountains of southwestern Transylvania, Romania, are home to a wide range of resources, including salt, tin, and some of the richest copper and gold deposits in Europe. The mountains are abutted by the Mureș River, which served as thoroughfare for the movement of goods and people throughout prehistory. During the Bronze Age this region thus acted as a significant cultural economic, and political crossroads due to the unique confluence of trade, traffic, and transportation that it made possible. While the area is home to a rich late prehistoric archaeological record, the biocultural backdrop of the region is poorly understood. This analysis presents the first major isotopic study of diet and mobility in the Apuseni region, including the results of over 60 analyses of carbon and nitrogen from bone collagen (approximately half faunal and half human) and 22 analyses of carbon and oxygen from human tooth enamel carbonate. The human samples encompass a number of key contexts frequently used in archaeological comparisons, including the mountains and the lowlands, cemeteries and settlements, and the Early and Late Bronze Age. Our results show no statistically significant differences between human carbon and nitrogen values for the uplands and the lowlands. However, our data do reveal significant increases in human $\delta^{13}\text{C}$ values over time when comparing the Early Bronze Age and Late Bronze–Early Iron Age, and well as significant differences in human $\delta^{15}\text{N}$ values between individuals buried in cemeteries and individuals buried in settlements.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie grant agreement No 746216.

She Knows Her Stuff: Modern and Ancient Expert Craftswomen in the Andes

SARA K. BECKER

Anthropology, University of California, Riverside

This research investigates skeletal evidence of labor (i.e., osteoarthritis and muscle enthesal changes), as performed by 525 females within the precontact Tiwanaku civilization (AD 500-1100) of the Bolivian and Peruvian Andes, and compares these laborers to those performed by their modern-day indigenous Aymara descendants who live in the same region and perform many traditional tasks (i.e., non-mechanized farming, carrying goods on the back over varying elevations, weaving, pottery production). Using ethnographic evidence from 21 interviews and 3D computer-aided video motion capture (mocap) of

traditional activities, data from these women were compared to prior published skeletal evidence of Tiwanaku tasks (Becker 2013, 2017, 2019). Results show that many of the tools used in prehistory, such as a sharpened and smoothed llama bone, are the same as those used over a thousand years ago during Tiwanaku times, and that intense labors, such as farming or craft production begins in pre-teen years in both the past and present. Specific enthesal comparisons also show a “chopping” motion females from prehistoric pastoralist communities perform that can be correlated to drop spindle weaving or weaving using mocap data. Osteoarthritis comparisons were not necessarily directly correlated between the modern and skeletal group. However, almost all individuals interviewed complained of back pain associated with repetitive tasks and this can be compared to skeletal evidence of lumbar osteophyte formation linked to both tasks and advancing age. Overall, focusing on laborers from the past and present can answer question about gendered labor and the importance of indigenous expert knowledge.

Funding for this research was provided by the National Science Foundation, the Hellman Foundation, and National Geographic.

Preliminary analysis of the nutritional composition of black-and-white ruffed lemur (*Varecia variegata*) diet in Ranomafana National Park, southeastern Madagascar

NINA BEEBY^{1,2,3}, JESSICA M. ROTHMAN^{1,2,3} and ANDREA L. BADEN^{1,2,3}

¹Anthropology, The Graduate Center, CUNY,

²Anthropology, Hunter College, CUNY, ³New York Consortium in Evolutionary Primatology, (NYCEP)

Characterizing primate nutrition is key to understanding the selective forces driving species' foraging strategies and ultimately how individuals are able to persist in their environment. Here, we present preliminary results describing the macronutrient contents of foods consumed by one community (n=30 individuals) of black-and-white ruffed lemurs (*Varecia variegata*) in Ranomafana National Park, Madagascar across six consecutive months of observation. We determine whether the fruits and leaves, which show considerable temporal variation in dietary proportions consumed, differ significantly in their macronutrient contents. Results reveal that animals dedicated 26% of their daily activity budget to feeding, during which time they consumed 89 different plant taxa (21 fruit, 19 leaf, two flower, and two leaf petiole). Of these, we analyzed 44 plant samples representing 41 consumed plant taxa which comprised 87% of the population's total feeding time. Subjects consumed foods that contained 2-20% crude protein (CP), 20-89% neutral detergent fiber (NDF), 10-75% acid detergent fiber (ADF), 2-37% acid detergent lignin

ABSTRACTS

(ADL), and 1-23% fats, calculated on a dry matter basis. The moisture content varied from 7% to 55%. Leaves had higher CP than fruits ($p=0.01$), yet fibers did not differ significantly (NDF: $p=0.29$, ADF: $p=0.33$, ADL: $p=0.19$). Fats did not vary significantly ($p=0.08$), suggesting fat intake is unlikely to be limited during the fruit-lean season. These data allow us to further characterize the diet of *V. variegata* and help to explain how resource availability and nutritional goals interact to constrain behavioral strategies.

Funding provided by Hunter College.

The "Hoo-Haa effect": An unfortunate name for a dramatic effect in female reproduction

JACINTA C. BEEHNER^{1,2}, ALICE BANIEL⁴, JACOB A. FEDER⁵, THORE J. BERGMAN^{2,3} and AMY LU⁴

¹Anthropology, University of Michigan, ²Psychology, University of Michigan, ³Ecology and Evolutionary Biology, University of Michigan, ⁴Anthropology, Stony Brook University, ⁵Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University

In 1978, Thelma Rowell discovered that novel males could stimulate immediate mating activity in female patas monkeys. Later, a report on hamadryas baboons observed that new males caused adolescent females to mature early, pregnant females to abort, and lactating females to resume fertility; each phenomenon accompanied by sexual swellings. Here, we summarize 13 years of data demonstrating all three phenomena in wild geladas (*Theropithecus gelada*) in Ethiopia, and we examine whether such responses provide fitness benefits for females. Geladas live in family units where dominant "leader" males sire nearly all offspring in the unit. Leader males are replaced every 3 years; and following takeovers, infants are at risk of infanticide. We found that immature females that experienced a takeover ($N=31$), matured earlier than those that did not ($N=49$; $p=0.01$). Moreover, earlier maturation predicted earlier first birth and first successfully weaned infant ($N=60$; $p<0.001$). Next, we confirm with new data that females abort pregnancies after takeovers. Finally, we found that lactating females that experienced a takeover ($N=86$) resumed cycling earlier than those that did not ($N=135$; 14 vs. 17.5 mos; $p<0.001$). Because these females did not conceive earlier ($N=55$ vs. $N=100$; 30.9 mos vs. 30.4 mos), we call these "deceptive" cycles. Deceptive cycles did lead to higher infant survival ($p<0.001$), however, these females also had the oldest infants. To unite these phenomena, Rowell

coined the term, "the Hoo-Haa effect". Although we will not resurrect this particular term, we propose that these phenomena share a similar mechanism and deserve further study.

Funding: The National Science Foundation (BCS-0715179, BCS-0824592, BCS-1723228, IOS-1255974, IOS-1854359); Leakey Foundation (multiple awards), National Geographic Society (Gr. #8100-06, Grant #8989-11; Grant #NGS-50409R-18), Fulbright, University of Michigan, Stony Brook University

50 years of fossil catarrhines from Rudabánya: sympatry and social organization

DAVID R. BEGUN

Department of Anthropology, University of Toronto

Between 1967 and 2017, 299 specimens have been catalogued into the primate collection from the late Miocene site complex of Rudabánya (Hungary.) 172 catalogued specimens are attributable to *Anapithecus*. These include both isolated teeth and associated dentitions, totaling 355 teeth, the largest pliopithecoid sample. 94 specimens are attributable to *Rudapithecus*. At R. II, the richest locality, *Anapithecus* is represented by at least 24 individuals and *Rudapithecus* by a minimum of 13. *Rudapithecus* is characterized by high size and canine sexual dimorphism, while *Anapithecus* has low molar size dimorphism (a proxy for body size) and large canine dimorphism. Both taxa are co-mingled within layers, providing the best evidence of sympatry between a hominid and a pliopithecoid. R.II *Rudapithecus* includes 8 adults (4 males and 4 females), 1 subadult male, 3 juveniles and 1 infant. R.II *Anapithecus* includes 12 adult females, 3 adult males and 8 infant/juveniles. The taphonomy of R.II resembles a catastrophic assemblage and low transport distance, suggesting that the distribution of sex/age categories in each taxon is roughly representative. *Anapithecus* and *Rudapithecus* are represented by dramatically different age/sex distributions, which is unexpected by chance. With equal representation of males, females and non-adults, *Rudapithecus* resembles a chimpanzee mixed-sex party and may represent the earliest evidence of this type of social organization in the hominine fossil record.

How Do Non-Primate Competitors Affect the Potential Distribution of Frugivorous Primates?

RACHEL B. BELL¹, KAYE E. REED⁴, JOHN ROWAN¹, LYDIA BEAUDROT³ and JASON M. KAMILAR^{1,2}

¹Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst, ²Department of Anthropology, University of Massachusetts Amherst, ³Department of BioSciences, Program in Ecology and Evolutionary Biology, Rice University, ⁴Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University

Global analyses of primate communities have found that modern climate and evolutionary history shape community structure. Interspecific competition among primates and with non-primate mammals may be an additional important factor to consider, though we have little knowledge of this potential effect. Competition with non-primate mammals may be particularly important in shaping frugivorous primate distributions due to the spatially and temporally patchy nature of fruiting resources. Our study comprehensively tests how non-primate competitors influence the predicted distributions of frugivorous primates by using a species distribution modeling approach in mainland Africa and Madagascar. We hypothesize that frugivorous non-primate mammals and primates will limit each other's distributions via competitive exclusion. We test this hypothesis by comparing abiotic and biotic species distribution models for 29 sub-Saharan African and 19 Malagasy primate species in MaxEnt. Biotic models incorporate potential competitor ranges as well as the environmental and climatic variables used in the abiotic models. We predict that the biotic models will produce more limited distributions compared to abiotic models by incorporating competitive exclusionary forces. We find that non-mammal competitors are more important predictors and limiting factors of mainland African primate distributions than of Malagasy lemur distributions. This suggests that non-primate competitors are not as important in shaping lemur distributions compared to primates in other broad geographic regions. The results of this study reflect the complexities of how interspecific interactions shape species distributions, as well as the influence of historical biogeography on community structure.

This research was funded by the National Science Foundation (NSF SBE Awards 1551799 and 1551810).

Effects of between group competition on cooperation and oxytocin in capuchins

MARCELA E. BENITEZ^{1,2} and SARAH F. BROSAN^{1,2,3}

¹Psychology, Georgia State University, ²Language Research Center, Georgia State University, ³Neuroscience Institute, Georgia State University

Parochial altruism, ingroup favoritism and outgroup hostility, is an important factor in promoting cooperation and prosocial behavior in humans. Numerous studies have shown that we are more cooperative with group members, even at a cost to ourselves, when competing against an outgroup, suggesting that cooperation and intergroup conflict may have coevolved. If parochial altruism is an important factor in the evolution of cooperation, other cooperative primates should, like humans, increase cooperation in the face of between-group conflict. Here, we examined whether socially-housed capuchin (*Sapajus apella*) monkeys cooperated more

ABSTRACTS

often when competing against another social group and the underlying hormonal mechanism that may promote increased cooperation during conflict. Using a tug-of-war based barpull apparatus, we found that capuchins were more likely to cooperate for inequitable, but not equitable, food rewards in the presence of between-group competition. Furthermore, a preliminary analysis (n=23 samples) suggests that urinary oxytocin was higher after competing with another group (M=124.28 pg/mg) compared to the no competition control (M=21.95 pg/mg) but only, again, when outcomes were inequitable. These results mirror studies in humans, supporting the hypothesis that both parochial altruism and the biological underpinnings of these behaviors are evolutionarily conserved in the primate taxa.

This research was funded by the GSU Brains & Behavior Seed Grant and the National Science Foundation (SBE 1919305)

Navigating identity politics in genomics research: a case study of Afro-descendants in Puerto Rico

JADA BENN TORRES

Department of Anthropology, Vanderbilt University, Vanderbilt Genetics Institute, Vanderbilt University

Within human population genetics, the concept of population is fundamental to addressing questions about the nature and dynamics of human genetic variation. Though typically defined as a geographically restricted (potentially) interbreeding group to the exclusion of other groups, the concept of population in reference to humans is multifaceted when accounting for historical factors that also shape mate choice. Defining a population is further complicated by identity politics, that is, social and political contexts that influence how people identify themselves as a member of a group or community. In groups that have experienced long-term social, economic, and political marginalization, identity and identity politics become especially critical in genomics work that aims to address questions about the roles that social structures have in shaping genetic variation.

In this paper I draw from my more recent fieldwork experience in collecting genetic samples from African-descended Puerto Ricans for a project designed to address questions about intra- and inter-island diversity and genetic ancestry. Because Puerto Ricans generally adhere to a national narrative proclaiming a 'tri-cultural heritage', that is descent from Native American, African, and European peoples, the ways in which people identify, or not, becomes a political statement in itself. By sharing the challenges that I have faced in deciding who to recruit and who ultimately enrolled in my study, I show that

intersubjectivity on questions of identity between the researcher and participants are fundamental to defining a population and the eventual success of this type of genomic work.

This research was funded with a grant from the Office of Equity, Diversity, and Inclusion at Vanderbilt University.

The application of GIS to three-dimensional scans of the auricular surface of the ilium to create a new age estimation method using the Hamann-Todd Osteological Collection

KRISTA E. BENNETT

Geography and Anthropology, Louisiana State University

The ability to accurately estimate age at death for adult skeletons has been the focus of bioarchaeologists and forensic anthropologists for decades. Most age estimation methods for adult remains provide age categories that are often too narrow, too broad, or too vague. The goal of this project was to combine 3D scans with GIS tools to produce physical morphology maps of the auricular surface in order to produce quantifiable characteristics for age assessment leading to narrower age ranges.

A NextEngine™ HD Desktop 3D scanner was used to scan the auricular surface of 200 os coxae from the Hamann-Todd Collection. ScanStudio HD Pro™ software was used to process the scans and produce xyz coordinate points. ESRI ArcMap™ software v. 10.6.1 was used to create digital elevation models and raster data for analysis. Three features were selected for mapping in ArcMap: exostosis on the retroauricular area, changes to the apical area, and porosity on the auricular surface. Samples were divided into seven groups by 10-year age increments (20-29, 30-39...70-79, 80+) and analyzed using analysis of variance (ANOVA). The ANOVA tests did not result in statistically significant p values between age groups and the three variables of interest.

Although the results for this method were not statistically significant, the study demonstrates the ability to use 3D scans in ArcMap to evaluate the morphological variations observed on the auricular surface. These findings suggest further testing with higher resolution scanners may capture more detail producing characteristics that can be quantified for age assessment.

This research was funded in part by a Robert C. West Graduate Student Field Research Award from the Department of Geography and Anthropology at Louisiana State University.

History of health in the Chinese Bronze Age: Results from five seasons of the Mogou bioarchaeology project

ELIZABETH BERGER¹, JENNA DITTMAR², IVY HUI-YUAN YE³, RUILIN MAO⁴, HUI WANG⁵ and GUOKE CHEN⁴

¹Anthropology, University of California, Riverside, ²McDonald Institute for Archaeological Research, University of Cambridge, ³School of Humanities, Nanyang Technological University, ⁴Archaeology, Gansu Provincial Institute of Cultural Relics and Archaeology, ⁵Research Center for Scientific Archaeology, Fudan University

From 2015-2019, the international team of the Mogou Bioarchaeology Project has collaborated with the Gansu Provincial Institute of Cultural Relics and Archaeology to examine the human remains from the large Bronze Age cemetery of Mogou (1750-1100 BCE), excavated between 2008 and 2012. The collection includes over 5000 sets of human remains of all age classes. The team has examined around 750 individuals for age, sex, postcranial metrics, oral health, and paleopathological lesions. The work is ongoing, but has so far revealed trends in health and demography that are suggestive of the interaction between social, environmental, behavioral, and biological factors. For instance, the prevalence of nonspecific indicators of physiological stress (41.6% of individuals with CO/PH, 43.1% of individuals with dental enamel hypoplasias, 47.1% of individuals with new bone formation on the appendicular skeleton) are higher than those at other published sites in the region. The population also seem to have experienced a notably high prevalence of interpersonal violence (11.4% of adults). The cemetery has also yielded individuals with lesions suggestive of a range of specific infectious, metabolic, and congenital illnesses (e.g. tuberculosis, scurvy, DISH, ankylosing spondylitis, carcinomas). This paper reviews the team's findings so far and their significance for our understanding of Bronze Age Northwest China.

NAP Start-Up Grant, Nanyang Technological University; Chinese National Social Science Grant (18ZDA225); Esherick-Ye Family Foundation; AAPA Cobb; Association for Asian Studies; Banco Santander, University of Cambridge; LRCCS University of Michigan

Demographics of 19th century Italian psychiatric patients: A review of the Siena Craniological Collection

JACQUELINE M. BERGER

Department of Anthropology, University of South Florida

Interest in archaeological study addressing historic institutional contexts has steadily increased, addressing the treatment of marginalized populations and the frequent collection of their remains in the furtherance of early anatomical study. Some of these analyses have specifically examined institutions for the treatment of the mentally

ABSTRACTS

ill, and how asylum demographics may differ from the general population. In general, a majority of studies concerning asylums have focused on contexts in English-speaking countries. The current study examined the Siena Craniological Collection (SCC) from Siena, Italy, specifically the patients of the *L'Ospedale Psichiatrico S. Niccolò* (San Niccolò Psychiatric Hospital - SNPH), as identified by the diagnoses listed in the collection *registri* (catalogs). The study analyzed the sex distribution of 200 patients from the SNPH, and compared these results to the 1861 census of the Province of Siena, to determine if there was any association between sex and status as a psychiatric patient. Chi-square analysis ($\alpha = 0.05$) found no significant difference ($\chi^2 = 1.613$, $df = 1$, $p = 0.204$) in sex distribution between the sample of SNPH patients and the general population of the Province of Siena in 1861. Additionally, age and primary psychiatric diagnoses, including potential sex-based differences, were examined. Based on these findings, sex was not a factor contributing to higher rates of hospitalization for a particular group, although there are more males than females in the asylum assemblage. Further investigation of the demography of SNPH patients is required to understand how various groups may have been marginalized through institutionalization.

Genomics of adaptation, convergence, and evolutionary conservation in haplorrhine primates

CHRISTINA M. BERGEY¹, AMBER E. TRUJILLO^{2,3}, TODD R. DISOTELL^{2,3}, ANTHONY J. TOSI⁴ and ANDREW S. BURRELL^{2,3}

¹Department of Genetics, Rutgers University,

²Center for the Study of Human Origins, Department of Anthropology, New York University,

³New York Consortium in Evolutionary Primatology,

⁴Department of Anthropology, Kent State University

A taxonomically diverse dataset of whole genome sequences allows comparative insight into adaptation, including positive and negative selection and parallel evolution. We have assembled the most taxonomically comprehensive genomic dataset of primates to date by sequencing over a dozen anthropoid genomes (including *Alouatta*, *Cebuella*, *Chiropotes*, *Leontopithecus*, *Pithecia*, *Saimiri*, *Sapajus*, *Trachypithecus*, *Nasalis*, *Presbytis*, *Semnopithecus*, *Lophocebus*, and *Mandrillus*) and aligning these and other available primate genomes. Using this dataset, we identify signatures of positive and negative selection on coding regions, as well as genomic regions of evolutionary conservation across primate lineages. The genome-wide dataset allows us to test hypotheses informed by primate behavior, ecology, and morphology using classes of genes united by functional annotation. For instance, of the 3,333 transcripts of genes in the human genome known to be associated with malaria,

an average of 2,286 were recovered for the newly produced genomes. We analyze the ratio of nonsynonymous to synonymous changes with a branch-site test for episodic diversification, identifying, for example, signatures of positive selection on genes implicated in malaria resistance in humans and mice. Conversely, we also identify signatures of evolutionary conservation, such as a variant in the Afro-papionins that is otherwise conserved in all other vertebrates surveyed, suggesting functional importance. As the variant is near the gene encoding bone morphogenetic protein 2 (*BMP2*), it warrants further study for its potential effect on skeletal development in the Afro-papionins. Our results illustrate the power of taxonomically dense genomic datasets for insight into primate evolution.

Funded by the National Science Foundation (BCS1640500 and BCS1717188)

How did mandibular morphology evolve in *H. sapiens*? A geometric morphometrics approach to the role of allometry during the emergence of our species

INGA BERGMANN, JEAN-JACQUES HUBLIN, PHILIPP GUNZ and SARAH E. FREIDLIN

Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Our study explores the morphological evolution of human mandibles during the last 300,000 years in order to discuss the taxonomic position of key specimens from the African Middle Pleistocene as well as the Levantine and Chinese early Late Pleistocene. These early *H. sapiens* are from the sites of Jebel Irhoud, Tabun, Border Cave, Klasies River Mouth, Skhul, Témara, Qafzeh, Dar-es-Soltane, El Harhoura and Zhirendong. While their faces show clear *H. sapiens* affinities, the mandibles display a mosaic morphology. Additionally, their generally large size could relate to archaic shape features. We use (semi)landmark geometric morphometrics methods to quantify mandibular shape among early *H. sapiens* ($n=13$), Upper Paleolithic *H. sapiens* ($n=87$), Holocene humans ($n=38$) and Neanderthals ($n=27$). We visualize allometric patterns for all groups and for the pooled sample, to explore how gracilization trends affect the expression of shape features.

Early *H. sapiens* variably possess derived traits unique to the taxon, including a lateral position of the mandibular notch crest, an antero-posteriorly decreasing corpus height and a chin. The retro-molar space is mostly absent. We identified a continuous shape and size trend within *H. sapiens* beginning in the Upper Paleolithic, associated with the gracilization of the mandible. Even though all groups possess a distinct allometric pattern, size always affects chin morphology, ramus width, corpus length and the degree of prognathism/

orthognathism. Accordingly, many so-called "archaic" features displayed by early *H. sapiens* and Neanderthals can be attributed to their large size.

Adaptation and human adaptability and its implications for the peopling of the Americas: a Big Data approach

DANILO V. BERNARDO^{1,2} and TATIANA F. DE ALMEIDA^{3,4}

¹Laboratório de Estudos em Antropologia Biológica, Bioarqueologia e Evolução Humana, Universidade Federal do Rio Grande, ²Programa de Pós-Graduação em Antropologia, Universidade Federal de Pelotas, ³Hospital Israelita Albert Einstein, ⁴Eretz.bio - Incubadora de Startups, Instituto Israelita de Ensino e Pesquisa

The contributions of Bioarchaeology as a discipline fundamentally based on an investigation of the biocultural interactions of past populations are crucial to understanding the occupation of the New World, allowing the proposition of models discussing origin, dispersion, and chronologies of Native Americans. In this context, the amount and diversity of data are enormous and results sometimes seems to be conflicting for different areas. Mathematical approaches once used to understand each of these areas are opening space to different strategies to analyze all data together and deliver one history for all disciplines. In the era of Big Data Bioarchaeology can make sense of genetics, morphology and other human marks and fill the gaps left by one or other discipline. From many times genetics were considered as the most trustable source of information regarding human evolution, but other areas, such as cranial morphology, are proving to be just as insightful. Here we present a study based on a Big Data approach to evaluate the biological affinities of New World autochthonous populations by means their craniometric measurements (taken in accordance with Howells' protocol) and genetic variation data. The populational structure of these affinities, were exploited by a series of tests of correspondence considering environmental and archaeological information, as a proxy of biocultural and adaptability constraints, for prediction of the best dispersion scenario of settlement of Americas. Our results suggest that a very complex scenario, with multiple possibilities may be considered as the more likelihood explanation for the origins of human in Americas.

A Partial Cremation from the Later Stone Age of Northern Malawi

ALEX BERTACCHI¹, JESSICA CEREZO-ROMÁN², JESSICA C. THOMPSON¹, JAY STOCK³, DOUGLAS KENNETT⁴, FLORA SCHILT⁵ and ELIZABETH GOMANI-CHINDEBVU⁶

¹Department of Anthropology, Yale University,

²Department of Anthropology, University of

Oklahoma, ³Department of Anthropology,

ABSTRACTS

Western University, ⁴Department of Anthropology, University of California, Santa Barbara, ⁵Institute of Archaeological Sciences, University of Tübingen, ⁶Malawi Department of Museums and Monuments, Ministry of Youth, Sports, and Culture

Later Stone Age (LSA) hunter-gatherer mortuary practices in sub-Saharan Africa do not include documented cremations. Here, we report the first evidence of intentional burning in an LSA mortuary context from the site of Hora 1, Northern Malawi. In 2017-2018, the Malawi Ancient Lifeways and Peoples Project recovered a fragmentary subfossil adult female skeleton consisting mainly of limb elements, clustered towards the center of a 20-30cm consolidated ash feature. Macro- and microscopic observations show that the feature, dated to 9540-9450 calBP (Uga-30618, OxCal 4.3) represents an *in situ* burning event. The individual fits within the range of phenotypic variation found among LSA hunter-gatherers from South Africa. Visual inspection of the bones revealed that 51% had some carbonization and 35% had some calcination, but only 2% were fully calcined. FTIR of four calcined specimens show incomplete heat-induced recrystallization, with one specimen evidencing surficial transformation. Bone breakage patterns are typical of direct heating of a fleshed body in an open fire, and cut marks indicate perimortem defleshing of long bones. Comparison with faunal remains show different depositional and thermal histories for the human and nonhuman assemblages. These data indicate intentional burning but incomplete cremation of the individual, potentially preceded by defleshing. This was followed by collection of remains into the center of the ash and removal of larger elements such as the skull. Four additional interments at the site – two infants and two adults – are unburnt and nearly complete, showing that this treatment was not typical of the time and region.

The fieldwork and laboratory analysis were funded by Emory University and the Wenner-Gren Foundation for Anthropological Research (Grant #9437).

The curious case of the fabella, an increasing common knee sesamoid bone

MICHAEL A. BERTHAUME^{1,2}, ERICA DI FEDERICO³ and ANTHONY M.J. BULL²

¹Division of Mechanical Engineering and Design, London South Bank University, ²Department of Bioengineering, Imperial College London, ³School of engineering and Material Science, Queen Mary University of London

The fabella is a sesamoid bone located in the tendon of the gastrocnemius behind the lateral femoral condyle. The fabella is ubiquitous in cercopithecines, present in lesser apes, absent from great apes, and present in humans. Here, we report on fabella prevalence in a Korean population (n = 106 individuals, CT scans) and perform a systematic review and meta-analysis to 1) examine human biological variation in

fabella prevalence rates and 2) the role of genetic and environmental factors in fabella development. Fabellae were present in 52.83/44.34% of our individuals/knees. No sexual dimorphism was detected in our sample, nor was fabella presence correlated to height or age. Interestingly, a Bayesian mixed effects linear model revealed fabella prevalence rates are ~3.5 times higher in 2000 than 100 years before, while prevalence rates for 10 other sesamoids in the hands and feet have remained constant. We hypothesize this is due to global increase in nutrition and body size. Our meta-analysis (n = 66 studies, 21,626 knees, studies from 1875-2019) revealed that, today, fabellae are ~2.5% more common in men than women, increasingly common with age, and there is antisymmetry within unilateral (one fabella/individual) cases, supporting the role of environment in fabella development. Conversely, the higher percentage of bilateral cases (one fabella/knee, 72.94%) and global, regional variation in prevalence rates support the role of genetics in fabella development. Taken together, we hypothesize the ability to form a fabella may be genetically controlled, but the mechanisms that trigger fabella ossification may be environmentally controlled.

This research was commissioned by the National Institute for Health Research using Official Development Assistance (ODA) funding.

From cementum microstructure to population structure. Reflection on the value of cementochronology for construction of age-at-death profiles

BENOIT BERTRAND^{1,2}, VADIM MESLI¹, ANNE BÉCART¹, SOPHIE VATTEONI^{1,3}, MARTINE VERCAUTEREN⁴, VALÉRY HÉDOUIN¹ and DIDIER GOSSET¹

¹EA 7367 UTML - Unité de Taphonomie Médico-Légale, Univ. Lille, CHU Lille, France, ²UMR 7194 HNHP - Musée de l'Homme, Muséum national d'Histoire naturelle, Paris, France, ³Direction de l'Archéologie, Douaisis-Aggl., ⁴Anthropology and Human Genetics, Univ. Libre de Bruxelles, Belgium

Accuracy and reliability of the methods for obtaining mortality data at individual level are central concerns in critiques of palaeodemography. Age estimation using dental cementum deposits is assumed to be the closest attribute to a chronometric measure of age-at-death. This assertion has generated interest in the applicability of cementochronology to assess mortality profiles. Recent advances demonstrated that cementochronology is a two-tier performance technique with lower accuracy for subjects over 60 and a precision that differs between age groups. Taking advantage of the correlation between chronological age and cementum annuli on a reference collection [$r=0.93$; $p=0.000$; $n=200$], we calculated matrix of age group frequencies for ten-annuli and five-annuli intervals. Following the *Age Length Key* method, we computed the age

distribution of a sample of a post-medieval population [$n=100$] and performed similar approach based on cranial suture closure. Results show the characteristic flattening of age distribution based on cranial suture while distribution based on cementum diverges and does not mimic the distribution of the reference sample. This absence of "age mimicry" can be attributed to the correlation between annuli intervals and age that is higher than for conventional indicators used in palaeodemography. Furthermore, the distribution resulting from the *probability vector method* applied to cementum differs from profiles computed from usual cementochronological estimates where elderly individuals are strongly underrepresented. Interestingly, age classes with higher precision and accuracy yield peaks suggesting that cementochronology could be a victim of its own performance for some age categories.

Variation in human eccrine sweat gland density and its relationship to heat dissipation

ANDREW W. BEST¹, DANIEL E. LIEBERMAN² and JASON M. KAMILAR^{1,3}

¹Department of Anthropology, University of Massachusetts, ²Department of Human Evolutionary Biology, Harvard University, ³Organismic and Evolutionary Biology, University of Massachusetts

Humans' capacity to cool by sweating far surpasses that of other primates and mammals and is linked with hallmark events in human evolution including expanded foraging and locomotor behavior, near-naked skin, and bigger brains, all of which depended upon increased ability to dissipate heat. Despite the significance of this trait to the human genus, the evolution of human sweat gland density and contemporary variation in gland density are poorly understood, as are its physiological implications. Here, we use a lab-based approach to quantify active sweat gland density and heat dissipation capacity. In particular, we used pilocarpine and iontophoresis to stimulate sweat glands in six body regions for 16 people. We used a whole room metabolic chamber to measure sweat volume during moderately strenuous exercise of eight people. Gland densities range from 63- 147/cm², with higher densities in the arms, torso and back than the legs, and high interindividual variation. We found that individuals native to warm climates produce less sweat in response to pilocarpine than temperate natives, and heat-trained endurance athletes sweat more than sedentary volunteers. In addition, we found that active gland density correlated with body surface area. Our results provide an initial insight into modern human sweat gland diversity and the evolution of this unique human trait.

Funded by the Leakey Foundation and the University of Massachusetts Amherst.

ABSTRACTS

An osteobiographical model of care: Case study of Carrier Mills, IL Individual 194

KALEIGH C. BEST¹, JESSICA R. SPENCER^{1,2}, KEVIN N. CABRERA^{1,2} and ALECIA SCHRENK³

¹Anthropology, Southern Illinois University, ²Center for Archaeological Investigations, Southern Illinois University, ³Anthropology, University of Nevada, Las Vegas

The prehistoric Midwest site of Carrier Mills (8000-2500 BP) provides a unique opportunity to examine the everyday life of individuals in a hunter-gatherer society with high levels of non-lethal violence, chronic illness, and increasing levels of disease. Individual 194, a 30-45-year-old late Middle Archaic male, exhibits an extensive amount of pathology and healed trauma combined with a chronic treponemal infection, which would have resulted in increasing levels of impairment throughout the course of his life. Individual 194 has a dislocated right hip, immobilized left elbow due to inflammation and bone growth, crushed and fused lower spine, destructive lesions to the cervical vertebrae and fractures to several ribs, right wrist, and nasal bones. There is also general periostitis present throughout the remains, the presence of treponemal disease, dental pathologies, and an osteoblastic reaction on the right humerus. The presence of cloacae and degree of bone formation suggests he survived for some time after the life-altering event(s). However, he would have had several impairments which would have limited his physical activities and he would have required help with many of his daily activities. This presentation constructs a general model of care for Individual 194's injuries using the Bioarchaeology of Care methodology. The results indicate that the healthcare provisioning provided by family or members of his community would have required extensive time and resources, which would have had an overall effect on the community. How individual 194's identity may have changed in the community and the potential community response is discussed.

Temporal Comparisons of Survivorship and Frailty in Late Prehistoric East Tennessee

TRACY K. BETSINGER¹, MARIA O. SMITH² and SHARON N. DEWITTE³

¹Anthropology, SUNY Oneonta, ²Anthropology, Illinois State University, ³Anthropology, University of South Carolina

The Late Mississippian period (AD 1300-1600) in East Tennessee was characterized by permanent aggregated settlements of intensive maize agriculturalists. There are two distinct cultural phases: the Dallas phase (AD 1300-1550), which is ubiquitous in the region, and the Mouse Creek phase (AD 1400-1600) in the Chickamagua Reservoir. Dallas sites have evidence of social status differences, while the Mouse Creek sites have less social differentiation. These disparities

along with differences in settlement organization and physiography may be reflected in distinct health patterns. Previous research assessing treponemal disease and general health indicators have found differences both within the Dallas phase and between the two phases. This study examines patterns of survivorship within and between the two phases. We hypothesize that at Dallas sites, higher status individuals will have better survivorship than lower status individuals, and that the Mouse Creek phase will have higher survivorship than the Dallas phase. To test these hypotheses, demographic data from eight Dallas sites (n=1586) and three Mouse Creek sites (n=719) were assessed for 1) all individuals, 2) just adult males, and 3) just adult females using Kaplan Meier survival analysis. Results indicate greater survivorship among higher status individuals at Dallas sites and that female survivorship declines from the Dallas Phase to the Mouse Creek phase, a pattern that is not found among males or the entire sample. These results suggest that social status/role, settlement organization, and physiographic differences play significant roles in morbidity and mortality.

Differential diagnosis of external auditory meatus atresia and scalp avulsion at the Fallen Tree site at St. Catherines Island, Georgia, USA

BARBARA J. BETZ¹, REBECCA MAYUS¹, KATHRYN E. MARKLEIN² and CLARK S. LARSEN¹

¹Anthropology, The Ohio State University, ²Anthropology, University of Louisville

Diagnosis of paleopathological processes in archaeological skeletal remains is often complicated due to the generalized nature of bone response to many diseases. A case study from the early contact-era St. Catherines Island Fallen Tree site (16th century CE) demonstrates the need for bioarchaeologists to consult clinical literature and incorporate expertise in human physiology and soft-tissue anatomy to improve diagnoses of pathological conditions within specific biocultural and archaeological contexts. The etiologies of two cranial pathological conditions found on the skeleton of an adult female individual were differentially diagnosed through examination of historical and current medical literature. The left temporal displays congenital atresia (absence) of the external auditory meatus. The individual would have experienced hearing impairment throughout life. Although microtia of the auricle was also possible, skeletal evidence is insufficient to determine the size or morphology of the outer ear. Additionally, a crescent-shaped lesion present on the external table of the frontal and parietal bones is accompanied by abnormal endocranial pitting consistent with documented cases of historical and industrial scalp avulsion. The extent of bone response suggests that the individual lived for a period of more than a month following injury

and experienced immune reactivity, likely due to infection, prior to death. Differential diagnosis of external auditory atresia and survived scalp avulsion illustrates the importance of incorporating clinical literature into bioarchaeological interpretations of pathological conditions to improve understanding of possible physical and social consequences experienced by individuals in the past.

This research was supported by the St. Catherines Island Foundation.

Great Ape Cerebral Organoids Recapitulate Evolved Differences in Gene Expression Observed in Primary Brain Samples

APARNA BHADURI¹, MOHAMMED A. MOSTAJO RADJI¹, MATTHEW SCHMITZ¹, MADELINE ANDREWS¹, TOMASZ J. NOWAKOWSKI¹, OLIVIA MEYERSON¹, SAINATH MAMDE¹, ELIZABETH DI LULLO¹, BEATRIZ ALVARADO¹, MELANIE BEDOLLI¹, TYLER D. FAIR¹, IAN T. FIDDES³, ZEV KRONENBERG², MARINA BERSHTEYN¹, EVAN E. EICHLER², ARNOLD KRIEGSTEIN¹, BRYAN J. PAVOLVIC¹ and ALEX A. POLLEN¹

¹Neurology, UCSF, ²Genome Sciences, University of Washington, ³Genomics Institute, UCSC

Primate brains vary dramatically in size and organization, but the genetic and developmental basis for these differences has been difficult to study due to lack of experimental models. Pluripotent stem cells and brain organoids provide a potential opportunity for comparative and functional studies of evolutionary differences, particularly during the early stages of neurogenesis. We hypothesized that human and chimpanzee brain organoids would preserve key features of gene expression observed during normal brain development and could reveal evolved changes in gene expression. We found that brain organoids preserve the majority of gene co-expression relationships observed in primary tissue, but also identified several differences related to elevated metabolic stress in organoid models. We next compared gene expression divergence observed between species using *in vitro* models with species differences observed in developing human and macaque cortex. We found that brain organoid models, but not non-neural cell types, recapitulated a significant proportion of species differences in gene expression. Our results suggest that great ape organoid models can be used to identify tissue-specific gene expression changes that evolved along the human lineage. Ultimately, great ape organoid models could be applied beyond studies of progenitor cell evolution to decode the origin of recent changes in cellular organization, connectivity patterns, myelination, synaptic activity, and physiology that have been implicated in human cognition.

ABSTRACTS

A theoretical mechanobiological perspective on shear stress as an osteogenic stimulus

HENNA D. BHRAMDAT and DAVID J. DAEGLING
Anthropology, University of Florida

Functional and mechanical interpretations of bone morphology posit a role for stress distributions experienced in growing skeletal elements and determination of their cross-sectional geometry. The potential role of shear stresses as signals for bone apposition during ontogeny, however, has been generally overlooked, partially due to the emphasis on beam models for retrodicting stress histories.

Assuming magnitude of torsional loads are roughly proportional to body size throughout growth, we utilize the formula for a twisted thin tube to characterize stress distributions during growth from initial geometries of asymmetric and symmetric ellipses. Growth is based on *Macaca nemestrina* females, with theoretical apposition rates (not exceeding those observed in vivo) calculated weekly for 10 years (German et al. AJPA 1994). Bone growth is determined from separate algorithms in which osteogenic activity responds to 1) local stress magnitudes proportionally and with respect to safety factor thresholds, 2) an invariant attractor stress magnitude, and 3) stress gradients, with steeper gradients inducing greater apposition. These three aspects of the stress environment have each been hypothesized to constitute the primary osteogenic signal in the skeletal mechanics literature.

In this model, stress gradients perform inadequately when compared to attractor and local stress stimuli, in that ultimate stress is exceeded before the end of model runs. Initial geometry influenced the relative efficiency of growth, in that mature cross-sections of initially asymmetric bones are notably thinner and achieve higher safety factors in the presence of shear stress compared to initially more symmetrical bones experiencing similar osteogenic parameters.

Supported by NSF BCS-1440532

Could woodworking have driven lithic tool selection?

REBECCA E. BIERMANN GÜRBÜZ and STEPHEN J. LYCETT

Department of Anthropology, University at Buffalo, SUNY

Understanding early stone tool technologies and their function, especially how this relates to form, is imperative to understanding the early archaeological record and the behavioral evolution of stone-tool-producing hominins. Stone flakes have potentially been used since at least 3.3 million years ago (mya), which may represent a key step in hominin evolution. Flake function, and its relationship to morphology, has long been

examined, almost exclusively for meat acquisition tasks. However, archaeological evidence for woodworking dates to at least 1.5 mya, at Peninj, Tanzania and Koobi Fora, Kenya. Furthermore, *Pan troglodytes* have been observed using sharpened sticks to hunt, thereby adding a phylogenetic argument to ancient woodworking. Nonetheless, woodworking has only been rarely examined in relation Paleolithic tool use. Here, we experimentally investigated stone flake cutting efficiency, as measured by time, during woodworking tasks and how this relates to flake size. Specifically, two groups of 15 participants each used simple (chert) flakes to remove a defined area (1 x 6 cm) from wooden shims. One group used "small" flakes (40-59 mm length) and another group used "large" flakes (70-109 mm length). The group using larger flakes was significantly (Mann-Whitney $U=51$, $p=0.01$) more efficient (took less time) for the woodworking task. Our results demonstrate that larger flakes could have been preferentially chosen by hominins for woodworking, consistent with previous data generated experimentally in other (non-woodworking) tasks.

Genomic adaptation to high altitude in the Andes

ABIGAIL W. BIGHAM¹, AINASH CHILDEBAYEVA², JULIEN WEINSTEIN³, MELISA KIYAMU⁴, GIANPIETRO ELÁAS⁵, MARIA RIVERA-CHIRA⁴, FABIOLA LEON-VALERDE⁴, FRANK S. LEE⁶ and TOM D. BRUTSAERT⁵

¹Anthropology, UCLA, ²Archaeogenetics, Max Planck Institute for Science of Human History, ³Anthropology, University of Michigan, ⁴Ciencias Biológicas y Fisiológicas, Universidad Peruana Cayetano Heredia, ⁵Exercise Science, Syracuse University, ⁶Pathology and Laboratory Medicine, University of Pennsylvania Perelman School of Medicine

Approximately 11,000 years ago, humans colonized the Andean Altiplano boasting an average height of 12,000 feet. Genome-wide scans for natural selection nominated *Egl-9 homologue 1* (*EGLN1*), whose protein product regulates the cellular response to hypoxia, as a robust candidate gene for high-altitude adaptation among Andeans. Subsequent work identified five genetic markers near *EGLN1* that were associated with higher aerobic capacity (VO_2max) in hypoxia among Peruvian Quechua. This finding supported the hypothesis that natural selection increased the frequency of an *EGLN1* causal variant that enhanced Quechua O_2 delivery or use during exercise at altitude. Nonetheless, the causative variant(s) contributing to Andean adaptation has not been identified. To do so, we rigorously characterized *EGLN1* sequence variation in the Andean population by performing next generation DNA sequencing for 48 Peruvian Quechua residents of high altitude and 48 Mexican Maya residents of low altitude. Evidence for natural selection was assessed using standard statistical

methods including LSBL, Tajima's *D*, and iHS. Next, SNPs with compelling evidence of functional importance were evaluated for significant associations with altitude-adaptive phenotypes using our full Andean Quechua cohort whose constituents allow us to control for the developmental effects high-altitude exposure. Finally, we measured *EGLN1* mRNA levels in a subset of 100 participants to determine if *EGLN1* SNP genotypes were associated with changes in *EGLN1* expression. By integrating evolutionary and functional approaches in the study of human adaptation to high altitude, this research provides critical insight into the molecular mechanisms governing functional, adaptive change.

This project was funded by the National Science Foundation, the Leakey Foundation

Allee effects in nomadic foragers

REBECCA BIRD

Anthropology, Pennsylvania State University

Throughout human evolutionary history, drastic population losses have accompanied dramatic shifts in climate. While models of habitat selection have typically been employed to predict settlement and mobility decisions under conditions when climate change reduces resource availability, they have typically not considered the demographic implications of living at low population density. Here, we draw on a unique record of Aboriginal responses to population losses in the late contact-era of Australia. In the context of reduced population density, ideal free distribution models predict landscape use should contract to the most productive habitats, and people should avoid areas that show more signs of extensive prior use. However, ecological or social facilitation due to Allee effects would predict that the intensity of habitat use should correlate positively with the presence of others. We analyzed recent fire footprints and fire mosaics from the accumulation of several years of landscape use that were visible on aerial photographs imaged between May and July 1953. Structural equation modeling revealed that, consistent with an Allee IFD, there was a positive relationship between the extent of fire mosaics, and the intensity of recent use, and this was consistent across habitats regardless of their quality. Our results suggest that even under conditions of low population density, when many high quality habitats are empty, people still aggregate in large social groups and are drawn back to persistent places on the landscape. We conclude that Allee effects may complicate simple predictions of habitat choice, especially under a demographic squeeze.

This research was supported by NSF grant SBR#1459880.

ABSTRACTS

A modern take on ancient goat herding: comparing the sustainable grazing practices of today to the biochemical results of Greek husbandry in antiquity

KATHERINE G. BISHOP¹, SANDRA GARVIE-LOK¹, MARGRIET HAAGSMA² and SOPHIA KARAPANOU³

¹Anthropology, University of Alberta, ²History and Classics, University of Alberta, ³Ephorate of Antiquities, Diachronic Museum in Larissa

Bioarchaeologists are showing an increased interest in animal-based studies to interpret how humans lived in the past. Stable isotope analysis of animal teeth has become an important tool for assessing how humans managed animals by providing insight into their diet and mobility. Ethnographic observations of modern shepherding practices also provide key insight into how humans interact with their animals and how animals behave in different environments. We present an ethnoarchaeological approach that combines observations of modern goat herders with the stable isotope values recorded from ancient Greek goat teeth. A sample of four goat third molars was collected from two sites in Thessaly, Greece dating to the Hellenistic (323 – 30 BCE) period. Intra-tooth isotope variation was measured from microsampled dental enamel to examine diet (carbon, $\delta^{13}\text{C}$), seasonality (oxygen $\delta^{18}\text{O}$), and mobility (strontium, $^{87}\text{Sr}/^{86}\text{Sr}$) of ancient goats. The resulting isotope values indicated management styles that varied according to available water and foraging source, mobility, and season. While working with a modern goat herder in Edmonton (Alberta) in 2019, the first author observed how modern shepherding strategies are strongly shaped by the dietary needs, digestive physiology, and behaviours of goats, and the landscape and resources available to the herd. These sentiments are also evident in ethnographic studies of modern Greek shepherds and ancient literary sources. Throughout our study we record commonalities in behaviours, actions, and decisions of goat herders across time and space. Ultimately we use an ethnoarchaeological approach to understanding goat herding today and thousands of years ago.

Funding was provided by the Social Sciences and Humanities Research Council of Canada, the Killam Trusts, various sources at the University of Alberta, and the Canadian Association of Physical Anthropology.

boneMachine: An R Package for Rotation and Analysis of Computed Tomography Scans and Other Three-Dimensional Data

AARON D. BLACKWELL¹ and AMY S. ANDERSON²

¹Anthropology, Washington State University, Pullman, WA, ²Anthropology, University of California, Santa Barbara, CA

The scoring and analysis of skeletal material and bone images from medical imaging is frequently done via manual, visual scoring. However, large datasets require standardized and automated

analysis. Our newly developed boneMachine package provides functions in R for working with three-dimensional data such as those produced by computed tomography (CT), magnetic resonance imaging, and other forms of medical imaging. We demonstrate the utility of boneMachine for biological anthropology and bioarchaeology by analyzing CT scans of crania from the Smithsonian National Museum of Natural History (n=23). We automatically score these scans for expression of porous cranial lesions (e.g., porotic hyperostosis and cribra orbitalia), which are often interpreted as skeletal indicators of systemic childhood stress. We then demonstrate the additional functions of boneMachine, which include the ability to create two-dimensional visualizations and statistical summaries of bone density, cortical thickness, and other characteristics. boneMachine includes functions for performing arbitrary rotations in three dimensions, remapping to square voxels, interpolating or downscaling to lower and higher resolutions, identifying object surfaces, calculating statistics from regions of interest (ROIs), and producing visualizations of slices or surfaces. The functions are particularly designed to allow for batch processing of 3D images to create comparable measurements for ROIs or the entire object. The boneMachine package will be released with open source code, allowing for customization for particular research needs. Although written with CT scans of bone in mind, the functions in boneMachine are written to be general purpose and might be applied to many other research questions involving three-dimensional data.

Dosimetry and ESR Analyses at Senèze, France: Dating Villafranchian Monkeys and Associated Fauna

BONNIE A.B. BLACKWELL^{1,2}, ERIC DELSON^{3,4,5,6,7}, KIERAN P. MCNULTY⁸, TERENCE D. CAPELLINI⁹, JOEL I.B. BLICKSTEIN², ANNE R. SKINNER¹, STEPHEN R. FROST¹⁰, EVELYNE DEBARD¹¹ and MARTINE FAURE¹²

¹Chemistry, Williams College, ²RFK Research Institute, ³Anthropology, Lehman College/CUNY, ⁴Vertebrate Paleontology, American Museum of Natural History, ⁵PhD Program in Anthropology, CUNY Graduate Center, ⁶NYCEP (New York Consortium in Evolutionary Primatology), ⁷Institut Català de Paleontologia Miquel Crusafont (ICP), Universitat Autònoma de Barcelona, Spain, ⁸Anthropology, University of Minnesota, ⁹Human Evolutionary Biology, Harvard University, ¹⁰Anthropology, University of Oregon, ¹¹Université de Lyon, UCBL, Villeurbanne, France, ¹²UFR Temps et Territoires, Université Lumière Lyon 2, France

The fossil mammal site of Senèze, located within a volcanic crater in the Massif Central, has yielded many nearly complete skeletons since 1892. The only primates are the holotype skull of *Paradolichopithecus arvernensis* and a partial ulna of *Macaca*. The site defines the late Villafranchian interval of early Pleistocene age, but its exact date

is controversial, estimated between 1.6 and 2.1 Ma. New fieldwork directed by Faure, Delson and the late Claude Guérin from 2001-2006 aimed to clarify stratigraphy, age, paleoenvironment and taphonomy. One fossiliferous horizon was bracketed by argon/argon dates of 2.21 and 2.16 (± 0.02) Ma; another horizon ca 300 m distant overlies a date of ca. 2.1 ± 0.03 Ma. Blackwell (assisted by Frost, McNulty and Capellini) collected data for ESR analysis in 2001 near the latter. TL dosimetry, Y spectrometry and neutron activation analyses measured the sedimentary dosimetry. Sedimentary water concentrations ranged 11-36 wt%. Volumetrically and time-averaged sedimentary and time-averaged cosmic dose rates ranged from 1.5 to 2.0 mGy/yr above and below the bone-bed, but up to 3.0-4.0 inside it. For each tooth studied, 5-8 subsamples were independently dated by standard ESR, while U uptake rates were analyzed by isochron analyses. Enamel U concentrations averaged 3-6 ppm, dentine 70-100 ppm, and bone 60-80 ppm depending on the tooth and subsample. Accumulated doses ranged from 2799 to 4721 Grays. Dates for two teeth suggest that bioturbation has mixed younger fauna into the Villafranchian deposits, but preliminary dates for *Dicerorhinus etruscus* teeth were 1.5-2.1 Ma, assuming $p = 4-8$.

NSF grants to Skinner, Blackwell and Delson. Fieldwork support: National Geographic Society, Leakey Foundation and CUNY. Logistical and financial support from ESR Foundation, Williams College, and RFK Science Research Institute.

How extreme are Kodhini's twinning rates? A Geospatial and Temporal Look at Indian Twinning Rates

RAYMOND BLAIR¹, JOSEPH BONNER², AADHYAA SHENOY¹, SAVANNAH EWING¹, GREGORY SAVARIMUTHU³, JANCY FRANCIS³ and LORENA MADRIGAL¹

¹Anthropology, University of South Florida, ²Precision Medicine, City of Hope National Medical Center, ³Department of Anthropology, Kannur University

India's twin-birth-rate (TBR) has varied considerably within both physical location and temporal space, ranging from 10.5 and 12.44 per thousand. In the current work, we show that the so-called "twin town" of Kodhini in the Southern state of Kerala has experienced a twinning rate significantly higher than the background rate of Indian twinning. We also compare Kodhini's rate with those of two other areas which have experienced an increase in twinning during the same time: in the Morena area of Madhya Pradesh and in Madurai, Tamil Nadu.

The population adjusted average twinning rate for India during the time period 1920-2015 was 10.65. In comparison, Madurai (Tamil Nadu) had a twinning rate of 56 percent from 1979-1982 (Thirumalaikolundusubramanian et al, 1986), and

ABSTRACTS

Morena (Madhya-Pradesh) had a twinning rate of 37.4 percent for the period 1963-1973 (Goswami, 1987). Kodinhi's twinning rate increased from a low of 14% in the 1920s to a high of 61% in the 2000s (Raker et al. 2018). Although these twinning rates were highly significant when compared with the background twinning rate, Kodhini's remains the highest of all.

Our work brings to light the importance of addressing the possible causes of the "twin epidemic" not only in Kodhini but also in these two other "twin foci". Kodhini is part of the Nannambra *panchayat*. Although it is a rural area, it is well connected by train and air. We wonder if during these decades these populations might have been exposed to insulin-like growth factors which may cause polyovulation.

Funded by an NSF EAGER award. Funded by the CAS Faculty Travel award.

Dental reduction, physiological stress, and changing subsistence: Alterations to dental characteristics associated with the transition to agriculture in prehistoric Ohio

ERIN C. BLANKENSHIP-SEFCZEK^{1,2}, JOHN P. HUNTER³, MARK HUBBE², ROBERT COOK² and DEBBIE GUATELLI-STEINBERG²

¹Cultural and Social Studies, Creighton University, ²Anthropology, Ohio State University, ³Evolution, Ecology and Organismal Biology, Ohio State University

Following the introduction of new dietary elements and/or food processing techniques during the transition to agriculture, dental reduction occurred in anatomically modern humans. The general trend associated with smaller teeth in human evolution is a simultaneous simplification in trait expression. Complicating our understanding of tooth size and morphological change in agricultural populations, is the pattern of increased physiological stress in groups transitioning to horticultural subsistence practices. Previous studies suggest the presence of developmental physiological stress resulted in an increase, rather than decrease, in the complexity of crown morphology. To measure the relative significance of systemic stress in dental morphology, this study explores the relationship between subsistence change, stressful events and dental size during the transition from hunting and gathering to agricultural subsistence in prehistoric Ohio. Crown sizes, cusp spacing, and dental morphology were recorded for the molar teeth of 62 hunter-gatherers and 108 agriculturalists from the Ohio Valley. Wilcoxon and Chi-squared tests were run to assess statistical significance. Results show that the agricultural group exhibited significantly smaller teeth ($p < 0.001$), increased prevalence of stress markers ($p < 0.001$), and a greater frequency and size of accessory cusps ($p = 0.012$). Thus, these findings support the association between physiological stress and increasing

molar crown complexity. Furthermore, results demonstrate that the trend of dental reduction and crown simplification are not necessarily associated. Based on these findings, increases in physiological stress with the transition to agriculture appear to result in more, rather than less, complex molar morphology even while teeth are reducing in size.

This research was funded in part by the Alumni Grant for Graduate Research and Scholarship and the Larsen Award.

Sex, gender, and gendered roles among the Purisimño Chumash: An integrative approach

MICHELE M. BLEUZE

Anthropology, California State University, Los Angeles

The demarcation between female and male subsistence-related activities among Chumash groups along the southern California coast became increasingly less distinct from the Early Period (~8500 BP-3000 BP) through the Late Period (~800 BP-missionization). It is unclear if this trend was a regional or local phenomenon partly because peripheral Chumash groups have not been as well-studied as the more centrally located groups in the Santa Barbara Channel area. This study examines sex differences in utilitarian burial accompaniments and midshaft femoral diaphyseal shape and robusticity in a sample of Middle Period (~3000 BP-800 BP) Purisimño Chumash from Point Sal, California, to assess the relationship between subsistence-related gendered roles and sex. For analytical purposes, utilitarian burial accompaniments were assigned a gender of "feminine" or "masculine" based on ethnohistoric and ethnographic data. Frequencies of gendered utilitarian burial accompaniments were not significantly different between the sexes. Significant sex differences in femoral diaphyseal shape suggest males may have engaged in more mobile activities than females. The relative strength of the femur, however, was not significantly different between the sexes. The mortuary and osteological data give somewhat conflicting results. Gendered utilitarian burial accompaniments in this Purisimño Chumash sample do not often align with sex, which is consistent with previous studies on other Chumash groups. When estimated sex based on standard osteological methods is ambiguous or when skeletal sex estimation is not possible, the use of utilitarian burial accompaniments to infer the sex of individuals at Chumash sites should be approached with extreme caution.

Crypt fenestration enamel defects have no association with childhood morbidity or mortality at Tlatelolco, a Mesoamerican urban center (1350-1521 CE)

KELLY E. BLEVINS¹ and JOSEFINA MANSILLA LORY²

¹School of Human Evolution and Social Change, Arizona State University, ²Dirección de Antropología Física, Instituto Nacional de Antropología e Historia

Evidence of adverse conditions during early life can be recorded in the skeleton. It has been demonstrated, however, that the presence of physiological stress indicators is not clearly associated with mortality risk. The relationship among stress indicators and metabolic and infectious disease has not been as intensively investigated, most likely due to the low frequencies at which these conditions manifest skeletally. Crypt fenestration enamel defects (CFEDs) are hypoplastic defects primarily identified on the deciduous canines. The proximate cause is thought to be traumatic injury during the first year of life to the developing tooth germ, which is vulnerable when the overlying cortical bone is abnormally thin. To determine if childhood morbidity and mortality are linked to early life adversity as recorded by CFEDs, CFEDs, evidence of metabolic and infectious disease, and age at death were recorded in juvenile skeletal remains from Tlatelolco ($n = 35$), the densely-populated commercial center of the Aztec empire. Individuals with ($n = 11$) and without ($n = 24$) CFEDs have a similar prevalence of metabolic and infectious disease, and survivability is similar between individuals with and without CFEDs. The overall high prevalence of infectious and metabolic disease in individuals with and without CFEDs (25-64%) shows that both groups survived in diseased states long enough to develop skeletal lesions. These data suggest that CFEDs do not represent a physiological trade-off or an adaptive response and are not suitable proxies for periods of physiological stress that have lasting effects on morbidity and mortality outcomes.

This research was funded by a Fulbright-García Robles Fellowship.

Self-Reported Childhood Socioeconomic Status and Dental Health in the William M. Bass Donated Skeletal Collection

LYDIA BLIZZARD and HALEY E. HORBALY
Anthropology, The University of Tennessee

Socioeconomic status (SES) has previously been used to measure health disparities in modern populations. Alongside post-secondary education and life-long occupation, access to health care is often variant among social classes. This study aims to explore the relationship between categories of SES using dentition within the William M. Bass Donated Skeletal Collection (WMB) and to understand how it relates to access to health care. The WMB at the University of Tennessee

ABSTRACTS

represents a modern population of individuals with varying self-reported SES. The self-reported SES of 186 individuals were scored on a scale of 1 to 4, with four representing the highest socioeconomic class. We evaluated the same individuals on a presence/absence basis for dental work (such as wisdom teeth removal, fillings, or veneer placements) as well as untreated dental pathology, periodontal disease, or dental caries. Descriptive statistics show that the majority of the donors included in the study (92.6%) had dental work present, while just over half (60.6%) exhibited untreated dental pathology. Mann-Whitney U tests indicate there is no significant difference in the presence of dental pathology ($p=0.4$) or dental work ($p=0.09$) among individuals of different SES groups. This finding indicates that socioeconomic status might not be a primary factor in the presence of dental work or untreated dental pathology among individuals in this sample.

Identification of disease at Verteba Cave, Ukraine

TRE BLOHM¹, JORDAN KARSTEN² and MERADETH SNOW¹

¹Anthropology, University of Montana,

²Anthropology and Religious Studies, University of Wisconsin-Oshkosh

As ancient DNA methods and techniques advance, researchers have become increasingly interested in obtaining DNA from the bacteria that may have infected individuals in the past. Using bioinformatics, researchers can identify bacteria at taxonomic levels as precisely as their species level. This can be immensely helpful in identifying disease in past populations and inferring their transmission and effect on the populations. A recent promising bioinformatic tool is the Heuristic Operations for Pathogen Screening (HOPS) tool. HOPS is suggested to be better than current metagenomic tools, highly specific, sensitive, and reliable (Hubler et al 2019). Given these suggestions, this project explores the metagenomic bacterial community of 106 genomes from the Tripolye culture from Verteba Cave, Ukraine using HOPS to identify bacteria to the genus and species level. This site is of interest because the Tripolye culture (4800-2900 cal BC) were one of the first archaeological cultures in Southeastern Europe to live an agriculturally rich lifestyle, pastoralize animals, and establish large settlements with high population densities (Karsten et al. 2014). This distinctive lifestyle would have had significant impact on their health relative to mobile hunter-gatherers previously living in the same area. The genomes from the individuals who resided here have suggested possible identification of *Mycobacterium tuberculosis* complex members using Kraken software previously (Blohm et al. 2019). The HOPS data show

that the population studied at Verteba Cave were influenced by disease, notably from the MTBC complex, as result of the biocultural conditions of the Neolithic package.

Seasonal-scale variability in diets of hominins from Turkana, Kenya

SCOTT A. BLUMENTHAL¹, THURE E. CERLING², KENDRA L. CHRITZ³, JULIA A. LEE-THORP⁴, FREDRICK MANTH¹⁵ and SHIRLEY STRUM⁶

¹Department of Anthropology, University of Oregon, ²Department of Geology & Geophysics, University of Utah, ³Department of Geography, University of Oregon, ⁴School of Archaeology, University of Oxford, ⁵Earth Sciences Department, National Museums of Kenya, ⁶Department of Anthropology, University of California, San Diego

The well-documented expansion of C_4 vegetation in eastern Africa since the Pliocene is accompanied by increasing consumption of C_4 foods by hominins and other mammals. Previous research on hominin diets has focused on inter-individual variation, and it is critical to investigate aspects of within-individual niche flexibility. We address diet change within the lifetimes of individual hominins from the Turkana Basin, Kenya using laser ablation isotopic analysis. We present results on intra-tooth isotopic variability for specimens identified as *Australopithecus anamensis* ($n=5$), *Kenyanthropus platyops* ($n=6$), *Paranthropus aethiopicus* ($n=3$), *Paranthropus boisei* ($n=6$), and *Homo* ($n=6$) ranging in age from 4.2 to 1.5 Ma. We find significant intra-tooth $\delta^{13}C$ variability among specimens of *A. anamensis* (mean range = 2.9‰), *K. platyops* (3.2‰), *P. aethiopicus* (4.8‰), and *Homo* (3.8‰), reflecting significant diet changes on intra- and inter-annual time scales. In contrast, we find lower intra-tooth $\delta^{13}C$ variability among specimens of *P. boisei* (mean range = 2.1‰). These results demonstrate that diets were highly variable even among early Pliocene hominins, notably including the early habitual biped *A. anamensis*. We contextualize these results with comparisons to laser ablation intra-tooth profiles from other extinct taxa, including *Theropithecus* ($n=18$), non-*Theropithecus* papionins ($n=4$), Colobini ($n=2$), herbivores ($n=3$), and extant *Papio* ($n=7$). The ecology of early hominins must be understood in the context of seasonal-scale shifts between C_3 and C_4 -dominated diets, which can influence selective pressures associated with resource availability, nutritional balance and competitive interactions.

We thank the Natural Environment Research Council and the National Science Foundation for support.

What a population is, and is not, matters: ancestry, evolution and racist science

DEBORAH A. BOLNICK^{1,2} and AGUSTÁN FUENTES³

¹Department of Anthropology, University of Connecticut, ²Institute for Systems Genomics,

University of Connecticut, ³Department of Anthropology, University of Notre Dame

The term "population" has a long and complex history. In evolutionary biology, at least since the maturation of the modern synthesis, scientists have generally followed Ernst Mayr and Theodosius Dobzhansky in seeing the "population" as the fundamental unit for assessing, interpreting, and describing evolutionary processes. However, even in most classic applications of this term, there is huge variability and much dissonance in how "population" is defined, used, and interpreted. It has become commonplace in many disciplines to treat populations more or less as an "I know it when I see it" category. This is deeply problematic, particularly in studies of human evolution, human biological diversity, and ancient DNA. When such non-synonymous and varied "units" as continental "populations", language groups, regional and local "culture" groupings, nationalities, ethnic groups, religion, geographic "races", socio-political-historical groupings, documented demes, assumed demes, single or low-sample paleo "species", and even unknown but measurable genetic signatures of "ghost" lineages are used in overlapping ways and treated as comparable "populations" for analytical purposes, it creates a risk of poor scientific outcomes, inaccurate racialized assertions, and grave mischaracterizations of complex and dynamic human histories and processes. Here we illustrate this substantive problem using examples from paleogenomic studies of European, American, and archaic "populations," demonstrating that the majority of ways we are thinking about, and using, "population" does not map accurately to human behavior, history, and structure. We end by considering possible new models to help us move towards more consistent, more valid, less racist, and more scientific practices.

Skeletal element distribution of immature *Homo naledi* remains in the Dinaledi Chamber, South Africa

DEBRA R. BOLTER^{1,2} and MARINA C. ELLIOTT¹

¹Evolutionary Studies Institute, University of the Witwatersrand, ²Anthropology, Modesto College

In 2013-2014, a large volume of *Homo naledi* fossil remains were recovered from the Dinaledi Chamber in the Rising Star Cave system in South Africa, and date to 335,000-236,000 years ago. A minimum number of 15 individuals were identified based on dental remains; 9 of which were immatures.

Of the 2013-2014 specimens, 76 represent immature postcranial elements. Remains were recovered from the surface, and to a depth of 16 cm below the surface of the Chamber floor. Of the immature material, 83% was recovered from the primary excavation pit. Surface immature postcrania mostly clustered to the southwest of the primary excavation pit. These

ABSTRACTS

remains are analyzed here, with specific attention to their placement in space, and depth. The goal is to assess skeletal element distribution in the Chamber, and to associate the postcranial remains by space, depth and maturity indicators.

Results indicate that 1) immature materials occur at all depths; 2) immature remains are intermingled with adult specimens; 3) immatures now number 10, bringing the total number of individuals represented in the assemblage to 16. The Dinaledi Chamber fossil assemblage is unique in paleoanthropology in that of 16 total individuals recovered, a remarkable 10 are immatures, and that they range across all life stages – infants, young and old juveniles, and sub-adult. This situation is unprecedented compared to other Pleistocene sites and provides a unique opportunity to study the ontogeny of a single regional *Homo* population.

The microbiomes of female lemurs vary structurally by species, body site, and ovarian hormone cycles

SALLY L. BORNBUSCH¹, NICHOLAS GREBE¹, SIERA LUNN², CHELSEA SOUTHWORTH², KRISTIN DIMAC-STOHL¹ and CHRISTINE M. DREA^{1,2}

¹Evolutionary Anthropology, Duke University,
²Biology, Duke University

Microbiomes, that differentially occupy epithelial surfaces of vertebrate hosts, play important roles in host health, reproduction, and behavior. Vaginal microbiomes help prevent sexually transmitted infections and promote reproductive success, whereas more external communities, such as labial and axial microbiomes, promote epithelial maintenance or aid in the manufacture of bodily odors used in chemical communication. Our understanding of the factors that shape host-associated microbiomes, and ultimately dictate their functions, derives principally from human studies and would benefit from a broader comparative approach. Using female ring-tailed lemurs (*Lemur catta*) and Coquerel's sifakas (*Propithecus coquereli*), we examined three microbiomes (the vaginal, labial, and axillary) across a full ovarian cycle to determine the relative influences of stable (species identity and mating system) versus transient (ovarian cycle and hormone concentrations) factors on microbiome structure. We used 16S amplicon sequencing of microbial samples to determine microbiome composition and enzyme-linked immunosorbent assays of blood samples to determine hormone concentrations. We found that microbial consortia significantly differed between lemur species and body sites, and that estradiol and progesterone concentrations predicted aspects of microbiome structure. For example, sifakas showed a similar relationship to that seen in humans whereby estradiol correlates with abundances of lactic acid bacteria in vaginal microflora, suggesting a similar estrogenic mechanism that influences primate reproductive

health. By illustrating the dual roles of stable and transient factors, and the importance of endocrine mediation in structuring various microbiomes, we add to the growing understanding of host-microbe dynamics and their implications for primate health and behavior.

Funding was provided by NSF BCS 1852151 REU Supplement for NSF BCS 1749465.

A child on display: Approaches in understanding a found mummified medical specimen

BAILEY B. BORRESON and ALLISON J. FOLEY

Sociology and Anthropology, College of Charleston

Despite its long history, the trade in, and display of, mummified human remains, has increasingly been met with sound criticism. While many of these ethical discussions center around archaeological remains, human remains intended for medical display warrant their own ethical analysis. In this study, we present the case of a mummified medical specimen, a young juvenile fixed to a stand/base with musculature, nerves, circulatory system (colored), and various organs preserved and displayed. Rumored to have been seized as the illicit "souvenir" of a naval officer returning from Asia, the mummy was transferred to the longtime custody of forensic anthropologist Dr. Ted Rathbun before its transfer and extended storage in the Charleston County Coroner's Office. The College of Charleston retained custody of the mummy, which exhibited substantial deterioration, in 2017.

The purpose of this case study is to not only analyze, understand, and conserve this mummy, but also to de-objectify this child, who, for the last several decades, has been passed around and displayed as a specimen rather than as a humanized individual. With respect to the first research goal, this presentation explores efforts to establish a provenience and health profile of the child through imaging, molecular analysis, and gross observation. In addition to these methods, we present on-going conservation and preservation efforts to diminish further decay of this individual. Providing greater context to this case study, we also present a history of medical mummification, a history of the trade in medical specimens, and an ethical analysis of this practice.

Metabolic iron and copper stable isotope fractionation in mature rhesus macaques (*Macaca mulatta*)

RENEE D. BOUCHER^{1,3,4}, HYLKE N. DE JONG^{1,3}, ERIN R. VOGEL^{1,3}, LINDA V. GODFREY² and SHAUHIN E. ALAVI⁵

¹Anthropology Department, Rutgers University, New Brunswick, ²Department of Earth and Planetary Sciences, Rutgers University, New Brunswick, ³Anthropology Department, Rutgers University Center for Human Evolutionary Studies,

⁴Anthropology Department, University of California, Santa Cruz, ⁵Department of Collective Behavior, Max Planck Institute of Animal Behavior, Konstanz

The isotopes of trace metals, such as iron (Fe) and copper (Cu) have been shown to be less in human adult males relative to females, and this sex effect has been linked to female menstruation. However, this variation has never been measured in non-human primates. We hypothesized that because rhesus macaques have a similar menstrual cycle to humans, the sex variation in Fe and Cu should be similar to adult humans. To test if there was a similar sex effect in rhesus macaques, we investigated the isotopic fractionation of $\delta^{56}\text{Fe}$ and $\delta^{65}\text{Cu}$ of 20 pre- and peri-pubescent rhesus macaques (*Macaca mulatta*) from the Caribbean Primate Research Center, Puerto Rico. We sampled bulk occipital bone and incisors, from which Fe and Cu were separated and measured by MC-ICP-MS. Our results show that there is a significant relationship between $\delta^{65}\text{Cu}$ fractionation and sex in rhesus macaque occipital bone ($p = 0.0014$), with $\delta^{65}\text{Cu}$ values higher by 1.4 ‰ in males compared to females. This effect was not present in incisors, which reflect earlier, pre-pubescent life stages. However, we found an interaction between age and sex that affects $\delta^{65}\text{Cu}$ fractionation in rhesus macaque occipital bone, suggesting that age could potentially influence $\delta^{65}\text{Cu}$ fractionation depending on the sex of the individual. We found no significant relationship between $\delta^{56}\text{Fe}$ values and sex in rhesus macaque occipital bone or incisors. Our results show that Cu metabolism has the potential to be a useful supplementary tool in future primatological, archaeological and paleo-anthropological studies.

Rutgers Center for Human Evolutionary Studies (CHES)
Barry C. Lembersky Undergraduate Research Award,
Aresty Research Center Undergraduate Research Fellowship, and Bigel Endowment in Anthropology

Ontogenesis of the manual and pedal motor systems in a comparative approach in the arboreal *Microcebus murinus* and mainly terrestrial *Papio anubis*

GREGOIRE BOULINGUEZ-AMBROISE^{1,3}, ANTHONY HERREL¹, GILLES BERILLON^{2,3} and EMMANUELLE POUYDEBAT¹

¹UMR 7179 CNRS, Adaptations of Living Organisms, National Museum of Natural History, Paris, ²UMR 7194 CNRS, Prehistory Department, National Museum of Natural History of Paris, ³UPS 846 CNRS, Primatology Station

The arboreal environment is very challenging for primate juveniles. Early effective locomotor abilities are thus crucial for survival. In this context, we can expect developmental strategies counterbalancing immaturity. In order to understand these strategies, we conducted an ontogenetic study, from birth to adulthood, on 2 species, a highly arboreal one, *Microcebus murinus* (longitudinal)

ABSTRACTS

and a mainly terrestrial one, *Papio anubis* (transversal). We investigated morphometric and performance (i.e. pull strength) traits for both limbs for both species and quantified grasping behaviour during locomotion in *Microcebus*. Results show that *Microcebus* are able to climb various substrates outside the nest, as soon as 8 days of age; young individuals display relative pull strengths that are even on par with adults, in links with their relative longer limbs and use more manual secure grasps than adults. Young baboons are carried during their first months; they display relative longer medial and proximal phalanges with larger joint surfaces, allowing strongly grasping the mother's coat. The metapodia then quickly grows, followed by the scapula, allowing effective arboreal behaviors at 2 months. Finally, our results point different functional roles of the hands and feet, with the hind limbs ensuring body balance on the substrates, freeing the upper limbs for manipulation. Such anatomical changes tracking behaviors can be discussed to better understand the functional, social (i.e. infant carrying) and ecological contexts that have driven the evolution of grasping in Primates.

This work was supported by the French National Center for Scientific Research. CT-Scans and osteological material (Papio anubis): CNRS-Institut écologie et Environnement International Research Network IRN-GDRI0870 and ANR-18-CE27-0010-01 HoBiS

Reconstructing Moty-Novaia Shamanka: A new Kitoi cemetery on the middle Irkut River

REBECCA L. BOURGEOIS¹, ANGELA R. LIEVERSE², HUGH MCKENZIE³ and VLADIMIR I. BAZALIISKII⁴

¹Archaeology and Anthropology, University of Saskatchewan, ²Archaeology and Anthropology, University of Saskatchewan, ³Anthropology, Economics and Political Science, MacEwan University, ⁴Scientific Research Centre, Irkutsk State University

Moty-Novaia Shamanka (MNS) is an Early Neolithic (7500-6800 cal. BP) Kitoi cemetery site located in the Baikal region of the Russian Federation. This ancient cemetery was originally situated on a large hill that stood out in the marshy landscape, but was bulldozed in the 1990s for the development of the village of Novaia ("New") Shamanka. The Baikal Archaeology Project conducted salvage excavations in 2014 and 2015, yielding 1246 human bone fragments scattered across 107 square meters. This paper presents the results of a six-week data collection period in May-June 2019 as well as the analysis of these data to reconstruct the people interred at MNS. It takes as its main research question, how can we develop methods to salvage information from highly disturbed human remains in order to better understand the context of the MNS cemetery and reconstruct the individuality of those interred within it? 192 human bone fragments

(21.65% of all identifiable fragments) were able to be rejoined into 70 conjoins, while multicomponent analyses of these data, including visual pair matching and GIS, have re-associated skeletal elements into discrete individuals. These, alongside further associations, were tested against the original MNI estimate by Russian anthropologist Dr. Denis Pazhetskii. Our results were used to synthesize a confidence scoring scale that can evaluate associations based on both qualitative and quantitative data. This research is significant to the broader field of bioarchaeology because it builds on faunal, forensic, and bioarchaeological methods to be able to better address issues of preservation in skeletal collections.

This research is supported by the Baikal Archaeology Project, Social Sciences and Humanities Research Council (SSHRC), Northern Scientific Training Program (Polar Knowledge), and University of Saskatchewan Department of History.

Testing Diffeomorphic Surface Matching versus 3D Geometric Morphometrics in Hominid First Metacarpals

LUCYNA A. BOWLAND and LESLEY H. EASON
Anthropology, University of Arkansas

Understanding the origins of the robust thumb in *Homo sapiens* requires an accurate means of quantifying shape differences across hominid taxa. Morphometric assessments of the thumb have long played a role in testing hypotheses concerning the origins of manual dexterity and tool use within hominins. Three-dimensional geometric morphometric (3D GM) landmark analyses are traditionally employed to quantify shape differences among primate taxa. However, traditional landmark analyses are subject to a high degree of methodological error due to the a priori nature of landmark placement and identification across specimens. Recent research demonstrates that diffeomorphic surface matching (DSM) has greater discriminatory power than traditional 3D GM when comparing hominid teeth. Thus, the same methods could potentially be useful for discriminating amongst hominoid postcrania. This project tests the discriminatory power of 3D GM analyses versus DSM techniques using 3D virtual renderings of the first metacarpal of *Gorilla* (*G. gorilla* [n=11] and *G. beringei* [n=25]), *Pan* (*P. paniscus* [n=16] and *P. troglodytes* [n=23]), *Pongo* (*P. abelii* [n=8] and *P. pygmaeus* [n=3]) and modern humans (n=40). Preliminary results indicate that DSM techniques better discriminate taxa than do traditional 3D GM analyses. If fossil taxa can also be discriminated using these methods, this study could have important implications for understanding the evolution of the modern human thumb and the origin of tool use within hominins. Researchers should consider employing DSM techniques to assess the pattern and magnitude of postcranial variation in the fossil record.

Large-scale cooperation in small-scale societies

ROBERT BOYD^{1,2} and PETER J. RICHERSON³
¹School of Human Evolution and Social Change, Arizona State University, ²Institute for Human Origins, Arizona State University, ³School of Environmental Science and Policy, UC Davis

Public goods play a crucial role in contemporary large-scale societies. Roads, public education, public order, and collective defense create very large benefits that are shared by all members of modern societies, and, absent third party sanctions, this motivates people to take the benefits of public goods without contributing to their production. Here we review evidence from historical accounts and archaeological data, mainly from western and northern North America, Australia and Pleistocene Europe, that indicates that people in nomadic hunter-gatherer societies also cooperated in large numbers to produce public goods. Foragers engaged in communal hunts; they often constructed shared capital facilities like drive lines, hunting nets and fish weirs; they made shared investments in improving the local environment through burning, irrigation and other habitat modifications; and they participated in warfare. The provision of these public goods often involved the cooperation of hundreds of individuals, and played a crucial role in subsistence, especially in temperate and arctic environments. Large-scale cooperation has not been reported among foragers studied by 20th century ethnographers. We will discuss why this might be the case. Large-scale cooperation in nomadic foraging societies suggests that contemporary large-scale cooperation is not solely the result of an evolutionary "mismatch." It also suggests that the psychological motivations for third party punishment is unlikely to have been favored by selection because of the benefits to the punisher of the increased cooperation induced by the punishment.

Artisanal gold mining and primate conservation: A threat hiding in plain sight

KELLY BOYER ONTL and KATHRYN LOVING
Anthropology, Ball State University

The greatest threats to non-human primates today are from anthropogenic activities, with the most severe and immediate impacts stemming from agriculture, extractive industries, and hunting. Here we present a review of published literature addressing artisanal and small-scale gold mining (ASGM) impacts on primates and discuss the need for further research. ASGM is broadly defined as labor-intensive gold mining of marginal deposits, with poor human health and safety measures and myriad negative environmental impacts. Despite thousands of publications on ASGM and associated harmful environmental impacts, we found very few studies relating these impacts to primates. Only 12 publications focused

ABSTRACTS

on primates and ASGM specifically; of these, four studied increases in bushmeat hunting related to ASGM, two looked at changes in primate behavior, three addressed the broad environmental impacts of ASGM and the assumed effect on primates, and three were a call to action. Most of the literature associated with ASGM focuses on human health impacts (particularly those associated with mercury usage), governance and policy, and environmental impacts. The environmental impacts of ASGM include deforestation, disruption of soils, and mercury toxins in the ecosystem, and have potential to severely impact on primate communities and their habitat. However, very few studies have attempted to quantify these impacts. In areas like Amazonia, southeast Asia, Central Africa, and Madagascar where high primate richness and critically endangered primates overlap with high rates of ASGM and mercury pollution, research is urgently needed to understand the dynamics between ASGM and primate communities.

Dental analysis of prehistoric populations in coastal Ecuador

CASSANDRA BOYER

Anthropology, Florida Atlantic University

This project compares the human dentition of three coastal populations in Salango, Ecuador, dating to Late Guangala (Site 141C: 100 B.C. – A.D. 800), Early Mantño (Site 35: A.D. 645 +/- 45 and A.D. 430), and Late Mantño (Site 140: A.D. 1300 – 1600). The human remains in Sites 141C and 140 have not been previously analyzed and provide new information about coastal Ecuador in the form of statistical analysis and osteobiographies. Dental pathologies such as caries, abscesses, calculus, hypoplasia, as well as dental wear patterns indicate subsistence, or diet, behavioral and cultural practices, and early developmental physiological stress. The data suggests that agriculture became more intensive during Site 35's occupation, whereas the other two sites simultaneously used the sea and agriculture for food, and neither practice dominated. Further, early developmental physiological stress became significantly more apparent during Site 140's occupation, suggesting these individuals were heavily affected by climate, Spanish colonization and subsequent disease, social struggles, and/or dietary deficiency. Site 140 also presents more intensive and abnormal wear on the anterior teeth, indicating an increase in specialized behavioral or cultural practices.

Variation in the anthropoid primate pelvis does not reflect differences in diet

EVE K. BOYLE^{1,3} and SERGIO ALMÉCIJA^{2,3,4,5}

¹Department of Anatomy, College of Medicine, Howard University, ²Division of Anthropology, American Museum of Natural History, ³Center for the Advanced Study of Human Paleobiology,

Department of Anthropology, The George Washington University, ⁴New York Consortium of Evolutionary Primatology (NYCEP), ⁵Institut Català de Paleontologia Miquel Crusafont (ICP)

Pelvic differences among hominins are suggested to reflect diet-related differences in gut size among species. This hypothesis emerges from the observation that animals with diets rich in leaves and other green plants exhibit larger guts than animals that rely on prey, and the expectation that differences in pelvic dimensions reflect accommodations for differently-sized guts. However, studies of extant primates provide little evidence supporting this hypothesis.

We test whether comparisons between pairs of similarly-sized, closely-related anthropoids reveal a link between diet and pelvic dimensions. Iliac flare, ilium width, and bi-iliac breadth were measured in 14 species (N = 234 individuals) using digital calipers. Percent time feeding on food categories were collected from the literature. Eleven comparisons were made; seven among species with different diets, and four among species with similar diet compositions. Welch's t-tests were used to test for differences in variable means between the species in each pair. We predict that more folivorous species will have pelvic dimensions reflecting a more capacious abdominal cavity and that there will be no significant differences in pelvic dimensions in species with similar diets.

Only four comparisons support the hypothesis that more folivorous species have broader pelvis than less folivorous species. The remaining comparisons yield results where: more folivorous primates have narrower pelvic dimensions, species with different diets show no differences in pelvic dimensions, or species with similar diets show differences in pelvic dimensions. These results indicate that differences in pelvic dimensions cannot reliably be used to infer differences in diet among anthropoid primates.

Funding provided by NSF (GRF, BCS 1316947), the Wenner-Gren Foundation (Dissertation Fieldwork Grant), the Agencia Estatal de Investigación (CGL2017-82654-P, AEI/FEDER EU), the Generalitat de Catalunya (CERCA Programme), and GWU.

Recent selective sweeps in bonobos (*Pan paniscus*): A machine learning approach

COLIN M. BRAND¹, TIMOTHY H. WEBSTER², FRANCES J. WHITE¹ and NELSON TING^{1,3}

¹Anthropology, University of Oregon, ²Anthropology, University of Utah, ³Institute of Ecology and Evolution, University of Oregon

Recent positive selection can leave distinct genomic signatures that are recognizable in population-level data. Further, it is possible to differentiate between novel mutations that arise, sweep, and fix in a population (a hard sweep) or extant variation that becomes favorable following

a change in the physical or social environment (a soft sweep). Here, we use a machine learning approach to identify genomic regions subject to recent selective sweeps in bonobos and the degree to which hard and soft sweeps have shaped recent bonobo evolution. We trained a convolutional neural network (CNN) using feature vectors calculated from data simulating neutral evolution and both types of sweeps. These simulated chromosomes were parameterized with demographic estimates for bonobos. Our classifier reached an accuracy of 0.809. We then calculated feature vectors for all autosomes from 13 reassembled bonobo genomes and applied the trained classifier to these data. We found evidence of selective sweeps in 339 out of 24,801 (1.4%) windows that overlapped 1,009 genes. These sweeps consisted of 34 hard and 305 soft sweeps. Our results highlight that soft sweeps appear to be the predominant mode of positive selection in recent bonobo evolutionary history. This study identifies candidate genes for subsequent research that may contribute to the complex and unique bonobo phenotype.

The influence of fruit availability and infant age on maternal behavior in wild Bornean orangutans (*Pongo pygmaeus wurmbii*)

TIMOTHY D. BRANSFORD¹, MARIA A. VAN NOORDWIJK², SRI SUCI UTAMI ATMOKO³ and ERIN R. VOGEL^{4,5}

¹Department of Anthropology, Northern Illinois University, ²Department of Anthropology, University of Zurich, Switzerland, ³Faculty of Biology, Universitas Nasional, Jakarta, ⁴Department of Anthropology, Rutgers University, ⁵Center for Human Evolutionary Studies, Rutgers University

Primate mothers differ in the behavioral strategies used to maintain energetic homeostasis across lactation, including varying dietary items and levels of activity. However, many primates are either seasonal breeders or exist in relatively predictable habitats, reducing the need for mothers to utilize multiple strategies. Orangutans nurse for up to eight years in habitats with unpredictable patterns of preferred food availability, making it difficult for mothers to maintain a stable energetic strategy. We examined if a mother orangutan's behavior and diet at the Tuanan Research Station, Central Kalimantan, Indonesia vary depending on fruit availability. We constructed generalized additive mixed models to investigate how activity budget and time feeding on specific food items from full-day focal follows on ten individuals (n = 1,924) vary throughout lactation periods and across different fruiting periods. During periods of high fruit availability, we found that while a mother's time spent feeding and resting didn't vary across lactation, she fed significantly more on ripe fruit with a two-year-old infant (p < 0.0001) and moved more as her infant aged (p = 0.031). Conversely, during low fruiting periods, mothers rested more

ABSTRACTS

while she had a two-year-old infant ($p=0.011$) and spent more time feeding on abundant items like leafy vegetation ($p=0.020$). Additionally, daily path length was significantly lower compared to high fruit periods ($p<0.0001$). These results suggest that mother orangutans with young infants seek to maximize energy intake during periods of high fruit availability, but change to an activity minimization strategy when fruit becomes scarce to reduce energetic expenditure.

This project was funded by the United States Agency for International Development, National Science Foundation, The Center for Human Evolution Studies, and the American Society of Primatologists.

Early *Homo sapiens* postcranial fossils from Middle Awash, Ethiopia

MARIANNE F. BRASIL

Department of Integrative Biology, Human Evolution Research Center, University of California, Berkeley

The emergence of anatomically modern humans has long been of great interest in human evolutionary studies. However, our knowledge of early modern human anatomy and evolution is constrained by the known fossil record, which at present samples our lineage's evolution irregularly across geography and through time. Furthermore, the fossil record is overwhelmingly craniodental, and the often fragmentary and isolated status of postcranial fossils limits our understanding of body size and shape evolution. Considering these limitations, additional fossils, and particularly individual skeletons, are necessary to further resolve the details of early modern human evolution.

The Middle Awash project has recovered an early *Homo sapiens* partial skeleton from a Middle Stone Age archaeological context at Halibee, preliminarily dated to ~100 kyr. Much of the skeleton is preserved, including portions of the vertebral column, shoulder and pelvic girdles, all long bones, and several hand and foot elements. Several additional postcranial elements ($n=7$ individuals) are also known from the same sedimentary package. These fossils are associated with a very rich Middle Stone Age assemblage and are part of a large and diverse faunal assemblage, situating the fossils within behavioral and ecological contexts. The chronological and geographic position of the Halibee fossils makes them crucial for understanding the evolution of modern human anatomy, as it places them within a population ancestral or closely related to anatomically modern humans.

This study was supported by the Leakey Foundation, NSF DDRIG-1732221, the Portuguese Studies Program and the Institute of International Studies at UC Berkeley, and the HERC Desmond Clark Graduate Fellowship.

Plio-Pleistocene hominin tool use and its context in the Koobi Fora Formation

DAVID R. BRAUN^{1,2}, SUSANA CARVALHO³, RENE BOBE^{3,4}, KEVIN UNO⁵, DAN PALCU^{6,7}, NIGUSS BARAKI¹, ASHLEY HAMMOND⁸, ELDERT ADVOKAAT^{7,9}, MARK SIER^{10,11}, CAROL WARD¹², J. W.K. HARRIS¹³, JONATHAN WYNN¹⁴, A. KAY BEHRENSMEYER¹⁵, AMELIA VILLASEÑOR¹⁶, MARION BAMFORD¹⁷ and DAVID PATTERSON¹⁸

¹Anthropology, George Washington University, ²Human Evolution, Max Planck Institute for Evolutionary Anthropology, ³Primate Models for Behavioral Evolution, Oxford University, ⁴Gorongosa National Park, Mozambique, ⁵Lamont-Doherty Earth Observatory, Columbia University, ⁶Oceanographic Institute, University of Sao Paulo, ⁷Fort Hoofddijk Paleomagnetic Lab, Utrecht University, ⁸Division of Anthropology, American Museum of Natural History, ⁹Department of Physical Geography, Utrecht University, ¹⁰CENIEH, Burgos, Spain, ¹¹Department of Earth Sciences, Oxford University, ¹²Department of Pathology and Anatomical Sciences, University of Missouri, ¹³Archaeology Division, National Museums of Kenya, ¹⁴Geology Program, U.S. National Science Foundation, ¹⁵Department of Paleobiology, National Museum of Natural History, ¹⁶Department of Anthropology, University of Arkansas, ¹⁷Evolutionary Studies Institute, University of the Witwatersrand, ¹⁸Department of Biology, University of North Georgia

The origins of our technological prowess remain poorly understood, yet a better understanding of the factors affecting the emergence of technological behaviour is critical to reconstructing hominin evolutionary history. The relationship between technology and hominin ecology is often considered to be a part of the generic level transition from Australopithecus to Homo, with the first stone tools appearing 2.6 Ma at Ledi-Geraru, Ethiopia. However, the recent discovery of an older and distinct stone tool technology at Lomekwi, Kenya, at 3.3 Ma and potential 3.4 Ma evidence of tool use in the Afar, Ethiopia, predate the appearance of Homo by 700,000 years. The apparent diversity of hominin behavior in the mid-Pliocene may reflect the apparent taxonomic and adaptive variation during this period of high hominin diversity. Here we present new results from seven seasons of systematic surveys and excavations at Pliocene and Pleistocene localities in the Koobi Fora Formation. We report on the ecological and temporal context of hominin behavior at multiple Pliocene localities within the Koobi Fora Formation. Hominin behavior appears to be focused on specific microhabitats. Results indicate that hominins likely implemented a variety of extractive foraging techniques well before the Plio-Pleistocene boundary.

This research is supported by the National Science Foundation Archaeology Program (Grant #1624398 and REU supplemental support #1930719)

How aging smooths a surface: GMM of pelvic symphysis roughness

GUILLERMO BRAVO MORANTE^{1,3}, FRED L. BOOKSTEIN^{2,3}, KATRIN SCHAEFER³, INMACULADA ALEMÁN AGUILERA¹ and MIGUEL BOTELLA LÓPEZ¹

¹Legal Medicine, Toxicology and Physical Anthropology, University of Granada, ²Statistics, University of Washington, ³Evolutionary Anthropology, University of Vienna

In skeletal forensics, one commonly exploited datum for age at death is the roughness of the pubic symphysis. Stoyanova et al. recently proposed an explicit quantification of this surface form. We modified their approach to bring it under the standard toolkit of geometric morphometrics (GMM).

400 symphyseal pubic surfaces from males aged 14 to 82 years (collection Laboratory of Anthropology, University of Granada) were surface scanned and landmarked with 102 fixed and surface semilandmarks. From that sample we selected the 381 specimens within Procrustes distance 0.05 of the side-specific average, rotated to the standard GMM basis of partial warp scores, and then, separately by side for ages under 50, correlated age with summed squared partial warps (PW) amplitudes over a wide range of plausible bandpass filters omitting the uniform term. Peak correlations with age were $r=-0.524$ both for the PW1-PW6 band on the right side and for the PW1-PW7 band on the left side, and the geometry of singular warps was virtually identical between the two analyses. The same filter predicts log age with a better correlation, -0.568, with a prediction standard error of 0.255 (-23% to +29% on the original age scale). Thus, the strong age signal in symphyseal surface shape is not a reduced roughness per se, as examined by Stoyanova et al., but rather a flattening at large scales.

The method is implemented in a version of the easy-to-use R statistical software package for combination with other GMM method in studies of other archival data samples.

This research was supported in part by Ernst Mach scholarship 56513 from the OeAD (Austrian Agency for International Cooperation in Education and Research) and by the Nvidia Corporation.

Paleogenomic reconstruction of diet and oral health in Pre and Post-contact individuals from Mexico

MIRIAM J. BRAVO-LOPEZ¹, CAROLINA ROCHA-ARRIAGA¹, JULIA PEREZ-PEREZ², JOEL HERNÁNDEZ-OLVERA², KEITLYN ALCANTARA-RUSSEL³, VIRIDIANA VILLA-ISLAS¹, AXEL SOLÁS-GUZMÁN¹ and MARÁA C. ÁVILA-ARCOS¹

¹International Laboratory for Human Genome Research (LIIGH), UNAM, ²School of Anthropology and History, INAH, ³Department of Anthropology, Vanderbilt University, Nashville, Tennessee

ABSTRACTS

Dental calculus (or plaque) has recently emerged as a rich source of ancient DNA (aDNA) from human archaeological samples. Besides preserving good-quality ancient human DNA, it is also an excellent substrate for recovering aDNA from oral microorganisms and food debris. To gain insights into oral health status, lifestyle and dietary habits of indigenous populations in Mexico, we analyzed Pre and Post-contact dental calculus samples from Mexico. We generated low-depth shot-gun sequencing data from samples from these two periods and used KRAKEN to compare the reads to a database composed of complete bacterial, archaeal, viral, and plants genomes in the NCBI's RefSeq database. We complemented these analyses with microbotanical analyses data (e.i pollen, starch grains and phytoliths) by optic and polarized microscopy of dental calculus. Data from Pre-contact individuals revealed reads assigned to *Streptococcus gordonii*, an opportunistic pathogen associated to endocarditis. Furthermore, Pre- and Post-contact individuals yielded reads matching to *Tannerella forsythia*, a Gram-negative bacterium associated with periodontal disease. Regarding the dietary sources in Pre-contact individuals, we identified starch particles of *Zea mays*, *Phaseolus vulgaris* and pollen grains of *Nicotiana* by both paleogenomics and microfossil analyses. Data from Post-contact individuals showed reads assigned to *Beta vulgaris* subsp. *Vulgaris*, *Zea mays* and *Gossypium hirsutum*.

Further genomic analyses of *T. forsythia* and *S. gordonii*, and dietary sources recovered from dental calculus of Pre and Post-contact individuals will provide additional evidence as to how Spanish colonization impacted past lifestyle, diet and genetic makeup of pathogens and hosts during this transitional period.

Wellcome Trust, DGAPA PAPIIT.

Fitness benefits of male chimpanzee social bonds at Gombe National Park, Tanzania

JOEL BRAY^{1,2} and IAN C. GILBY^{1,2}

¹School of Human Evolution and Social Change, Arizona State University, ²Institute of Human Origins, Arizona State University

Strong social bonds are associated with fitness benefits in several species. To date, however, the strong, equitable, and stable bonds formed between male chimpanzees have not been linked to improved health, greater longevity, or higher mating and paternity success. Using 34 years of behavioral data (N = 24 adult males) from Gombe National Park, Tanzania, we examined whether the strength of a male's bonds with other males predicted his mating success with maximally-swollen, parous females. In Analysis 1, we identified each male present in a party during all matings between males and maximally-swollen, parous females, marking each male as having

mated or not. In Analysis 2, we examined all days on which a parous female was maximally-swollen and identified whether each male in the community mated with her or not. In Analysis 3, we repeated Analysis 2 while including only matings that could be confidently identified as having occurred during a female's periovulatory period. Overall, we found that a male's maternal relatedness to a female and his rank were the strongest and most robust predictors across all three analyses. Additionally, the strength of a male's bonds positively predicted his mating success when all mating data were included. In the dataset that included only matings during the periovulatory period, however, these effects were more variable and less clear. These data provide preliminary evidence that strong social bonds may be associated with increased reproductive success in male chimpanzees, but the magnitude and meaning of this effect requires further investigation.

Funding provided by the Jane Goodall Institute, the National Science Foundation, the National Institutes of Health, the Leakey Foundation, and the National Science Foundation Graduate Research Fellowship.

New perspectives on Nubian ancestry: Paleogenomic investigation of the ancient Middle Nile Region

ABAGAIL M. BREIDENSTEIN¹, JUDITH NEUKAMM^{1,2}, CHIARA BARBIERI³, GIADA FERRARI⁴, AGATA T. GONDEK-WYROZEMSKA⁵, MOHAMED SAAD ABDALLAH^{6,7}, MAHMOUD SULIMAN BASHIR⁷, MURTADA BUSHARA⁷, ROBERT J. STARK⁸, JOANNA CIESIELSKA⁹, ARTUR OBLUSKI⁹, BASTIAAN STAR⁴, HISHAM YOUSIF HASSAN¹⁰, FRANK RÜHLI¹, VERENA SCHUENEMANN¹ and ABIGAIL W. BIGHAM¹¹

¹Institute of Evolutionary Medicine, University of Zürich, ²Institute for Bioinformatics and Medical Informatics, University of Tübingen, ³Institute of Evolutionary Biology and Environmental Studies, University of Zürich, ⁴Centre for Ecological and Evolutionary Synthesis, Department of Biosciences, University of Oslo, ⁵Norwegian College of Fishery Science, Faculty of Biosciences, Fisheries, & Economics, University of Tromsø, The Arctic University of Norway, ⁶Bolheim Bioarchaeology Laboratory, Khartoum, ⁷National Committee for Antiquities and Museums, Khartoum, ⁸Department of Anthropology, McMaster University, ⁹Polish Centre of Mediterranean Archaeology, University of Warsaw, ¹⁰Banoon ART & Cytogenetics Centre, Bahrain Defense Force Hospital, ¹¹Department of Anthropology, University of California Los Angeles

The kingdoms of Nubia, located in the Nile River Valley of modern-day northern Sudan, served as an important corridor of migration for millennia. Since little is known of the ancient genetic landscape, there is a lack of understanding of population movements from Nubian times through the Arab expansion. Here, we created a time-transect of genetic diversity in this region, using whole mitochondrial genome analysis of ancient DNA of samples obtained from several

Middle Nile archaeological sites spanning nearly two thousand years, from the Meroitic period (ca. 350 BCE) to before the Arab expansion (ca. 1450 CE). We trialed 40 individuals, extracting DNA using newly developed methods, including petrosal bone extraction, non-heat sample processing, enzymatic pretreatments, and DNA capture techniques, optimized for samples with very poor DNA preservation. We retrieved whole mitogenomes (MT) for six individuals: two with African ancestry and four with Eurasian ancestry. The ancient Nubians showed most genetic affinity with modern East Africans, Middle Easterners, and Egyptians. These results indicate that Nubians had a strong African component with evidence of gene flow from Eurasia dating back to at least Meroitic through Christian times. Although these individuals encompass varying archaeological contexts and span over two thousand years, these initial results hint at the complexity of the region's genetic makeup and begin to reconstruct the impact of migrations from outside Africa. Lastly, our work represents the first successful retrieval of full MT sequence data from Middle Nile inhabitants, further demonstrating the viability of paleogenomic work in northeast Africa.

This work was funded by an Early Career Grant provided by the National Geographic Society (EC-224R-18).

Health & Well-being in Pre- & Post-Black Death London: An Assessment of Sexual Stature Dimorphism

EMILY J. BRENNAN and SHARON N. DEWITTE
Anthropology, University of South Carolina

Given evidence that physical growth for males is more sensitive to environmental fluctuations while immune responses in females may provide better buffering against environmental conditions, the degree of sexual stature dimorphism (SSD), the ratio of male to female height, may be an indicator of living standards. The degree of SSD is expected to decrease as resource availability declines. This association has been observed in living contexts, and the aim of this study is to assess SSD as an indicator of living standards in medieval London in the context of repeated famine events before the Black Death (c. 1348-1350) but improved wages and diet afterwards. This study compared adult individuals from pre-Black Death (n=325) and post-Black Death (n=289) cemeteries from London. Maximum tibial length was used as a proxy for stature, and SSD was calculated as the ratio of male to female mean tibial length. Both sexes achieved taller adult stature in the post-plague environment. Results revealed only a slightly higher degree of SSD after the Black Death. When considering SSD by age at death, trends in both stature and SSD were more similar between the early pre-Black Death sample (c. 1000-1200) and the post-Black Death sample (c. 1350-1540), compared to the late pre-Black Death group (c. 1200-1250). Differentials in male

ABSTRACTS

to female heights driving SSD values across these time periods may indicate differences in resource allocation by sex. This study underscores the importance of examining indicators of well-being by age-at-death category within their specific biohistorical context.

The mother infant dyad: Use of the neonatal line in dentine in the first permanent molar and primary teeth

MEGAN B. BRICKLEY, BONNIE KAHNON and LORI D'ORTENZIO

Department of Anthropology, McMaster University

The presence of the neonatal line (NL) in enamel has long been used in histological investigations of the perinatal period and growth and development. Dentine precedes enamel formation and we reviewed previously published literature to establish that a NL is present in the first permanent molars (M1s) and all primary teeth of live births. Incremental dentine formation was plotted for the complete dentition and a new method for locating the NL, which is not always clearly visible in dentine, was devised. A measurement is taken from the NL in the enamel to the dentino-enamel junction (DEJ), and an equal distance was measured from the DEJ into the dentine to establish the baseline for in utero formation in teeth with a NL. This information was then used to investigate the mother infant dyad using Interglobular dentine (IGD) as evidence for vitamin D deficiency in Canadian sample of M1s from living (n=9, Ontario) and archaeological individuals (n=9, 18th century Quebec). Four individuals had IGD, one modern and three archaeological. Two archaeological individuals, both from Quebec City, had prenatal IGD. The densely built environment of the growing city and social ideals on clothing for women, resulted in deficiency in pregnant females. We investigated IGD, but these techniques could also be used in investigation of stable isotopes. The neonatal line accurately demarcates tooth formation from the prenatal versus postnatal period, allowing detailed investigations of in utero health and providing a window into the experiences of women in past communities and potentially public health debates.

This research was undertaken, in part, thanks to funding from the Canada Research Chairs program. Canada Research Chair 231563, SSHRC

Women Warriors among Central California Hunter-Gatherers

KRISTEN A. BROEHL¹, MARIN A. PILLOUD¹, AL W. SCHWITALLA² and TERRY L. JONES³

¹Anthropology, University of Nevada, Reno, NV, ²Millennia Archaeological Consulting, Sacramento, CA, ³Social Sciences, California Polytechnic State University, San Luis Obispo, CA

Archaeological studies often assume immutable gender roles within hunter-gatherer societies, which can trivialize the role of women within society. Generally, women are assumed to be gatherers with limited roles in warfare and hunting. This study explores the role of women in violent behaviors as evidenced in bioarchaeological and ethnographic records from central California. Osteological data were retrieved from the Central California Bioarchaeological Database (n>18,000) that spans 3050 BC to AD 1899. A sub-set of males (n=289) and females (n=128) with only sharp force trauma were investigated to identify sex-based patterns of experienced trauma. Additionally, ethnographic records were investigated to identify mention of warfare, which was further subdivided by tribe, sex, the type of activity, and the equipment (i.e., weapon) used.

Bioarchaeological data indicate that males experienced a slightly higher prevalence of sharp force trauma than females. However, the patterns of trauma are very similar between males and females. Postcranial elements affected are analogous, with humeri and vertebrae showing the highest incidences in both sexes. The timing of injury is also comparable between males (87.03% perimortem; 12.97% antemortem) and females (81.34% perimortem; 18.66% antemortem). The trajectory of injury is also similar with a posterior trajectory identified in 42.62% of males and 40.54% of females. Ethnographic data support these findings as well as provide possible context for the skeletal patterns. Overall, results indicate males and females were active combatants whose experience in terms of violent behavior and sharp force trauma was very similar.

Using 3D prints of primates to teach evolution through comparative anatomy: a multi-modal educational module

HEATHER M. BROOKSHIER¹, DAWN M. MULHERN¹ and NADIA C. NEFF²

¹Anthropology, Fort Lewis College, ²Anthropology, University of New Mexico

Primate classification and comparative skeletal anatomy provide an excellent context for introducing basic principles of evolution. Educational modules for kids (ranging from 6 to 16) were developed by Fort Lewis College undergraduates and put into practice at the Powerhouse Science Center and MakerLab, a children's discovery center in Durango, Colorado.

Models of a variety of primate skulls were 3D printed to allow for hands-on discovery of the anatomical features within Order Primates. Scaled lesson plans were created to accompany this collection of prints so that the activity can be led by museum educators as a more formalized, field-trip activity, an intern-led gallery floor or off-site outreach activity, or an independently-guided exhibit for the Powerhouse Science

Center. Since the files are free and available on the internet, this module and its lesson plans can be shared with educators who have access to 3D printers, eliminating the need for a collection of expensive replica cast models. By engaging in the activity, learners are introduced to adaptations resulting from environmental pressures, as well as the biological similarities between humans and other living primates.

Three key outcomes of this project have been encouraging undergraduate students to develop educational outreach modules for the community, using 3D printing technology as a cost-effective way to make these modules available to those without teaching collections, and creating activities that improve students' life-long self-efficacy and therefore performance in science, whether they pursue anthropology or other scientific disciplines.

Ancient Human DNA Recovered From Promontory Caves Cordage

NASREEN Z. BROOMANDKHOSHBAKHT^{1,2}, HEATHER J. MILNE³, JOHN W. IVES³, LARS FEHREN-SCHMITZ^{1,2} and BETH SHAPIRO^{2,4}

¹Department of Anthropology, UC Santa Cruz, ²UCSC Paleogenomics, UC Santa Cruz, ³Department of Anthropology, University of Alberta, ⁴Department of Ecology & Evolutionary Biology, UC Santa Cruz

The topic of destructive analysis for ancient DNA research can be a source of tension between researchers and descendant communities, particularly if disturbing human remains goes against the beliefs of the descendant community involved. Recovering trace DNA from environmental samples (such as soil) or from artifacts that were heavily used during their service life (such as cordage or footwear) provides an opportunity to assuage many concerns of the community while still obtaining data pertinent to the research questions developed by the archaeologists and geneticists in conjunction with the indigenous communities involved. From a small sample of cordage excavated from Promontory Caves in Utah, we extracted and sequenced what appears to be authentic ancient human DNA. We look forward to working with indigenous communities in further exploring mitochondrial genome capture enrichment experiments. While there are many advantages and disadvantages to this method, our results show it is possible to recover authentic ancient human DNA from artifacts such as cordage samples.

ABSTRACTS

Craniodental fossils from a new locality in the Rising Star Cave System

JULIET K. BROPHY^{1,2}, MARINA C. ELLIOTT²,
TEBOGO MAKHUBELA³, DARRYL J. DE RUITER^{2,4},
JOHN HAWKS^{2,5} and LEE R. BERGER²

¹Geography and Anthropology, Louisiana State University, ²Evolutionary Studies Institute, University of the Witwatersrand, ³Geology, University of Johannesburg, ⁴Anthropology, Texas A&M University, ⁵Anthropology, University of Wisconsin

Homo naledi has been described from the Dinaledi and Lesedi Chambers in the Rising Star Cave System, South Africa. Recent explorations in the cave system have revealed a new fossil bearing site referred to as Grid S2000W800. This difficult to access area was identified in a narrow fissure 12 m southwest of the original Dinaledi Chamber excavation. Surface collections have recovered twenty-eight hominin cranial fragments and six hominin teeth. The largest refittable cranial fragments surround the region of bregma, including pieces of frontal and both parietals. Internally, an asymmetric frontal crest is visible with two concave features on either side. The right side is deeper and more concave than the left side, indicative of petalia. The teeth consist of left and right deciduous second molars (ldm², rdm²), a right permanent first incisor (RI¹), a right permanent second incisor (RI²), a right permanent fourth premolar (RP⁴), and a right permanent first molar (RM¹). The deciduous molars are moderately worn but the permanent teeth are unworn suggesting they were not in occlusion at the time of death. The cranial fragments and teeth are at similar stages of development and, as such, likely come from the same sub-adult individual. The morphology of the new specimens is consistent with that of *H. naledi* from the other localities in the Rising Star Cave system. The Grid S2000W800 craniodental materials provide evidence of *H. naledi* from a third locality in the Rising Star Cave system, and further support a homogeneous morphology for *H. naledi*.

Funding for this research was provided by National Geographic Society, South African Centre for Excellence in Palaeosciences, Palaeontological Scientific Trust, University of the Witwatersrand, and Louisiana State University.

Trabecular bone variation in the mandibular condyle and its association with diet in different Macaque species

ELLA J. M. BROWN¹ and JAY T. STOCK^{1,2,3}

¹Department of Archaeology, University of Cambridge, Cambridge, UK, ²Department of Anthropology, Western University, London, Ontario, Canada, ³Department of Archaeology, Max Planck Institute for the Science of Human History, Jena, Germany

Mandibular shape and size variation, in relation to diet, has been analysed extensively in different primate species. Variation exists in the

mechanical properties of foods consumed by primates and is considered to have an effect on the biomechanical loading, resulting in changes to the morphology of the mandible. In this study we test whether variation in the trabecular bone of the mandibular condyle corresponds with habitual dietary differences between Macaque species.

We compare Macaques from Africa and Asia, specifically: *Macaca mulatta*, *Macaca fascicularis* and *Macaca nemestrina* who are primarily frugivorous and occasionally folivorous, with *Macaca sylvanus* and *Macaca fuscata* who are considered hard-food eaters, particularly *fuscata*, which relies heavily on tree bark during winter. Data was collected via the Nikon XTH 225 ST HRCT Scanner at the Cambridge Biotomography centre and the Natural History Museum, London. Analyses consisted of volumetric measurements of trabecular bone in the condyle, including bone volume fraction (BV/TV), connective density (Conn.D) and degree of anisotropy (DA), which all contribute to the mechanical strength of bone.

ANOVA results illustrated significant variation between species in the degree of anisotropy, connectivity and bone volume fraction. Connectivity differed significantly between dietary groups. There were noteworthy differences in all trabecular variables between *Macaca fuscata* and all other Macaque species, indicating that climate or phylogenetic distance may have an impact on bone development. Results indicate a relationship between trabecular properties and dietary categories, however climate and phylogenetics also appear to influence the morphology of condylar trabecular bone.

This study was funded by the Cambridge AHRC Doctoral Training Partnership and the Isaac Newton Trust, and ADaPt Project, ERC grant number 617627 to JTS.

Early-Life Stressors in Pre-and Postcontact Peru: Evidence from Incremental Enamel Microstructures

GENEVIEVE BROWN, DANIEL TEMPLE and HAAGEN KLAUS

Sociology and Anthropology, George Mason University

This study seeks to understand how populations in the Lambayeque Valley Complex, north coast Peru, were affected by Spanish colonialism by analyzing linear enamel hypoplasia (LEH). Here, we compared two late pre-contact samples from Chotuna and Huaca de los Sacrificios (AD 1470-1532) with a sample from Eten dating to the Early/Middle Colonial era (AD 1535-1620). The three samples represent indigenous Muchik peoples from three distinct contexts (community cemetery, sacrifice victims, and postcontact mission cemetery). To characterize the timing of early-life biological stress, high resolution impressions were used to produce tooth crown replicas and studied under an engineer's measuring microscope.

Perikymata were measured from the most occlusal region of the imbricational enamel along the length of each tooth to the cemento-enamel junction. Accentuated perikymata were used as indicators for LEH and identified using z-scores and a moving average. Employing constants for crown initiation and cuspal enamel formation for each tooth and an eight-day periodicity for each perikymata, age-at-defect-formation was calculated. Age-at-defect formation ranged from 1.2 to 3.8 years. The interquartile range was between 1.6 and 2.9 years for the Eten sample, and 1.9 and 3.2 years for Chotuna/Huaca de los Sacrificios. These results suggest a shift in the timing of stress following contact, with an earlier onset of stress in the Colonial era compared to pre-contact samples. Combined with historical data and previous bioarchaeological studies, this work supports the understanding that Colonial populations endured elevated levels of stress early in life compared to those from pre-contact samples.

Redefining what it means to win an intergroup conflict among red-tailed monkeys (*Cercopithecus ascanius*) in Kibale National Park, Uganda

MICHELLE BROWN^{1,2} and MELISSA E. THOMPSON³

¹Dept of Anthropology, University of California, Santa Barbara, ²Ngogo Monkey Project, ³Dept of Anthropology, University of New Mexico

Group-level contests for access to food resources are hypothesized to have important fitness effects on individuals and groups. Few studies, however, have directly measured the short-term consequences of winning or losing these conflicts, and none have considered that what humans label a 'win' might not correspond with success from the perspective of the study subjects. To address these issues, we observed 86 intergroup encounters among six groups of red-tailed monkeys (*Cercopithecus ascanius*) at the Ngogo site in Kibale National Park, Uganda and tracked changes in energy balance – the difference between energy inputs and outputs – by measuring levels of urinary C-peptide of insulin. We first ran a complete model using all urine samples to model the effects of season, group, and individual identity, then used the residuals in a second model to estimate the effects of travel distance 90 min before and after an encounter. We found that energy balance immediately after an encounter is more strongly and positively predicted by travel before the encounter than by post-conflict movements (mixed-effects regression, $N = 111$, Wald $X^2_3 = 20.53$, $P < 0.001$). Moreover, groups that would normally be classified as winners traveled farther before encounters than losing groups (linear regression, $N = 74$, $F_{(2,71)} = 5.65$, $P = 0.005$). We suggest that the timing of a departure from

ABSTRACTS

a conflict site is likely a function of motivation – i.e., whether the group has had an opportunity to consume local resources – and not necessarily an indication of competitive inferiority.

Funded by the National Science Foundation (award #1103444), the Leakey Foundation, the Hellman Foundation, and the UCSB Academic Senate and the Institute for Social, Behavioral, and Economic Research.

Leprosy in Medieval Denmark: a multi-tissue and multi-isotopic approach to investigate life histories

ANASTASIA BROZOU¹, BENJAMIN T. FULLER¹, VAUGHAN GRIMES^{2,3}, GEERT VAN BIESEN⁴, NIELS LYNNERUP⁵, JESPER L. BOLDSSEN⁶, MARIE LOUISE JØRKOV⁵, DORTHE DANGVARD PEDERSEN^{6,7}, JESPER OLSEN⁸ and MARCELLO A. MANNINO¹

¹Department of Archaeology and Heritage Studies, Aarhus University, ²Department of Archaeology, Memorial University of Newfoundland, ³Department of Earth Sciences, Memorial University of Newfoundland, ⁴Core Research Equipment & Instrument Training Network (CREAIT), Memorial University of Newfoundland, ⁵Department of Forensic Medicine, University of Copenhagen, ⁶Department of Forensic Medicine, University of Southern Denmark, ⁷National Museum of Denmark, ⁸Department of Physics and Astronomy, Aarhus University

Leprosy is a chronic infectious disease with severe debilitating and crippling implications. During the medieval period, numerous leprosy hospitals were established in Europe. Even though historians still debate the true aim of leprosy hospitals (e.g. isolation vs. nursing), their establishment during a period when the notion of contagion was not fully understood provides key insights into medieval attitudes towards diseases and social relations. Combining archaeology, historical sources, biological anthropology and isotopic analysis ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$, $\delta^{34}\text{S}$, $^{87}\text{Sr}/^{86}\text{Sr}$, $\delta^{13}\text{C}_{\text{AminoAcids}}$), we investigate how leprosy affected both institutionalized individuals and Danish medieval society as a whole. We follow a multi-tissue and multi-isotopic approach to generate data on individual life histories, which is essential when dealing with the issue of stigma attached to disease. We further explore the organizational structure of these institutions (Næstved and Odense; 13th – 16th c.) by investigating dietary differentiations with local, contemporary communities and between sex, age and social groups. Isotope analyses on bulk collagen and amino acids indicate that the leprosy patients changed their diet during the last few years of life, which is compatible with institutionalization. Furthermore, sulfur and strontium isotope analyses found that the leprosy patients were local to the regions of the leprosy

hospitals. This combination of different threads of evidence weaves together a clearer and more detailed understanding of the social implications of leprosy in medieval Denmark.

Research funded by the Faculty of Arts, Aarhus University, the Aarhus University Research Foundation (M. A. Mannino); Danish & European Diets in Time, the Elisabeth Munksgaard Fonden (A. Brozou).

Habituation, Avoidance Strategies, and Social Learning in Wild Bornean Orangutans in Gunung Palung National Park, Indonesia

LAURA A. BRUBAKER-WITTMAN¹, ERIN E. KANE¹, TRI WAHYU SUSANTO² and CHERYL D. KNOTT^{1,3}

¹Anthropology, Boston University, ²Biology, National University of Indonesia, ³Biology, Boston University

Habituation, or the process of an animal becoming comfortable with human observers, is an essential part of wild primate observational studies. Despite the importance of this process, questions remain as to what counts as habituated for a particular species, how individuals and species react to humans, and how age-sex classes differ in these responses. To address these questions, we analyzed data from over 25 years of research on wild Bornean orangutans from Gunung Palung National Park, Indonesia, drawing from 8,383 follows and 82,413 hours of observation. We categorized the degree of agitation with humans by totaling the number of alarm vocalizations, giving each follow a score of 1-10. We then looked at behavioral measures using a GLMM to control for individual and food availability. This revealed that individuals with the highest vocalization scores spent a greater percentage of the day traveling ($b=40.5$, $p < 0.0001$), stayed higher in the canopy ($b=16$, $p < 0.0001$) and spent less time eating ($b=205$, $p < 0.0001$) than did animals that did not vocalize. Our analysis also revealed a less common, but frequently observed, opposing response to humans, which was to hide, often inside of a day nest, and emit no vocalizations. Individual orangutans were observed to switch between these two 'strategies' to evade human observers. We discuss the implications of this behavior as well as present evidence that the reaction of other orangutans mediates the response of focal individuals to humans, suggesting the importance of social learning in this behavior.

NSF (9414388, BCS-1638823, BCS-0936199); National Geographic; USFish/Wildlife (F18AP00898, F15AP00812, F13AP00920, 96200-0-G249, 96200-9-G110); Leakey; Disney Conservation Fund; Wenner-Gren; Nacey-Maggioccalda; Conservation-Food-Health; Woodland Park Zoo.

Extrinsic and intrinsic effects on nutritional strategy in redbtail monkeys (*Cercopithecus ascanius*)

MARGARET A. H. BRYER^{1,2} and JESSICA M. ROTHMAN^{1,2,3}

¹Anthropology, The Graduate Center of the City University of New York, ²New York Consortium in Evolutionary Primatology, ³Anthropology, Hunter College of the City University of New York

An animal's nutritional requirements and intake fluctuate by extrinsic spatiotemporal variation in food availability and food nutritional composition as well as by intrinsic variables like reproductive status. We examined the effects of fruit availability and reproductive status on nutrition of female redbtail monkeys (*Cercopithecus ascanius*) in three study groups in Kibale National Park, Uganda. When ripe fruit availability was low, daily intake of available protein ($b = 1.01$, $t(112) = 3.12$, $p = 0.002$) and fiber ($b = 1.09$, $t(112) = 3.40$, $p < 0.001$) was higher. Redtail monkeys gained protein from young leaves, insects, and some unripe fruits, leading to increased protein intake in low ripe fruit periods. When availability of fruit of any ripeness (ripe and unripe) was low, daily intake decreased for protein ($b = -1.16$, $t(112) = -4.05$, $p < 0.001$) and fat ($b = -0.82$, $t(112) = -2.38$, $p = 0.02$), explained by redtails using some unripe fruits as protein and fat sources. Reproductive status did not affect daily intake of metabolizable energy, nonprotein energy, fiber, nonstructural carbohydrates or fat, indicating that mobilizing fat stores could provide energy for reproduction. How primates alter their nutritional strategy when faced with dynamic food availability and physiological states gives us insight into how animals interact with their environment to reach nutritional goals enabling survival and reproduction.

This study was funded by NSF BCS 1540369 (DDRI Bio Anth), NSF BCS 1521528, NSF BCS 0922709, and NSF DGE 0966166 (NYCEP IGERT).

Sex differences in bilateral asymmetry of the clavicle and humerus in medieval Giecz, Poland

EMMA T. BRZEZINSKI and AMANDA M. AGNEW
Department of Anthropology, Skeletal Biology Research Lab, The Ohio State University

Bilateral asymmetry of skeletal elements of the upper extremities provides an important record of functional adaptation and workload in present and past populations. Variation in skeletal asymmetry is partially attributed to effects of mechanical loading due to dominant limb use associated with "handedness". Furthermore, asymmetry differences between males and females can reveal a sexual division of labor. The objective of this research was to evaluate sex differences in bilateral asymmetry of the clavicle and humerus in a medieval Polish population.

ABSTRACTS

The sample included skeletally mature males (n=89) and females (n=53) from the early Medieval (11th-12th c.) cemetery in Giecz, Poland, site Gz4. Across all variables for both elements, there was significant sexual dimorphism, with males being larger (Kruskal-Wallis test, $p < 0.0001$). In the humerus, asymmetry values between males and females were significantly different (Kruskal-Wallis test, $p < 0.05$) for maximum length with a right-side bias, but not for midshaft dimensions. The clavicles showed significant asymmetry between sexes for maximum length with a left-side bias ($p = 0.019$) and superior-inferior diameter with a right-side bias ($p = 0.007$), but not anterior-posterior midshaft diameter ($p = 0.075$). These findings suggest a general tendency in the population to be right-handed. Since bone length is likely more influenced by growth and development and less by physical activity in adulthood, values at midshaft should be prioritized for interpretations of workload. Asymmetry was most pronounced in midshaft dimensions despite the general lack of sexes differences, suggesting that physical activity placing differential mechanical demands on each upper limb may have been similar between sexes in Giecz.

The effects of admixture in the pelvis

LAURA T. BUCK^{1,2}, DAVID C. KATZ^{2,3}, REBECCA ROGERS ACKERMANN^{4,5}, LESLEA J. HLUŠKO⁶, SREE KANTHASWAMY⁷ and TIMOTHY D. WEAVER²
¹School of Biological and Environmental Sciences, Liverpool John Moores University, ²Department of Anthropology, University of California Davis, ³Cell Biology and Anatomy, University of Calgary Cumming School of Medicine, ⁴Department of Archaeology, University of Cape Town, ⁵Human Evolution Research Institute, University of Cape Town, ⁶Department of Integrative Biology, University of California Berkeley, ⁷School of Mathematical and Natural Sciences, Arizona State University

Recent advances in genetic analyses have uncovered evidence of multiple admixture events during human evolution; yet, the role of admixture in determining gross anatomy is still poorly understood. In this context the pelvis is particularly interesting, due to its complex shape and interactions between the constraints of locomotion and parturition. The pelvis is also amongst the most divergent regions between *Homo sapiens* and Neanderthal skeletons, leading to potential ramifications for hybrid offspring. Here we use a large, multigenerational sample of Chinese and Indian rhesus macaques (*Macaca mulatta*) and their admixed progeny as a proxy to investigate the role of admixture in hominin pelvic evolution. Unlike many non-human hybrid studies, our sample includes animals with a range of admixture proportions, from low percentages of Chinese ancestry to low percentages of Indian. This range of admixture is a good representation of what we expect in natural hybrid zones and in

the fossil record. Our geometric morphometric approach indicates that, while sexual dimorphism is the strongest determinant of morphology as expected, there is a weak admixture signal in pelvic shape. The magnitude of the admixture signal likely reflects a relatively small pelvic shape difference between the macaque subspecies, in contrast to the relatively disparate morphology of *H. sapiens* and Neanderthals. We discuss potential functional constraints on admixture expression in different skeletal regions and the implications of our results for identifying hybrids in the fossil record.

This research was funded by grants #1623366 and #1720128 awarded by the National Science Foundation (USA) and by The Leakey Foundation.

The Aquatic Neolithic: isotope, aDNA, radiocarbon, and osteological data analysis reveal asynchronous behavior in early prehistoric human societies of Ukraine

CHELSEA BUDD¹, INNA POTEKHINA², CHRISTOPHE SNOECK³ and MALCOLM LILLIE¹

¹Department of Historical, Philosophical and Religious Studies, Umea University, ²Institute of Archaeology, National Academy of Sciences of Ukraine, ³Analytical, Environmental & Geo-Chemistry (AMGC), Vrije Universiteit Brussel

In Europe the characterization of the Neolithic period is traditionally dominated by the advent of agro-pastoralism. Neolithic populations in the Dnieper Valley region of south-central Ukraine are notably divergent from this trend. From the Epi-Palaeolithic-Neolithic periods (ca. 10,000 - 6000 cal BC), evidence for the adoption of agro-pastoral technologies is absent from archaeological assemblages. It is not until the Eneolithic period (ca. 4500 cal BC) that we observe the beginnings of a transition to farming in the Dnieper region. One hypothesis suggests that spikes in aridity propagated a hunting crisis in Mesolithic populations, which prompted a delay in the transition and the reshaped of Mesolithic subsistence practices to focus on freshwater aquatic resources to supplement terrestrial herbivores such as boar and deer.

This research presents 300+ human and faunal samples (including 80 unpublished results), using multi-disciplinary techniques such as DNA analysis and various isotope applications, alongside osteological analysis, to provide holistic individual life histories. The results show long-term continuation of fishing practices from the Epi-Palaeolithic to Neolithic periods - no distinct shift from hunting to fishing practices took place. DNA results show the predominance of indigenous hunter-gatherers, with limited genetic inclusions from proximal Anatolian farming populations. Thus, despite the availability of plentiful dietary resources and the westward influence of extra-local farming populations, the prehistoric communities of the Dnieper

region remained resistant to change and resilient in terms of their subsistence strategies, with freshwater resources providing a 'buffer' against any perceived impacts from climate variability.

Enthesal Change within St. Gregory's Priory: An Assessment Based on Age, Sex, and Social Status

JOSHUA BUINICKY and EMMY BOCAEGE
School of Anthropology and Conservation, University of Kent

Changes seen within enthesal attachments—areas where connective tissues attach to the bone—are useful to recreate human activity through scoring bony changes due to habitual movement. The aim of this study is to verify the significance between age, sex, and social status of entheses, as well as, their feasibility to generate a biological profile, found within the skeletal collection of St. Gregory's Priory medieval burial site in Canterbury, England. Using the Coimbra method, nine fibrocartilaginous entheses, from 58 individuals, were assessed. Significance was found factoring for sex, but not for age or social status. Observational trends showed greater expression within male individuals, and along the left side of the body. Using a Mann-Whitney U test, five of the nine attachment sites resulted in significant values ($p < 0.05$) based on sex. Assessing for age and social class no significant results were found. This research concluded that the use of enthesal change in regards to building a biological profile is only feasible for sex determination.

A reassessment of E. A. Hooton's metric analyses of crania from Madisonville, an Ohio Fort Ancient site (1275-1640 C.E.)

M. LORING BURGESS and MICHÈLE E. MORGAN
Osteology Department, Peabody Museum of Archaeology and Ethnology, Harvard University

100 years ago, E. A. Hooton published a monograph with craniometric and nonmetric data on individuals from Madisonville. Hooton used these data to make numerous observations about cranial shape variation based on very little comparative data; for example, noting that Madisonville individuals had relatively short, broad palates for their facial proportions compared to other populations. Our study aims to verify the comparability of Hooton's craniometric data to other commonly-used archival craniometric datasets and to reevaluate Hooton's conclusions about the morphology of Madisonville individuals through comparisons to archival data from other populations.

We independently remeasured 50 individuals from Hooton's original study following his described protocol, with repeated measures ANOVA used to compare each measurement between the three observers. Results were largely similar across

ABSTRACTS

observers, suggesting that Hooton was collecting craniometric data consistently with his cited standards. One exception is upper facial height, which post-hoc tests with family-wise error rate of .05 found was significantly shorter in the more recent measurements. This questions Hooton's assertions about palate and facial shape in Madisonville. Comparison of Hooton's data from Madisonville with craniometric data collected by Hrdlička on other indigenous North American populations did not show that Madisonville individuals differed significantly from other groups in relative palate dimensions (ANOVA, $p > .05$). While some prior interpretations of these datasets have been problematic, the primary data themselves have intrinsic value for understanding human variation. This preliminary reassessment is part of a larger multidisciplinary project seeking to improve documentation on Ohio archaeological collections and stimulate further engagement and research.

Bioarchaeological (Un)Change in Woodland Period Louisiana

STEVEN N. BYERS

N/A, Retired

Skeletal biological data from four Louisiana Woodland period sites, dating from all of the sub-periods, were analyzed to elucidate any bioarchaeological trends that might have occurred through time. The teeth and bones of 493 mainly incomplete individuals from Little Woods (Early Woodland), Lafayette Mounds (Early Woodland), Crooks (Middle Woodland) and Greenhouse (Late Woodland) were observed for the usual bioarchaeological traits. Analysis revealed a number of inter-site differences, but with no clear trends. That is, parameters like stature or tooth loss or frequency of porotic hyperostosis did not increase or decrease through time. Nor did one site consistently display differences from the other three for all (or even most) of the traits. Also, when differences did occur, they did not correlate with traits that should also have showed differences (e.g., a site with more caries than expected did not show greater rates of periodontitis, calculus, abscesses, and antemortem tooth loss). Only one fairly clear trend was noted: an increase in the frequency of artificial cranial deformation through time. Thus, the data gathered in this study indicates very little human biological change during the Woodland period of Louisiana, despite culture changes elucidated by archaeology.

Signatures of adaptive evolution in Neotropical primate genomes with a focus on capuchin monkeys

HAZEL BYRNE^{1,2}, PATRICIA IZAR⁴ and JESSICA W. LYNCH^{2,3}

¹Department of Anthropology, University of Utah, ²Institute for Society & Genetics, UCLA,

³Department of Anthropology, UCLA, ⁴Department of Experimental Psychology, University of São Paulo

Neotropical primates (Platyrrhini) are a diverse mammalian clade with five families, 21 genera and over 170 species – as with their sister clade (Catarrhini), a plethora of forms, behaviours, and life histories are found across this group. Capuchin monkeys are characterised by a diverse behavioural repertoire; the “apes of the Neotropics” show many striking similarities to Hominidae including social conventions and local culture, intelligence, delayed life history, high dexterity, tool use and extractive foraging. To gain insight into the evolutionary trajectory of capuchin monkeys, a *de novo* draft genome assembly for robust capuchins (*Sapajus apella*) was constructed and scaffolded using Dovetail's proximity ligation data to obtain a highly contiguous assembly with a scaffold N50 of 27.1Mb (29 scaffolds). Following standard genome annotation and preparation pipelines, we employed a suite of evolutionary models in PAML to uncover genes with accelerated rates of evolution and/or with positively selected sites in Neotropical primates. We focused on four extant lineages; the encephalised capuchin monkeys (both *Sapajus* and *Cebus*), as well as the miniaturised marmoset (*Callithrix*), and the highly social squirrel monkey (*Saimiri*). The results of these analyses shed light on the evolution of lineage-specific traits within these groups of Neotropical primates including the unique twinning reproductive biology of the marmoset and the differing capuchin phenotypes. We also assessed the ancestral branch to Neotropical primates to understand the targets of selective pressures putatively related to their adaptation to the novel environment of the Neotropics, with accelerated rates inferred across genes related to immunity.

Strain Energy Variation Relates to Food Effects while Strain Orientation Relates to Individual Effects in Robust and Gracile *Cebus* Morphotypes

CRAIG D. BYRON¹ and CALLUM F. ROSS²

¹Biology, Mercer University, ²Organismal Biology and Anatomy, University of Chicago

Laboratory trained *Cebus* monkeys of both robust and gracile morphotypes were used to record suture strain and muscle activity simultaneously while subjects fed on several different foods with contrasting material properties. This included three gage sites along the sagittal suture (bregma, middle, and lambda) and several EMG recording sites within masseter and temporalis muscles. In this study we sought to explain variance in suture strain energy and orientation during feeding on various item types. Using RStudio (version 1.1.456) a series of mixed effects models were calculated with random factors (Individual and Food Item Type) as well as fixed factors (Chew

Side, Chew Cycle Type, and Strain Gage Site). For measures of strain magnitude (Log10Max, Log10Min, and Strain Mode ratio) the food effect explains more variance than the individual effect. For strain orientation data the individual effect explains more variance than the food effect. One interpretation is that food has a greater impact on masticatory strain magnitudes than the individual subject in our experiment. Conversely, strain orientations transduced through the sagittal suture at different strain gage recording sites are explained more by individual effects and not as much by the specific food being consumed. Results show significant variation in strain regimes along the sagittal suture. Strains are laterally directed but strain mode data does not suggest this is strongly in tension. However, for the very robust specimen, many of the chew cycle observations on nuts and nut shells are tensional, especially at the posterior end of the suture.

This research was funded by the NSF HOMINID grant (BCS 0725147).

For Sale: A Study of the Primate Pet Trade in the United States

SYDNEY N. CAHOON¹ and MELISSA S. SEABOCH^{1,2}

¹Anthropology, University of Utah, ²Anthropology, Salt Lake Community College

The depiction of wild animals in the media can lead to an increased desire to own one, such as the increase in the sale of owls following the Harry Potter movies. We are interested in whether this is the case for primates. There are over 15,000 pet primates in the U.S. despite agreement among primatologists and veterinarians that they do not make good pets. Capuchin monkeys are the most common monkey featured in films (e.g. Night at the Museum, Pirates of the Caribbean), and in TV shows (e.g. Friends) while the Madagascar franchise popularizes lemurs. Based on this media influence, we hypothesized that capuchins and lemurs will be the most common type of primate for sale. We recorded the type of primate for sale twice a month from six exotic pet-trade websites. There were 373 primates for sale between May and September 2019 with 19% strepsirrhines, 72% platyrrhines, and 9% catarrhines; no apes were for sale. Marmosets were sold most often (28.7%, $n=107$) followed by lemurs (18.8%, $n=70$), and capuchins (17.4%, $n=65$). Five types of primates (marmosets, lemurs, capuchins, squirrel monkeys, and tamarins) made up 87% of all primates for sale; it is noteworthy that all are smaller primates. Contrary to our hypothesis, lemurs and capuchins were not the most common type of primate, though they were second and third respectively. While we cannot confirm whether media depictions have increased the desire for certain types of primates, the inclusion of lemurs, the only non-platyrrhine, in the top five is intriguing.

ABSTRACTS

Social stratification and its differential experience at Middle Kingdom (2050-1650 B.C.) sites in Egypt

ALYSON C. CAINE

Department of Anthropology and Heritage Studies,
University of California, Merced

The imperialist position of the Middle Kingdom (2050-1650 BC) and subsequent demographic diversity of Egyptian territory led to societal stratification. While elite narratives have dominated archaeological research and interpretations, there is little known of non-elite individuals. This research studies elites and non-elites from two Middle Kingdom Egyptian sites, Naga-ed-Dêr and Mesheikh, to understand the biocultural effects of social stratification through the analysis of paleopathological conditions. The results of this analysis provide insight into differential experiences of elites and non-elites contextualized through mortuary information.

A total of 187 individuals (Naga-ed-Dêr $n=115$; Mesheikh $n=76$) were observed for pathological conditions that may reflect social inequality, including those that may result from differential social treatment and/or differential access to resources. Among all individuals presented in this study, 18% ($n=33$) were observed with trauma, 59% ($n=109$) were observed with evidence of metabolic disease, and 19% ($n=35$) were recorded with at least one abscess. A Fisher's exact test found the rate of metabolic disease and abscess in Naga-ed-Dêr individuals to be statistically significant, ($p<0.0001$) and ($p=0.0245$) respectively, while the rate of trauma observed was not statistically significant, according to a Fisher's exact test ($p=0.6166$). Of these individuals, material culture associated with 64 individuals from Naga-ed-Dêr which has been combined with osteological analysis to understand how social status manifests in the mortuary context. Multidimensional correspondence analysis has indicated that individuals identified with pottery and jewelry had no evidence of trauma or abscesses suggesting individuals buried with these artifacts may have been of a higher social status.

Surviving Raids in Small Scale Societies: Finding Hidden Females Fighters in the Ancient Southwest

MARYANN CALLEJA and DEBRA L. MARTIN

Anthropology, University of Nevada, Las Vegas

When examining violence in archaeological contexts, the roles of females are minimized. This is because (male) researchers use models of fighting and warfare in historic and more recent times and overlay those on to indigenous people in precontact times as an *a priori* assumption. Ancient indigenous females are often relegated to more passive roles or roles of diminished significance. In an effort to provide a more nuanced representation of the women living in the ancient

southwest, we conducted a bioarchaeological analysis of skeletal remains from two distinctly separate sites within relatively close proximity, Point of Pines Pueblo (~AD 1260-1400) and Kinishba (~AD 1160-1320). Despite similarities in cultural composition, time periods, and geographic locations, notable differences were found between and within each site. A comparison of adult crania from Point of Pines Pueblo and Kinishba ($N=111$ and $N=57$, respectively) indicate that an equal or greater percentage of women than men from both sites had one or more healed cranial depression fractures forensically interpreted to be due to violence (versus accidental or occupational). The size, location, angle, placement, and orientation of the head wounds are similar to forensic cases supporting face to face fighting. Ethnographic, forensic, archaeological and bioarchaeological lines of evidence suggest that females likely participated in raiding and sustained head wounds as active participants. The combined data sets offer a more nuanced interpretation of violence in general and violent women in particular who up until now have been both hidden and invisible in interpretations about raiding in the ancient southwest.

Applications of spatial analyses in Holocene Later Stone Age southern African bioarchaeology

MICHELLE E. CAMERON

Department of Anthropology, University of Toronto

Holocene Later Stone Age (LSA) southern Africans from the Cape coast have been well-studied in terms of bone collagen stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope ratios and cross-sectional geometric properties (CSGPs). Some individuals have isotopic ratios indicative of marine resource exploitation and most individuals have CSGPs indicative of highly mobile lifeways. Ecological factors may have affected LSA skeletal variability. However, it is challenging to assess the degree of skeletal variation that arose in response to ecological conditions among past groups. LSA skeletal properties are often compared among groups from different ecologies such as the forest and fynbos regions of the Cape coast. These regional analyses may mask the contribution of site-specific variation in skeletal properties. Spatial analyses of skeletal variation on the Cape coast were conducted using Geographic Information Systems to assess spatial distributions of LSA stable isotopic and biomechanical properties. Spatial autocorrelation analyses (Global Moran's I) and interpolation were used to assess if particular skeletal traits clustered in specific ecologies or at specific locales. Burial and archaeological site locations of LSA southern Africans ($n=40$) were used to locate individuals on the landscape. Previously published $\delta^{13}C$ and $\delta^{15}N$ values and CSGPs for LSA individuals were incorporated into spatial models. Preliminary results indicate that

meaningful clusters of stable isotopic or biomechanical data may best be defined based on the archaeological site or burial location where individuals were recovered. Inter-site variation may best explain the patterns evident in these skeletal properties rather than regional comparisons based on ecology.

University of Toronto Faculty of Arts & Science Tri-Council Bridge Funding Program

Reinterpreting Human Sacrifice in Ancient Egypt: New Conclusions from Old Data

ROSELYN A. CAMPBELL

Scholars Program, Getty Research Institute

Surrounding the tombs and funerary enclosures of the earliest kings of Egypt are hundreds of subsidiary burials of officials, craftsmen, and members of the royal court. The majority of these subsidiary burials were plundered in antiquity, but many were excavated and recorded in the early 20th century. The apparent lack of skeletal trauma combined with circumstantial evidence for human sacrifice has led to much debate about the nature of these burials, and whether they were sacrificial in nature. The incomplete and altered nature of these remains, due to 20th century interventions and taphonomy, has caused them to be largely ignored.

This study assesses 48 crania from subsidiary burials associated with two kings and one queen of the late fourth millennium BCE and describes new data that was recovered through comparison with modern forensic cases. Though scholars have consistently stated that the remains show no evidence of trauma, this study found clear examples of lethal perimortem cranial fractures, strongly suggesting human sacrifice. By re-analyzing the physical remains as well as the context of these burials, it becomes clear that expediency was a primary concern of the sacrificial burials, but that other factors such as sex and social status may also have played a role in the mode of death and burial. Identifying the clear evidence for trauma in these remains, and assessing the reasons for variation in the traumatic injuries within the context of ancient Egyptian culture, provides new interpretations of the practice of human sacrifice in the nascent Egyptian state.

Step cycles in three sympatric cercopithecids

TESSA H. CANNON¹, JORDAN TRAFF², DAVID J. DAEGLING² and W. SCOTT MCGRAW¹

¹Department of Anthropology, The Ohio State University, ²Department of Anthropology, University of Florida

Relationships between primate limb structure and behavior are often investigated using proportions of positional repertoires such as time spent leaping, climbing, or moving quadrupedally.

ABSTRACTS

Recent biomechanical analyses suggest several aspects of bone architecture are more readily interpreted using number of loading cycles compared to maximum loads. If true, then relationships between individual positional behaviors and the corresponding number of cycles (e.g., steps) should be established. The primates of Cote d'Ivoire's Tai Forest provide an excellent opportunity to investigate associations between specific cycle quantities and percentages within locomotor profiles because these cercopithecids display a relatively high positional diversity across a narrow body size range. Here we report step data during quadrupedalism in three sympatric taxa collected during all day follows. One adult female red colobus (*Ptilocolobus badius*), Diana monkey (*Cercopithecus diana*), and Sooty mangabey (*Cercocebus atys*) was followed for 30 days and the total number of quadrupedal steps performed each hour recorded. Average steps per minute for each taxon were compared to activity budgets, locomotor profiles and home range size. The three taxa differ dramatically in the frequency their limbs are loaded during locomotion ($p < 0.001$): mean steps/minute for red colobus, Diana monkeys and Sooty mangabeys were 4.04, 12.23, and 33.9, respectively. Step rates do not consistently co-vary with percent of activity budget spent moving quadrupedally but do correlate with home range size. We conclude that attempts to interpret the structure of limb bones will enjoy greater success if field researchers count step cycles in addition to building general positional behavior profiles.

Supported by NSF BCS-1440278 and -1440532

Ethnoprimateology: Preliminary Results of An Applied Approach to Highway Construction in Costa Rica

T A. CAPEL, MELISSA J. REMIS and STACY LINDSHIELD

Anthropology, Purdue University

Humans and nonhuman primates live together in numerous locations, including the Refugio de Gandoca-Manzanillo, Jario Mora Sandoval (REGAMA), Costa Rica. Even in areas with long-term human-nonhuman primate relationships, a sudden increase in human activity can have unintended effects, including deforestation and resource loss. There are plans for a highway to be built through REGAMA, so this project aims to assess the state of the forest before construction begins. This data set will be used as a baseline to assess future changes in the area. A mixed methodology was used to collect 59.01km of transect data and conduct 28 semi-structured interviews. This project also uses applied frameworks to provide local conservation organizations with important conservation data. Preliminary results show more visual encounters of nonhuman primates (1.17 groups/sq km) than humans (0.83/sq km) along the transect.

Alouatta palliata (mantled howler monkey) are the most commonly seen (1.02 groups/sq km) and heard (2.99 groups/sq km) monkey. *Cebus imitator* (white-faced capuchin) and *Ateles geoffroyi* (black-handed spider monkeys) were rare but seen on the transect at 0.10 groups/sq km and 0.05 groups/sq km, respectively. Interview data suggests the monkey species are considered useful animals, especially in relation to tourism. It also revealed the most valued animal species are those hunted for sustenance. This dataset will be shared with local conservation projects and can be compared to future planned data collections, allowing researchers to assess change over time.

College of Liberal Arts, Purdue University: Promoting Research Opportunities to Maximize Innovation and Scholarly Excellence (PROMISE) Grant

Cataloging the Regulatory Landscape of Human Skeletal Development Via Functional Genomics: Insights into Human Pelvic Evolution

TERENCE D. CAPELLINI, MARIEL YOUNG, PUSHPANATHAN MUTHURULAN, VISMAYA KHARKAR and DANIEL RICHARD

Human Evolutionary Biology, HARVARD UNIVERSITY

Underlying the vast skeletal differences between species as disparate as humans, chimpanzees, and mice are thousands of regulatory changes in each genome. While many molecular pathways are conserved between species, justifying the use of the mouse model to shed light on conserved developmental processes, derived human skeletal traits likely have little shared biology with mice. Therefore, to move beyond the mouse model, we have performed assays on rare human skeletal samples acquired from the Roadmap Epigenomics Project. Skeletal preparations spanning gestational day (E)54-94 reveal that at the level of chondrogenesis, derived human girdle and limb skeletal traits are present early prenatally and prefigure adult morphology much earlier than previously documented. Using the functional genomics assay ATAC-seq on E54 and E67 tissues (N=3 per timepoint), we reveal a catalogue of 68,604 previously undocumented genomic regulatory regions utilized in human skeletal development. Of these, 49,600 are active in the pelvis and scapula at E54, and only 38.2% overlap with stage-matched mouse regions, highlighting substantial regulatory divergence. A subset of these regions also display evidence of positive selection: 195 overlap Human Accelerated Regions (HARs), of which 38 are pelvis-specific and 41 are scapula-specific. Given the unique morphology of the human ilium, we have targeted 7 iliac-specific regulatory regions overlapping HARs that may underlie derived biology. By investigating these and other regions across the skeleton, we aim to link genotype to phenotype

and pinpoint where in the human genome natural selection targeted in order to create such different skeletal phenotypes between humans and chimpanzees.

This research was funded by Harvard University Dean's Competitive Fund

Experimental investigation of phytoliths and combustion features and their relevance for the 'Cooking Hypothesis' from East Turkana, Kenya

TAMARA CAPPS¹, GEORGIA OPPENHEIM², JEANWON KIM³, DEANNA MAYBEE⁴, MICHAELA HOWELLS¹, DAVID R. BRAUN⁵ and SARAH HLUBIK⁵

¹Anthropology, University of North Carolina Wilmington, ²Anthropology, Wellesley College, ³Anthropology, New York University, ⁴Anthropology, SUNY Binghamton, ⁵Center for the Advanced Study of Human Paleobiology, The George Washington University

The Cooking Hypothesis proposes that human use of fire was responsible for major biological changes seen in the Homo lineage (~2 mya), yet there is little archaeological evidence of fire usage during this time period. Confirmed identification of combustion features associated with hominin behavior in the Early Pleistocene archaeological contexts requires a greater diversity of proxies for FxJ20AB. We report on experimental research to identify the possible use of phytoliths as proxies for use of fire. Phytoliths are silicate particles of plants that resist degradation and may discolor when burned at high temperatures. We examined phytoliths from experimental fires to assess the reliability of this proxy for identifying concentrated fires in open-air contexts. Experimental fires (n=18) were set for variable time lengths (15 minutes - 12+hours) while maintaining the temperature (>700°C). We collected sediment samples before and after burning to contextualise pre- and post-fire contexts. We analyzed phytoliths for evidence of burning and changes in taxonomic proportions in phytolith assemblages. Preliminary analyses indicate that phytolith movement is difficult to predict with burned phytoliths found in both pre- and post-fire assemblages, highlighting the need for more research. We expected pre-fire assemblages to contain greater amounts of grass due to frequent die offs and post-fire assemblages to reflect a greater amounts of wood due to stoking the fires. When examining the phytoliths, we discovered the opposite was occurring. A larger sample size is needed to determine if phytoliths are an adequate proxy for determining Early Pleistocene fire in open-air contexts.

This research funded in part by the NSF Archaeology program #1624398 and a supplemental REU #1930719.

ABSTRACTS

An examination of the variation in enthesal changes in human skeletal remains discovered in a 15th century necropolis in Mistihalj, Montenegro

GABRIELLA K. CARD¹ and SEAN D. TALLMAN^{1,2}

¹Anthropology, Boston University, ²Anatomy and Neurobiology, Boston University School of Medicine

This study examines the variability in enthesophytes on human skeletal remains in an archaeological collection from the former Yugoslavia. Twenty entheses on 125 individuals (f=42; m=83) from the Mistihalj, Montenegro collection housed at the Harvard University Peabody Museum of Archaeology and Ethnology were examined for enthesal changes (EC). EC, also known as musculoskeletal stress markers, have been utilized to aid in the reconstruction of past populations' activity patterns. In particular, this study examined which variables (age, sex, body size) may affect EC expression for the investigation of the relationship between EC and activity patterns. EC scores were measured on a 0 to 3 scale and an aggregate EC score was generated for each individual. Humeral measurements were utilized as proxies to body size. Aggregate EC scores were found to correlate significantly with age ($p < 0.001$), sex ($p = 0.005$), and body size ($p < 0.001$). However, after controlling for body size, aggregate EC score and sex were no longer significantly correlated ($p = 0.933$). This suggests that differences in EC score between sexes are more likely due to body size rather than a sexual division of labor. Age also impacts seven EC scores, with age groups 16-24 years and 45-54 years showing the most difference. These results highlight some of the variables that may affect EC expression which is important when evaluating the relationship between EC and activity patterns. Though it is difficult to compare across studies due to a lack of standardization of methods, further research will examine similarities and differences between this population and others.

This research was funded by the Boston University Undergraduate Research Opportunities Program.

Patterns in and determinants of cortical thickness and rigidity in the humeral diaphysis of Holocene *Homo sapiens*

KRISTIAN J. CARLSON^{1,2}, MARK R. DOWDESWELL³, ELISA CHENG¹, KIMBERLEIGH A. TOMMY⁴, EMILY ZHU¹, NICHOLAS B. STEPHENS⁵, LILY J. DEMARS⁵, JAAP P.P. SAERS⁶, JOHN R. JOHNSON⁷, TACY KENNEDY⁷, JAY T. STOCK^{6,8}, TIMOTHY M. RYAN⁵, ADAM D. GORDON⁹ and TEA JASHASHVILI^{10,11}

¹Department of Integrative Anatomical Sciences, University of Southern California, Keck School of Medicine, ²Evolutionary Studies Institute, University of the Witwatersrand, ³School of Statistics and Actuarial Science, University of the Witwatersrand, ⁴School of Anatomical Sciences, University of the Witwatersrand, ⁵Department of Anthropology,

Pennsylvania State University, ⁶Department of Archaeology, University of Cambridge, ⁷Department of Anthropology, Santa Barbara Museum of Natural History, ⁸Department of Anthropology, Western University, ⁹Department of Anthropology, University at Albany, SUNY, ¹⁰Molecular Imaging Center, Department of Radiology, University of Southern California, Keck School of Medicine, ¹¹Department of Geology and Paleontology, Georgian National Museum

Modern humans are widely considered to have undergone postcranial gracilization since the Late Pleistocene. Hints of greater complexity than would be characterized by a linear trend in skeletal gracilization are emerging, however. What drives this complexity is uncertain. Here we systematically evaluate humeral diaphyses from eight diverse modern human groups, focusing on visualizing and quantifying cortical bone thickness and rigidity around and along shafts. We assess whether factors such as activity levels or patterns, geography, subsistence strategy, diet, and substrate may contribute to structural variability.

Using image data acquired through medical and high-resolution computed tomography, we digitally quantify cortical bone from 20% to 80% diaphyseal length in 82 human humeri representing North American, African, and European populations. We measure cortical thickness and second moments of area around and along diaphyses. We use color maps to visualize and qualitatively evaluate observed patterns and apply penalized discriminant function analyses to quantitatively evaluate them.

Among the considered intrinsic and extrinsic (e.g., environmental and behavioral) factors, purported group activity patterns differentiate not only magnitudes in cortical thicknesses and second moments of area, but also relative locations of high levels in both. Additional factors contribute to the observed variability. Since the patterns observed in humeral diaphyses do not correspond precisely to those expressed in other elements from the same sample, limb specific effects (e.g., usage) are deemed partly responsible for the observed variability. Analysis of bilateral asymmetry in humeral diaphyses may shed further light onto behavioral inputs driving variability in upper limb skeletal structure.

Funding: NSF BCS-1719140, NSF BCS-1719187, NRF-DST (South Africa), ERC under European Union's Seventh Framework Programme (FP/2007-2013)/ERC Grant Agreement n.617627, RCUK/BBSRC grant BB/R01292X/1, USC Provost grant for Nikon Metrology XTS225ST micro-CT.

A biochemical approach to women's identities and migration in the Moquegua Valley, Peru during the later LIP (ca. 1250-1476 CE)

DANIELLE E. CARMODY¹, BENJAMIN J. SCHAEFER^{2,3,4}, BETHANY L. TURNER¹ and NICOLA O. SHARRATT¹

¹Department of Anthropology, Georgia State University, ²Department of Anthropology, University of Illinois at Chicago, ³Department of Gender and Women's Studies, University of Illinois at Chicago, ⁴Department of Latin American and Latino Studies, University of Illinois at Chicago

Circa 1000 CE, two expansive Andean polities, the Wari of central highland Peru and the Tiwanaku of the Lake Titicaca *altiplano*, underwent sociopolitical decline and eventual collapse. During this time of turmoil, both withdrew from the Moquegua Valley of southern Peru. In the altered political landscape of the subsequent Late Intermediate Period or LIP (1000-1476 CE), the valley's residents resettled in new villages situated in defensive hilltop locations. However, the degree to which Moquegua Valley LIP populations and individuals engaged in long-distance movement and migration remains debated.

This poster focuses on the individuals of Estuquiña that were sexed female and buried with material objects associated with women to explore multiple dimensions of female identity during the tumultuous LIP in Moquegua. Naturally mummified hair recovered from the LIP site of Estuquiña was analyzed for endogenous cortisol and both heavy and light isotopes to reconstruct and theorize patterns of migration, paleodiet, and psychosocial stress. Our results indicate that although most of the female individuals were local to the Moquegua Valley, several had relocated to the valley months before their deaths. Segmented cortisol levels range between 34-824 nMol/L suggesting that the embodied lived experiences during the LIP altered the regulation of hormone production. Paleodietary reconstructions evince that females were provisioned with kiwicha and local marine resources from the valley. The variation in seasonal diet may be related to wider social and environmental processes that were endured during political reorganization in the Moquegua valley.

Grants-in-Aid of Research, Sigma-Xi (2018), Massachusetts Cultural Council (2017-2019)

Alternative energy: evidence for gut microbiome-mediated buffering of human energy balance

RACHEL N. CARMODY
Department of Human Evolutionary Biology,
Harvard University

The availability of energy and its efficient allocation underpin survival and reproductive success in any species. For past and present human

ABSTRACTS

populations with chronically limited energy supplies and/or short-term volatility in energy balance, any physiological or behavioral system that provided a buffer against shortfalls in net energy availability would likely have conferred important advantages. Using data from three of our recent studies in humans and mice in which energy intake was manipulated through cooking-induced changes in starch digestibility, energy expenditure was manipulated through ultra-distance running, and the development and function of the gut microbiome was manipulated through early life antibiotic treatment, I show that: (1) the composition and function of the gut microbiome adapts quickly in response to short-term changes in energy intake and expenditure; (2) the resulting gut microbiome can enhance host net energy availability in a causal manner; and (3) the gut microbiome contributes to the maintenance of host energy balance through various mechanisms including regulation of hunger and satiety, enhanced rates of energy salvage in the colon, reductions in resting metabolic rate, and developmental tradeoffs in expensive tissue growth. Although interactions between humans and our resident microbial communities are complex and often competitive, our combined dataset suggests that the gut microbiome could have contributed importantly to human evolution by serving as a dynamic buffer against energetic stress, thus helping to lower constraints on the human energy budget that are today reflected in unique features of our anatomy, physiology, life history, and patterns of behavior.

This work was supported by the National Institutes of Health (1F32DK101154), Leakey Foundation, William F. Milton Fund, Harvard Dean's Competitive Fund for Promising Scholarship, and Harvard Department of Human Evolutionary Biology.

The impact of riparian and anthropogenic edge effects on mantled howler monkeys (*Alouatta palliata*) in a fragmented rain-forest in Costa Rica

ANNA J. CARTER

Political Science, University of Louisville

Forest fragmentation increases primate species' exposure to anthropogenic edges, altering their environment and behavior. While edges occur naturally in ecosystems, deforestation increases the area of edges compared to interior zone, making edge effects an important research topic for primatologists. I explored the impact of riparian and anthropogenic edges on mantled howler monkey (*Alouatta palliata*) activity budgets, food item selection, and sociality at the La Suerte Biological Field Station in north-eastern Costa Rica. This site is a riparian forest fragment, making it highly suitable for this study. I hypothesized that howlers would exhibit more social behaviors and spend more time feeding at riparian edges compared to anthropogenic edges.

I also predicted that howlers would have different activity budgets at edge zones compared to interior forest zones, exhibit wider variety in food item selection at riparian edges compared to anthropogenic edges, and exhibit more affiliative interactions at riparian edges compared to anthropogenic edges. 25 hours of data was collected during the wet season in July 2019 using 30 minute point samples. Results did not support my hypothesis, showing similar feeding and social times at riparian edges and anthropogenic edges. Howlers had different activity budgets, resting more and feeding less, in interior forest zones compared to edge zones. There was little difference in food item variety or sociality between edge zones. These results point to the need for further research on edge effects to understand how ecologically flexible species like mantled howler monkeys persist in modified habitats.

Teaching Evolution in Creationist Country: Strategies for Effective Engagement

KATE CARTER

Community Science, National Center for Science Education

While evolution acceptance has made great strides over the past 40 years, the United States is still near the bottom among developed countries. As the causes for evolution denial are varied and complicated, scientists need to be mindful of best practices for sharing evolutionary science broadly. However, best practices for reaching a science-inclined audience are different than reaching more hesitant audiences, and more work on understanding these audiences is needed. Previously, the National Center for Science Education has found anecdotal success bringing evolutionary informal science activities into communities, without substantial pushback, by 1) providing inquiry-based activities, 2) placing activities within appropriate community context, and 3) ensuring volunteer facilitators receive "no-conflict" training. To evaluate the impact that these approaches have on reaching target audiences, I analyzed the effectiveness of three evolution activities—human bipedalism, flight, and digesting cellulose—in six different regional sites where evolution denial is high. Each activity focused on subject matter while also teaching an underlying evolutionary concept: last common ancestors, systematics, and adaptation, respectively. I used a mixed-methods approach that combined pre/post surveys with interviews with volunteers and participants. Results suggest the importance of a visitor-led experience, where visitors are allowed to make observations and explore on their own. Activities that taught evolutionary concepts before labeling them as such also showed greater visitor engagement. Finally, activities that

reached families were more effective in reducing pushback than those targeted to children alone. Overall, these strategies allow for integration of evolution content into critically important regions.

Playful teasing: evidence of joking in non-human primates?

ERICA A. CARTMILL, JOHANNA ECKERT and SASHA WINKLER

Anthropology, UCLA

Teasing walks a fine line between aggression and play. The risk of crossing that line and souring a positive interaction with a social partner requires that the teaser predict their partner's reactions and closely monitor their behavior. Teasing thus presents an opportunity to investigate prediction of others' behaviors and attribution of others' mental states. In studies of animal behavior and cognition, teasing is typically discussed as an aggressive behavior (if explicitly mentioned at all), or lumped into the category of play and not examined further. Recent developmental studies suggest that non-verbal "playful teasing" is already present in human infants in the first year of life. Human infants tease their parents by performing unexpected acts, appearing to deliberately violate their expectations, mutual understandings, or shared conventions in order to provoke a reaction. Here we explore the evolutionary antecedents of human teasing by analyzing the dynamics of spontaneous "object teasing" events in zoo-housed orangutans (*Pongo pygmaeus* and *Pongo abelii*). In these events, one orangutan extends an object towards another and retracts it just when the other reaches for it. These teasing events take the form of games, often repeated several times, and with both parties willingly participating. These games likely require inferences about the others' actions and mental states. In this way, they can be seen as playing with one's own inferences and predictions of other minds. These types of exchanges in orangutans suggest that playful teasing is evolutionarily old and may have been an antecedent to human joking.

Work supported by a grant from the Templeton World Charity Foundation (TWCF0318) "Play, Humor, and Joy in Great Apes"

What, if anything, is *Australopithecus afarensis*?

MATT CARTMILL^{1,2} and FRED H. SMITH^{3,4}

¹Anthropology, Boston University, ²Evolutionary Anthropology, Duke University, ³Sociology and Anthropology, Illinois State University, ⁴Anthropology, University of Colorado - Boulder

Recent fossil discoveries, especially of partial foot skeletons, have brought about a gradual recognition that there were probably at least two hominin species coexisting in East Africa around 3.5 My ago. Yet most analyses continue to assume that all, or nearly all, of the East African

ABSTRACTS

material from this period represents a single species, *Australopithecus afarensis*. We suggest that we no longer have any conclusive reasons for thinking that A.L. 288-1 "Lucy" (3.18 My), the Dikika infant (3.32 My), KSD/VP/1-1 "Kadanuumuu" (3.6 My), and the LH 4 type specimen of *A. afarensis* (3.6 My) all sample the same species, or for assuming that parts of the skeleton known for one tell us much about unknown parts of any other. It is unclear in the present state of our knowledge how many species are represented in the "A. afarensis" congeries, or where the boundaries are between them. We nevertheless contend that if we free ourselves from the presumption that all evolutionary analysis must start with a fully resolved phylogenetic hypothesis, it is possible to say interesting and important things about early hominin evolution in terms of a fuzzy phylogeny.

Rodent stable isotopes provide new data on Miocene ape environments in the Siwaliks and the Vallès-Penedès Basin

ISAAC CASANOVAS-VILAR¹, YURI KIMURA², LAWRENCE J. FLYNN³, DAVID PILBEAM³, SALVADOR MOYÉ-SOLÉ^{1,4,5} and DAVID M. ALBA¹

¹Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, ²Department of Geology and Paleontology, National Museum of Nature and Science, Japan, ³Department of Human Evolutionary Biology, Harvard University, ⁴Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, ⁵Unitat d'Antropologia (Dept. BABVE), Universitat Autònoma de Barcelona

Apes originated in Africa, but by the beginning of the middle Miocene they expanded their range into Eurasia and underwent a remarkable evolutionary radiation. This group is relatively well represented in the long and continuous Miocene records of the Siwaliks (Pakistan) and the Vallès-Penedès Basin (Catalonia, NE Spain). In the Siwaliks only the genus *Sivapithecus* is recorded, whereas in the Vallès-Penedès several different apes occur (*Anoiapithecus*, *Pierolapithecus*, *Pliobates*, *Dryopithecus*, *Hispanopithecus*). Here we use molar enamel stable isotopes of murid rodents to infer climate and vegetation in fossil sites covering all the stratigraphic range of apes in both areas (ca. 14-8.5 Ma in the Siwaliks, ca. 12.5-9 Ma in the Vallès-Penedès). Carbon isotope values indicate pure C3 diets throughout the interval. The $\delta^{13}\text{C}$ values are also used to estimate mean annual precipitation and environment after applying theoretical correction factors for biological fractionation, altitude, latitude and variations in $\delta^{13}\text{C}$ of atmospheric CO_2 over geologic time. Results show that in both regions ape-bearing sites consistently represent the more humid environments. In the Vallès-Penedès, most ape-bearing sites are in the isotopic range of tropical deciduous forests and a few correspond to evergreen warm mixed forests, in agreement with other faunal and paleobotanical data. In the Siwaliks, current small mammal enamel analyses

suggest that *Sivapithecus* was associated with drier environments, which is at odds with faunal, floral, and other proxy data from the Pakistan, India and Nepal. Caution is called for in applying micromammal isotopic analyses to paleoenvironmental interpretation.

Funded by MINECO (RYC-2013-12470 to I.C.V.), AEI/FEDER EU (CGL2016-76431-P and CGL2017-82654-P), and the Generalitat de Catalunya (2017 SGR 116, 2017 SGR 86, and CERCA Program).

Voices in the sky: Mantled howler monkey (*Alouatta palliata*) howl responses to changes in weather in a fragmented tropical rainforest in Costa Rica

MAKENZIE E. CASH

Anthropology, Appalachian State University

The mantled howler monkey (*Alouatta palliata*), named for its distinct male long call, is known to use howling in conflict avoidance, spatial distribution, alarm calls, and in response to low pitch noises. Most studies of howler monkey vocalizations focus on the role of howls in spacing groups, production of loud calls, and classification of the vocalizations in the male and female repertoires. In this study, I investigated the relationship between weather conditions (e.g., rain, thunder, wind) and howl production by mantled howlers at the La Suerte Biological Field Station in Limón, Costa Rica over 27 hours from July 4 to July 10. I proposed that howl rate per hour would correspond with changes in weather, with a greater rate of howls per hour during rain than when not raining. Using all-occurrences sampling, I recorded the occurrence and duration of all howl bouts produced by focal males and the environmental stimuli, including rain, wind, thunder, and anthropogenic noises, that prompted them. Mantled howler monkeys howled more often during rain (13.4 howls/hour) than when not raining (8.86 howls/hour) but average bout duration was higher when not raining (56 seconds) than when raining (35 seconds). Howler monkeys responded to neighboring howls 100% of the time when not raining and 0% of the time when raining. The results of this study suggest that rain significantly constrains intergroup communication. Future studies should examine how changes in weather influence intergroup communication in terms of spatial distribution and conflict.

Genomic perspectives of the Tupí Expansion

MARCOS A. CASTRO-SILVA¹, ALEXANDRE PEREIRA², MARIA C. BORTOLINI³, FRANCISCO M. SALZANO³, DAVID COMAS⁴ and TÁBITA HÜNEMEIER¹

¹Department of Genetics and Evolutionary Biology, University of São Paulo, São Paulo, Brazil, ²Instituto do Coração, Hospital das Clínicas da Faculdade de Medicina, University of São Paulo, São Paulo,

Brazil, ³Departamento de Genética, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil, ⁴Institut de Biologia Evolutiva (CSIC-UPF), Departament de Ciències Experimentals i de la Salut, Universitat Pompeu Fabra, Barcelona, Spain

The Tupí expansion is the main linguistic expansion in South America, however, relatively little is known about this event. Among the Tupí-speakers, the Tupí-Guaraní family has assumed an expansionist character over the last 2,000-3,000 years, populating the Brazilian southwest, northeast, and the entire coast. Based on archeological and linguistic evidence, two contrasting hypotheses on the expansion routes taken by the Tupí can be found in the literature. The first proposes that the Tupí reached the Atlantic Coast after coming from southwest Brazil, originating from the same Tupí-Guaraní branch of the Guaraní. The second hypothesis assumes that one branch of the Tupí first moved eastwards reaching the coast and then southwards along the coastline, originating the coastal Tupí, whereas the other branch went southwards from the Amazon, originating the Guaraní populations. Here we leveraged genomic data from the last remaining representatives of the Tupí coastal branch, a Tupiniquim community, as well as data of a Guaraní-Mbyá population from Southern Brazil and of three native Amazonian populations. Our results showed evidence of a direct migration from the Amazon to the Northeast Coast in pre-Columbian time, giving rise to the Tupí Coastal populations, and a single distinct migration going southwards which originated the Guaraní people from Brazil and Paraguay. Our results are consistent with the first hypothesis, primarily constructed on the divergence between the Guaraní and Tupinambá potteries. In this context, the expansion was caused by a search for new lands to cultivate, undertaken by populations of ceramists and incipient agriculturalists.

The project was funding by FAPESP (2018/013716; 2015/26875-9).

New insights on the Neanderthal knee-joint loading environment from the endostructural configuration of the patellae from Krapina, Croatia

MARINE CAZENAVE¹ and DAVORKA RADOVČIĆ²

¹Anatomy and Histology, Sefako Makgatho Health Sciences University, ²Geology and Paleontology, Croatian Natural History Museum

The Neanderthal patella is anteroposteriorly thicker and shows more symmetric articular facets associated with higher angles than in recent humans. While it does not appear to be a close relationship between the degree of patellar facet asymmetry and the configuration of the distal femur, which is similar among Neanderthals, fossil and recent humans, the functional implications of such differences are still debated.

ABSTRACTS

By using micro-focus X-ray tomography (isotropic voxel size range: 24-50 μm), we characterized the endostructural pattern of six Neanderthal patellae representing five individuals from the OIS 5e site of Krapina, Croatia, and compared the results to those from a sample of 31 patellae representing 22 adult recent humans of various origins and socio-economic patterns.

For the cortico-trabecular complex and trabecular thickness, the Neanderthal values fall within the human range of variation. Conversely, in Krapina cancellous bone density (BV/TV) in the medial aspect is higher, and the degree of anisotropy in the inferior aspect is lower than measured in humans. Also, while a bone reinforcement in the lateral and superior aspects is present in humans, in Krapina it is only found laterally. Interestingly, as commonly observed in humans, in Krapina the BV/TV is higher in the left patella.

The only other evidence available from an adult Neanderthal patella, Regourdou 1 (France, OIS 4), does not fully overlap the average signal recorded in Krapina. Endostructural differences of the patella thus reveal differing knee-joint loading environments between Neanderthals and humans, as well as inter-individual variation likely age-, sex- and/or physical activity-related.

Funding support to M.C. provided by the Erasmus Mundus program Bakeng se Afrika.

Differences in sexual dimorphism between two Central European populations evaluated using external morphology of the frontal bone

MARKETA CECHOVA¹, JAN DUPEJ^{1,2}, JAROSLAV BRUZEK¹, SARKA BEJDOVA¹, RADOSLAV BENUŠ³ and JANA VELEMINSKA¹

¹Department of Anthropology and Human Genetics, Faculty of Science, Charles University, ²Department of Software and Computer Science, Faculty of Mathematics and Physics, Charles University, ³Department of Anthropology, Faculty of Natural Sciences, Comenius University in Bratislava

Sex estimation is an important issue in forensic anthropology and bioarchaeology. Along with the pelvic bone, the skull is the most important source of sexual dimorphism. The upper third of the face (i.e. the frontal bone) is one of the most significant sexually dimorphic structures on the human skull. Nevertheless, traits on the skull are population-specific. The expression of sexual dimorphism on the skull varies across populations. The present study deals with the variability of the entire external surface of the frontal bones from a contemporary Slovak and Czech populations and evaluates differences in expression of their sexual dimorphism. Frontal bones were evaluated using geometric morphometric analyses: coherent point drift-dense correspondence analysis (CPD-DCA), principal component analysis (PCA) and support vector

machine (SVM). The ability to sex estimation was successfully tested on 196 individuals from two contemporary European populations. The whole external frontal surface was significantly different between males and females both in form and shape. In the previous study, sex estimation was carried out applying the virtual method developed on the frontal bones of individuals from Czech population. In this study, the model was successfully verified on the Slovak population. Using this combined dataset was made more reliable and robust classifier. The estimation method reached a success rate from 83 to 88 % using individual samples and their combination.

This research was supported by the Grant Agency of Charles University (grant number 1590218).

Relationships between macroparasite infection and cardiovascular/metabolic health among indigenous Amazonians experiencing rapid economic development

TARA J. CEPON-ROBINS¹, THERESA E. GILDNER², MELISSA A. LIEBERT³, SAMUEL S. URLACHER⁴, FELICIA C. MADIMENOS⁵, GEETA N. EICK⁶, LAWRENCE S. SUGIYAMA⁶ and J. JOSH. SNODGRASS⁶

¹Department of Anthropology, University of Colorado Colorado Springs, ²Department of Anthropology, Dartmouth College, ³Department of Anthropology, Northern Arizona University, ⁴Department of Anthropology, Baylor University, ⁵Department of Anthropology, Queens College (CUNY), ⁶Department of Anthropology, University of Oregon

Cardiovascular disease (CVD) is rare among subsistence populations; it has been hypothesized that soil-transmitted helminths (STHs) reduce CVD-risk in these populations by regulating immune-function and directly consuming blood lipids/glucose. Here, we test relationships between current STH infection and markers of cardiovascular/metabolic health among 205 Shuar adults (89 men, 116 women; ages ≥ 15 years). *Ascaris lumbricoides* and *Trichuris trichiura* were detected via microscopy in stool samples using Kato-Katz thick smears. Markers of cardiovascular/metabolic health measured from finger-prick blood samples include total cholesterol, high- and low-density lipoprotein (HDL; LDL) cholesterol, triglycerides, and fasted glucose. Blood pressure was assessed via automatic blood pressure monitor. Sex-specific analysis of covariance tests (controlling for age/body mass) compared health markers by infection type. Unexpectedly, some cardiovascular/metabolic measures were elevated among infected individuals. Men who were singly infected with *Ascaris* had higher LDL cholesterol than uninfected men ($p = 0.005$) and men singly infected with *Trichuris* ($p = 0.029$). Coinfected women had higher LDL cholesterol than uninfected women ($p = 0.004$) and women singly infected with *Ascaris* ($p = 0.008$). Coinfected men had higher glucose levels

than uninfected men ($p = 0.001$) and men singly infected with either species ($p < 0.01$). These findings indicate a double-burden of chronic and infectious diseases associated with economic development. We examine these relationships in conjunction with biomarkers of long-term macroparasite infection (Immunoglobulin E) and inflammation (C-reactive protein), as well as lifestyle factors (house construction, water source), to determine if immune responses to STHs mediate CVD-risk related to lifestyle transitions.

Support: Wenner-Gren Foundation; NSF DDIG (BCS-134-1165, BCS-0824602, BCS-1650674, BCS-0925910), IBSS (1329091), GRFP (2011109300); American Philosophical Society Lewis and Clark Fund; Sasakawa Young Leaders Fellowship Fund; Leakey Foundation; University of Oregon.

Identification of skeletal remains using vertebral body osteophytes

MARIANNA CERVANTES

Chemistry, University of Leicester, Archaeology, Simon Fraser University

Osteophytes have a complex etiology which produces quantifiable individual variation applicable to the identification of human remains.

Two hundred computerized tomography (CT) scans of thoracic and lumbar areas of 80 females and 120 males, obtained from The Cancer Imaging Archive, were examined. The right, anterior, and left parts of the superior and inferior margins of the vertebral bodies were scored using a 0-4 system. Frequency and likelihood ratio (LR) of each score at each data point was calculated.

Spearman's Rho tests identified points with negligible ($-0.30 < p < 0.30$) correlation. The resulting matrix illustrates independently occurring osteophytes. Independent LRs can be multiplied, increasing specificity. A Kruskal-Wallis test identified the impact of age and sex. Regarding sex, 98% of points resulted in $p > 0.05$. Sex had no significance. In testing age $p < 0.05$ on 78% of data points, age was deemed significant. The population was grouped in 10 year increments > 30 and < 80 for application of the identification method.

On three sample cases, the least frequently occurring scores at data points on available vertebrae were selected, and using the matrix produced from the Spearman's Rho test independent data points were identified. The LR for each score was ascertained within the appropriate age group, then multiplied. A LR of 6.68, 41, and 56.61 for individuals 34, 51, and 69 years, respectively.

This preliminary method can be definitive for small pools of possible identities, and can be combined with likelihood ratios associated with other aspects of the skeletal biography.

ABSTRACTS

Fats are differentially fattening: Host-microbial interactions in energy harvest from dietary lipids

KATIA S. CHADAIDEH and RACHEL N. CARMODY
Human Evolutionary Biology, Harvard University

Energetic models of ancestral and modern human diets assume that all dietary fats are isocaloric. However, consumption of different dietary fats has been linked to differences in numerous metabolic phenotypes, including obesity. To examine whether host-microbial interactions in energy metabolism might explain the divergence between prediction and observation, we performed two experiments to assess how different dietary fats and their impacts on the gut microbiota shape host energy gain. In a first experiment, we fed mice isocaloric high-fat diets (45% w/w) varying only in the dominant type of fat present: saturated fat (milk fat), monounsaturated fat (olive oil), Ω -3 polyunsaturated fat (flaxseed oil), or Ω -6 polyunsaturated fat (safflower oil). After 12 weeks, mice fed saturated fat exhibited higher adiposities and divergent gut microbial communities compared to mice fed Ω -3 ($p_{\text{adiposity}}=0.010$, $p_{\text{microbiota}}=0.002$) or Ω -6 ($p_{\text{adiposity}}=0.006$, $p_{\text{microbiota}}=0.009$) polyunsaturated fat, with mice fed monounsaturated fats exhibiting intermediate host and microbial phenotypes. To isolate the microbial contribution to differences in host adiposity, we next transplanted gut microbial communities conditioned on isocaloric saturated fat or Ω -3 polyunsaturated fat diets into germ-free mice cross-fed these diets in a fully factorial design. Gut microbial communities exhibited interactions reflective of both the conditioning diet and the current diet, and recipient animals exhibited differences in adiposity reflecting these microbial dynamics that could not be ascribed to differences in caloric intake. Our results challenge conventional models of the caloric value of fats, and encourage a holobiont view of fat metabolism in efforts to model human energy budgets past and present.

This study was supported by the National Science Foundation (BCS-1919892), the William F. Milton Fund, the Harvard Dean's Competitive Fund for Promising Scholarship, and the Harvard Department of Human Evolutionary Biology.

Individual predictors of participation in intergroup encounters among urban-dwelling rhesus macaques (*Macaca mulatta*)

BIDISHA CHAKRABORTY^{1,2}, STEFANO S. K. KABURU³, PASCAL MARTY², KRISHNA BALASUBRAMANIAM², BRIANNE BEISNER^{2,4}, LALIT MOHAN⁵, SANDEEP K. RATTAN⁵ and BRENDA MCCOWAN^{2,4}

¹Animal Behavior Graduate Group, University of California, Davis, ²Department of Population Health & Reproduction, School of Veterinary Medicine, University of California, Davis, ³Department of Biomedical Science & Physiology, School of

Sciences, University of Wolverhampton, ⁴California National Primate Research Center, University of California, Davis, ⁵Himachal Pradesh Forest Department, Shimla, Himachal Pradesh

Primates commonly engage in intergroup encounters (IGEs), ranging from peaceful displacement to intense aggression. While most of the studies in nonhuman primates have highlighted how groups tend to assess numerical asymmetries to determine whether to engage in intergroup conflict or not, the role of individual differences during IGEs is still poorly understood. Moreover, there is still little information on how within-group social relationships can influence participation in IGEs, and vice versa. Different individuals or different classes of individuals might vary in the benefits accrued and costs incurred as a result of participation, and examining these costs and benefits might shed light on the determinants of participation in IGE. In this study, we investigated individual predictors of participation in IGEs among urban rhesus macaques (*Macaca mulatta*) in Shimla, North India. We collected data from 2016 to 2018 on three groups of macaques and recorded a total of 226 IGEs. We found that males ($\beta = 0.12$, $p < 0.01$), subordinates ($\beta = -0.07$, $p < 0.01$) and individuals central in the grooming network participated more ($\beta = 0.06$, $p < 0.01$) in intergroup encounters. We also found that individuals actively involved in giving and receiving coalition support were more likely to participate in IGEs ($\beta = 0.04$, $p = 0.05$). Our results confirm inter-individual differences in participation in IGEs in urban rhesus macaques. In view of the apparent relationship between intergroup encounters and intragroup affiliation, we speculate on the implications of our results for a better understanding of macaque social structure.

This work was funded by the U.S. National Science Foundation (#1518555)

Strontium Isotope Testing of Deciduous Molars from Maya Sacrificial Victims

AMY CHAN
Anthropology, California State University, Los Angeles

Excavated in 2008-2010, the Midnight Terror Cave contains the comingled remains of at least 118 Maya sacrificial victims from the Classic Period (250 CE - 925 CE). Questions remain as to who the victims were and how they were obtained. Previous research on the collection has established a large portion of subadult remains originating from throughout the Yucatan along with a high number of females. At least 60% of permanent teeth tested have been established as local to the Belize River Valley. But, strontium isotope testing has yet to be carried on deciduous teeth to determine the geographic origin of infants from the Midnight Terror Cave. Due to the young age of these children, the victims would have to have been born locally or carried in a great distance to be sacrificed.

Two right maxillary deciduous second molars were photographed, molded, and sent to the Stable Isotope Lab at Washington State University for testing. Results showed trends similar to those of the permanent teeth's isotopic signature, placing the infants from outside of the Belize River Valley. The first infant came from the Northern Lowlands while the second came from the Central Maya Area. Infants from outside the Belize River Valley could have been obtained specifically for sacrifice through gift exchange between *caciques*, possibly through purchase or kidnapping, and brought to the Midnight Terror Cave. Infants could also have been carried in by their mothers or family members as it would have been difficult to nurse a child over long distances.

Funding provided for by the Office of Graduate Studies at California State University, Los Angeles

Evaluating Pressures on Lemur Demographic Histories in Ranomafana National Park, Madagascar

APARNA CHANDRASHEKAR¹, CARLO PACIONI^{2,3}, AMANDA N. MANCINI^{4,5}, TONI L. MORELLI^{6,7}, EDWARD E. LOUIS JR.⁸ and ANDREA L. BADEN^{1,4,5}

¹Anthropology, City University of New York Hunter College, ²Terrestrial Ecology, Arthur Rylah Institute for Environmental Research, ³School of Veterinary and Life Sciences, Murdoch University, ⁴Anthropology, The Graduate Center of City University of New York, ⁵Evolutionary Primatology, The New York Consortium in Evolutionary Primatology, ⁶Department of Environmental Conservation, University of Massachusetts Amherst, ⁷U.S. Geological Survey, DOI Northeast Climate Science Center, ⁸Center for Conservation Research, Omaha's Henry Doorly Zoo and Aquarium

Ranomafana National Park (RNP) has one of the highest levels of primate biodiversity in the world, containing thirteen species of lemurs, three of which are critically endangered. While over 50% of the park is primary forest, the remainder has been subject to varying levels of logging and other anthropogenic and natural disturbance. To evaluate the effect of these pressures, we are reconstructing population demography across five diurnal lemur species that vary in size, locomotor pattern, dietary diversity, and life history variables. Seven sites within RNP were visited and 38 *Varecia variegata*, 40 *Eulemur rufifrons*, 41 *Haplemur griseus*, 42 *Eulemur rubriventer*, and 85 *Propithecus edwardsi* were genotyped using 10-17 microsatellite markers. Mode shift and heterozygosity excess tests were used to test for signatures of a historical bottleneck within all five taxa. Three mutation models were used for heterozygosity excess tests: the stepwise mutation model (SMM), two-phase model (TPM), and infinite allele model (IAM). Though the mode shift test did not strongly indicate the presence of a historical bottleneck, heterozygosity excess was indicated under IAM and TPM models for V.

ABSTRACTS

variegata, *E. ruffifrons*, *E. rubriventer*, *H. griseus*, and IAM only for *P. edwardsi*. Additionally, Extended Bayesian Skyline plots revealed that *Varecia variegata* once had large effective population sizes (~4,000) prior to a bottleneck, which then decreased gradually by 84% within the last 1,500 years. This comparison across morphologically and behaviorally diverse lemur species will allow us to investigate if and how anthropogenic and natural pressures impact population demography within the same habitat.

An Examination of the Subpubic Region, Greater Sciatic Notch, and Obturator Foramen Variation in Thai Individuals Using Elliptical Fourier Analysis

RACHEL E. CHANEY, SEAN D. TALLMAN and GREGG HARBAUGH

Department of Anatomy and Neurobiology, Boston University

While features of the os coxa, including the subpubic region, greater sciatic notch, and obturator foramen, are frequently used for sex estimation in bioarchaeological and forensic anthropological contexts, little is known about how these areas are affected by other biological or ecogeographic factors. This project uses Elliptical Fourier Analysis (EFA) to examine the relationship between these three features, with sex, age, stature, weight, and pelvic dimensions of modern Thai individuals to ascertain how these variables impact pelvic morphology. A total of 214 os coxae ($f=108$; $m=106$) aged 20-97 years from the Khon Kaen University Human Skeleton Research Centre were analyzed. Each os coxa was photographed to obtain standardized images of the three regions. Each of the features was traced in Procreate, and the outlines analyzed for variation using SHAPE, an EFA software. Exploratory Factor Analysis and Multivariate ANOVAs were performed to examine the effects of sex, age, stature, weight, and pelvic dimensions on the three regions. Preliminary results indicate that shape appears to be well described by a 20-harmonic solution. Age is not statistically associated with any of the seven dimensions of the factor analysis; however, sex is statistically associated with three of the first seven dimensions (factor3, factor4, and factor7). This study provides a greater understanding for the range of variation in the three sexually dimorphic regions of the os coxa and how these regions are affected by inter-related biological variables that are frequently left out of sex estimation studies. Additionally, the study emphasizes the need for population-specific research.

Funding for this project was provided by the Program in Forensic Anthropology at the Boston University School of Medicine.

Preliminary evidence for distance and land cover influences on genetic differentiation among endangered lemur populations

CHLOE CHEN-KRAUS¹, ELAINE E. GUEVARA², NJARATIANA A. RAHARINORO³, MARLI RICHMOND⁴, RICHARD R. LAWLER⁵ and BRENDA J. BRADLEY⁴

¹Department of Anthropology, Yale University,

²Department of Evolutionary Anthropology, Duke University, ³Mention Zoologie et Biodiversité

Animale, Université d'Antananarivo, ⁴Department of Anthropology, The George Washington University,

⁵Department of Sociology and Anthropology, James Madison University

Verreaux's sifaka (*Propithecus verreauxi*), a critically endangered lemur species endemic to southwest Madagascar, occur at high densities at Bezà Mahafaly Special Reserve (BMSR), but it remains unknown how connected the BMSR population is with sifakas inhabiting other forests in the region. We surveyed BMSR as well as four forests within 50km of the reserve, and collected sifaka fecal samples from individuals at each site. To examine the genetic connectivity of sifakas across this human-altered landscape, we performed landscape genetic analyses via microsatellite genotyping ($N=135$ individuals across five sites). We found evidence for varying degrees of genetic differentiation between sites ($F_{ST}=0.026-0.182$) and that genetic distances are correlated with Euclidean distances between sites ($r=0.790$, $p=0.007$). Beyond the effects of geographic distance, land cover types (e.g., forests, grasslands, settlements, and agricultural fields) may differentially impede gene flow across the landscape. Our initial investigation suggests that geographic distance and forest connectivity are main factors influencing patterns of sifaka gene flow. Pairwise genetic distances are greater between sifakas at sites that are geographically distant and not connected by substantial forest corridors. Without genetic connectivity, sifaka populations are at higher risk for inbreeding depression and ultimately extirpation. Our preliminary results highlight the importance of protecting forest corridors and taking a landscape scale approach to conservation for this species.

This research was funded by the National Science Foundation (NSF-BSC-1745371), National Geographic Society (EC-420R-18), Explorers Club, Yale University Macmillan Center, and Yale Department of Anthropology.

Discovery of early Paleocene *Purgatorius* from a new fossil locality in the Fort Union Formation of southeastern Montana, USA

STEPHEN G. B. CHESTER^{1,2,3}, GREGORY P. WILSON⁴, TYLER R. LYSON⁵ and ERIC J. SARGIS^{5,7}

¹Department of Anthropology and Archaeology, Brooklyn College, City University of New York, ²Department of Anthropology, The Graduate Center, City University of New York, ³New York Consortium in Evolutionary Primatology, ⁴Department of Biology, University of Washington, ⁵Department of Earth Sciences, Denver Museum of Nature & Science, ⁶Department of Anthropology, Yale University, ⁷Division of Vertebrate Paleontology, Yale Peabody Museum of Natural History

Recent phylogenetic analyses support purgatoriid plesiadapiforms as the oldest known stem primates or stem primatomorphans (Primates + Dermoptera). Purgatoriids were among the first placental mammals to diversify in the early Paleocene Puercan North American Land Mammal Age (NALMA) following the Cretaceous–Paleogene (K–Pg) mass extinction event, but only several isolated teeth of purgatoriids have been reported from the oldest Puercan (Pu1) NALMA interval zone. Here we report a new sample of *Purgatorius* teeth from the Pu1 Camel Butte

ABSTRACTS

locality, Fort Union Formation, Fallon County, southeastern Montana. This represents the southernmost occurrence of purgatoriid and one of the oldest records of plesiadapiforms worldwide. The locality is at the base of a channel-lag deposit that lies 29 cm above the Fort Union–Hell Creek formational contact and 125 cm above the palynologically defined K–Pg boundary. Camel Butte is assigned to Pu1 based on the presence of “archaic ungulates” such as *Protungulatum* and *Oxyprimus* and provides an intermediate stage of mammalian taxonomic diversity between the low diversity “disaster” and higher diversity “recovery” faunas documented in northeastern Montana. *Purgatorius* teeth from Camel Butte have some features known only in the geologically younger *P. coracis* and *P. pinecreensis* from Saskatchewan, Canada (e.g., small P4 with incipient metacone) but share other features with *P. janisae* from northwestern Montana (e.g., less transverse upper molars with mesially canted protocone). Specimens from this poorly sampled interval contribute to our understanding of taxonomic diversification of purgatoriid and may help further clarify the divergence of primates from other mammals.

Yale Peabody Museum of Natural History Division of Vertebrate Paleontology, PSC CUNY Award jointly funded by The Professional Staff Congress and The City University of New York

Correlations between growth disruptions and adult mortality risk: comparisons between documented and archaeological samples using consistent methods

COLLEEN M. CHEVERKO

Anthropology & Heritage Studies, University of California, Merced

Several studies in modern human variation demonstrate that early life conditions can affect adult health and mortality risk. Based on these findings, bioarchaeologists have applied the Developmental Origins of Health and Disease (DOHaD) framework to understand patterns of past heterogeneity of risk, with mixed results that lead to questions about whether interpretations are driven by differences in context and/or analytical protocols between studies. This paper incorporates a life history approach derived from human biology to investigate the role of early life stress and adult mortality risk in the past, using samples from two distinct biocultural contexts. Evidence of growth disruptions (i.e., linear enamel hypoplasia, vertebral neural canal diameters, and stature and body proportions) were recorded in adult individuals from an archaeological sample (Hotchkiss Mound, precontact California, $n = 132$) and reference sample (Terry Collection, $n = 209$). Consistent methods were used between samples to record these childhood and adolescent stress markers to understand the long-term impact of early life stress across two periods of

growth and development. Comparisons were made between evidence of growth disruptions and adult age-at-death as a proxy for mortality risk. Each sample was analyzed individually, with a qualitative discussion of how patterns differ between samples. The results highlight how interpretations can differ between varying cultural and geographic contexts when applying consistent methods across studies, lending support to arguments that correlations explained using the DOHaD framework are affected by context and depend on a suite of factors that affect individuals throughout their lives.

This work was supported by the Ohio State University Office of Energy and the Environment, a Larsen Travel Award, and a Coca Cola Critical Difference for Women Grant.

DNA methylation changes are associated with an incremental ascent to high altitude

AINASH CHILDEBAYEVA^{1,2}, TAYLOR HARMAN³, JULIEN WEINSTEIN¹, JACLYN M. GOODRICH⁴, DANA C. DOLINOY^{4,5}, TREVOR A. DAY⁶, ABIGAIL W. BIGHAM^{1,7} and TOM BRUTSAERT³

¹Department of Anthropology, University of Michigan, ²Archaeogenetics, Max Planck Institute for the Science of Human History, ³Department of Exercise Science, Syracuse University, ⁴Department of Environmental Health Sciences, University of Michigan, ⁵Department of Nutrition, University of Michigan, ⁶Department of Biology, Mount Royal University, ⁷Department of Anthropology, University of California

Genetic and non-genetic factors are involved in high-altitude acclimatization. However, epigenetic factors are not well understood in the context of short-term, high-altitude exposure. To understand the effects of increasing high-altitude exposure on DNA methylation, we recruited 21 healthy adult participants of European ancestry ($n=21$) trekking to Everest Base Camp. We collected saliva samples in Kathmandu (1400m; baseline) and three altitudes: Namche (3440m; day three), Pheriche (4240m; day seven), and Gorak Shep (5160 m; day 10). We used quantitative bisulfite pyrosequencing to determine DNA methylation levels at the line LINE-1 repetitive elements and regulatory regions of hypoxia inducible factor (HIF) pathway associated genes *EPAS1*, *EPO*, *PPAR α* , and *RXR α* . We identified significantly lower DNA methylation between baseline (1400m) and high altitudes in LINE-1, *RXR α* , and *EPO* (4240m only). In addition, we found increased methylation in *EPAS1* (4240m only) and *PPAR α* . Positive associations also were found between *EPO* methylation and systolic blood pressure as well as *RXR α* methylation and hemoglobin. Our

results demonstrate that incremental exposure to hypoxia can affect the epigenome, suggesting that epigenetic changes may in part underlie high-altitude acclimatization.

This work was supported by the University of Michigan, M-LEEd NIEHS, Marshall Weinberg Award, National Geographic Early Career Award, and Natural Sciences and Engineering Research Council of Canada Discovery grant.

The rhesus macaque brain cell census reveals heterogeneity in aging across cell types

KENNETH L. CHIOU^{1,2}, ALEX R. DECSIEN^{3,4}, MICHAEL J. MONTAGUE⁵, SAMUEL E. BAUMAN⁶, NICOLE R. COMPO⁶, OLGA GONZÁLEZ⁷, HANNAH A. PLINER⁸, CAILYN H. SPURRELL⁸, LEA M. STARITA^{8,9}, LAUREN J. N. BRENT¹⁰, JAMES P. HIGHAM^{3,4}, MELWEEN I. MARTINEZ⁵, JAY SHENDURE^{11,12,8,9}, MICHAEL L. PLATT^{13,14,5} and NOAH SNYDER-MACKLER^{1,15,2}

¹Department of Psychology, University of Washington, ²Nathan Shock Center of Excellence in the Basic Biology of Aging, University of Washington, ³Department of Anthropology, New York University, ⁴New York Consortium in Evolutionary Primatology, ⁵Department of Neuroscience, University of Pennsylvania, ⁶Caribbean Primate Research Center, University of Puerto Rico, ⁷Southwest National Primate Research Center, Texas Biomedical Research Institute, ⁸Brotman Baty Institute for Precision Medicine, ⁹Department of Genome Sciences, University of Washington, ¹⁰Centre for Research in Animal Behaviour, University of Exeter, ¹¹Howard Hughes Medical Institute, ¹²Allen Discovery Center for Cell Lineage Tracing, ¹³Department of Psychology, University of Pennsylvania, ¹⁴Department of Marketing, University of Pennsylvania, ¹⁵Center for Studies in Demography & Ecology, University of Washington

Primate brains are complex organs capable of supporting a wide array of social behaviors and cognitive functions. Underlying these abilities are myriad cell types and anatomical regions integrated into neural circuits and their support networks. Age-related declines in behavior and cognition stem from disruptions to the normal functioning of this network, but our understanding of these changes is hampered by an incomplete knowledge of cell types and their activities across the brain. To address this gap, we are using a scalable high-throughput approach, sci-RNA-seq, to profile single-brain-cell transcriptomes from free-ranging macaques of Cayo Santiago. We first sequenced transcriptomes from 16,675 nuclei isolated from the primary visual cortex of 2 middle-aged adults. Preliminary analysis of these data revealed 8 primary clusters corresponding with known neuronal and glial cell types, subdivided into 45 “subclusters” reflecting heterogeneity within cell types. Clusters were differentiated in part by previously undescribed marker genes. We next used our data to train a classification model and evaluated the resulting

ABSTRACTS

classifier on a published dataset of 15,928 human cortical cells. Our classifier assigned cell types to 93.5% of human cells, with only 1.6% conflicting with published classifications, revealing overall phylogenetic conservation in cell-type identity. Continuing with this framework, we are currently expanding our transcriptomic "cell atlas" to target millions of cells across dozens of brain regions and spanning the macaque lifespan. These data will lend novel insights into proximal mechanisms underlying age-related behavioral changes in primates and pave the way for fine-grained evolutionary comparisons of brain aging across species.

This work is supported by the National Institutes of Health (NIMH U01-MH121260, NIA R01-AG060931, NIA R00-AG051764, NIMH R01-MH108627, NCR/ORIP P40-OD012217, NIA T32-AG000057) and the National Science Foundation (BCS 1752393).

Trabecular bone morphology in early Pleistocene hominins from Koobi Fora, northern Kenya

HABIBA CHIRCHIR^{1,2}, CAROL WARD³ and JOB KIBII⁴

¹Biological Sciences, Marshall University, ²Human Origins Program, National Museum of Natural History, Smithsonian Institution, ³Department of Pathology & Anatomical Sciences, University of Missouri School of Medicine, ⁴Department of Paleontology and Paleoanthropology, National Museums of Kenya

Modern humans have unusually low trabecular bone density (bone volume fraction, BVF) in limb joints compared to early hominins indicative of gracilization. Research suggests an increase in skeletal gracility over time among hominins and recent modern humans, often attributed to increasing sedentism. So far, data from Plio-Pleistocene hominins, indicate that they share less, though variable, skeletal gracility than recent humans despite differences in relative hindlimb joint size, taxonomy, and body size. However, factors underlying variation in gracilization among hominins still need to be studied. Here, we investigate BVF in early Pleistocene hominins from Koobi Fora, Kenya, to understand whether the observed pattern of low gracility in Plio-Pleistocene hominins of South Africa and late Pleistocene of Europe is also seen in these East African fossils. We microCT scanned three specimens; KNM-ER 1481 (*Homo*) femur and tibia, and KNM-ER 1503 (*Paranthropus*) femur. 3D images were segmented using the MIA clustering tool. We quantified BVF in all three specimens and compared them with data from *A. sediba*, *A. africanus*, *Australopithecus* sp., early *H. sapiens*, possible *Paranthropus*/early *Homo*, chimpanzees, and recent humans. KNM-ER 1481 and KNM-ER 1503 display high BVF, similar to australopithecines and greater than early modern humans or neanderthals. These data support the hypothesis that BVF is unrelated to joint size or possibly

variation in locomotor behavior. Whether this is a temporal trend is uncertain. While still tentative, these results demonstrate the efficacy of using microCT imaging to test questions on the origin of gracilization.

Linear enamel hypoplasia frequencies with the rise of urbanism at Tel Megiddo

CECELIA CHISDOCK¹, ALISON BROOKS², ERIC CLINE³, DAVID HUNT⁴ and SUSAN SHERIDAN¹

¹Anthropology, University of Notre Dame, ²Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, ³Department of Classical and Near Eastern Languages and Civilizations, The George Washington University, ⁴Anthropology Division, Smithsonian National Museum of Natural History

The rise of urbanism has often been linked to changing patterns of physiological stress corresponding with population density and resource availability. In this study, we compared the pre-urban Chalcolithic (4300-3300 BCE) and the urbanized Late Bronze Age (LBA) (1550-1200 BCE) skeletal collections from Megiddo, Israel-Palestine, housed at the Smithsonian Institution. Linear enamel hypoplasias were used as a general stress indicator and compared by employing chi-square and Fisher's exact tests ($n=744$; $p<0.05$). There was no significant difference between the permanent teeth of the two periods ($p=0.47$). Anterior teeth showed considerable sensitivity to LEH formation compared to posterior teeth ($p<0.00001$), but still lacked significant difference by period ($p=0.069$). The Chalcolithic tombs had large enough samples to compare between them. The most well-built (probably highest status) tomb, T-910, showed significantly higher incidence than either T-903U ($p<0.00001$) or T-1103 ($p=0.0037$), implying a link between status and stress before the amplified social stratification of urbanism. While urbanism is typically linked to higher stress due to increasing population density and subsequent decreasing resource availability, there was no discernible difference in this sample. Possible causes include the fact that LBA Megiddo, as a wealthy hierarchy center, imported much of its food from the Jezreel Valley. It also experienced the region-wide trend of de-urbanization, alleviating the density of the large population. This increase of resources and decentralization of the populace may have helped off-put the stressors associated with urbanization.

Luther Rice Undergraduate Fellowship, The George Washington University; Presidential Fellowship, University of Notre Dame; Conference Funding from the Dean of the College of Arts and Letters, University of Notre Dame

Pelvic variation and sexual dimorphism in East Asian populations

ELIZABETH O. CHO and LIBBY W. COWGILL

Department of Anthropology, University of Missouri

The pelvis is of evolutionary, obstetric, and forensic interest due to the impact of body size and breadth on thermoregulation, pelvic canal dimensions on childbirth, and utility of feature dimorphism for sex estimation. While well-studied in European and African populations, studies of Asia are few and typically limited to comparisons of a small number of select populations. Climate adaptation studies have identified a dissimilarity in bi-iliac breadth clines between the Americas and Old-World populations. Evidence of pelvic canal variation between populations of similar latitudes also suggests some independence of pelvic shape despite the identification of general global proportional trends at higher and lower latitudes. This study examined the articulated pelvises of individuals ($N=654$) from multiple East Asian countries (Mongolia, China, Korea, Japan, Thailand, and the Philippines). Dimensions of the pelvic inlet, midplane, outlet as well as canal depth, bi-iliac breadth, bi-acetabular breadth, and breadth of the superior and inferior anterior iliac spines were collected. Data was analyzed using t-tests, ANOVA, and Tukey tests, and dimorphism indices and ratios of the pelvic planes calculated. Bi-iliac breadth of Asian populations increases with latitude, but this trend is clearer in males. Pelvic inlet anterior-posterior diameter compresses compared to its transverse diameter as latitude increases, while the pelvic outlet anterior-posterior diameter elongates. Significant differences between male and female proportions are more prevalent in lower latitude populations. The findings of this study support the necessity of further evaluation of this geographic region to better understand global pelvic variation and selective pressures.

Wenner-Gren Dissertation Fieldwork Grant (Grant number: 9693) and NSF Biological Anthropology DDRIG (Grant number: 1847486)

Condensed Tannins and Nutritional Quality of Bornean Orangutan (*Pongo pygmaeus wurmbii*) Foods in Gunung Palung National Park, West Kalimantan, Indonesia

ISHRAT CHOWDHURY¹, MADELINE M. EORI¹, ERIN KANE¹, NANCY CONKLIN-BRITTAIN², TRI WAHYU. SUSANTO⁴ and CHERYL KNOTT^{1,3}

¹Anthropology, Boston University, ²Human Evolutionary Biology, Harvard University, ³Biology, Boston University, ⁴Biology, National University of Indonesia

Orangutan habitats are characterized by fluctuations in the availability of ripe fruits. During non-fruiting periods orangutans typically incorporate more lower-quality foods such as pith and bark in their diet. Condensed tannins (CT) are secondary plant compounds that bind to proteins, thus impeding the digestibility of proteins, and tending to make foods bitter or unpalatable. We analyzed condensed tannin content in 129 plant samples collected from Gunung Palung

ABSTRACTS

National Park in Borneo, Indonesia between 1994 and 2001. We predicted that CT concentrations would be highest in bark, and that there would be a correlation between protein and condensed tannin content. We used ANOVA with Bonferroni's method for post-hoc comparisons to test for differences in tannin content between plant parts, and Pearson's correlation to test for relationships between tannin concentrations and other nutrients. There were significant differences in condensed tannin content ($F(4)=2.70$, $p=0.03$) but no differences after adjusting the alpha-level for post-hoc comparisons. Whole fruit (including the skin) tended to have the highest CT concentration. However, we found no correlation between CT and concentration of nutrients including crude protein ($R=0.12$, $p=0.19$, $N=127$), free simple sugars ($R=-0.09$, $p=0.40$, $N=100$), or fiber ($R=-0.38$, $p=0.67$, $N=128$). This underscores that plants rich in desirable nutrients may also be rich in antifeedants, posing challenges for orangutan consumption and digestion even as they provide a source of high-quality energy. Additionally, for some food categories where high tannin content is predicted, such as bark, orangutans may be choosing to eat species that are lower in these compounds.

BostonUniversity UROP, NationalScienceFoundation (BCS#0936199, 9414388, 1613393); NationalGeographicSociety; L.S.B. Leakey Foundation; WennerGren Foundation; US Fish and Wildlife Service (F15AP00812, F12AP00369, 98210-8-G661); Conservation, Food and Health Foundation; Focused on Nature; Orangutan Conservancy; Disney Conservation Fund; Woodland Park Zoo and Nacey Maggioncalda Foundation.

Serum inflammation in Guamanian Amyotrophic Lateral Sclerosis and Parkinsonism Dementia: A nested case-control pilot study

RISANA N. CHOWDHURY¹, ERIN CULVER², UMER WATTOO², FARRAH MARGOLIN³, THU NGUYEN², RALPH M. GARRUTO^{1,2}, KATHERINE WANDER¹ and KOJI LUM^{1,2}

¹Anthropology, SUNY-Binghamton, ²Biological Sciences, SUNY-Binghamton, ³Integrative Neurosciences, SUNY-Binghamton

In 1945 Guam, the leading cause of premature death in the local population was a neurodegenerative disease that had symptoms of either Parkinsonism-dementia (PD) or Amyotrophic Lateral Sclerosis (ALS). Guamanians developed these symptoms—a combination of tremors and dementia or progressive motor function loss at 40-50 times worldwide average. Many ALS patients lived unusually long (20+ years) without respirators or medical treatment.

The purpose of this study was to observe change in serum inflammation of Guamanian ALS and PD patients before and after disease onset. Among longitudinally sampled participants, incident cases were identified, and pre-diagnosis and

post-diagnosis specimens were evaluated ($n=21$). Two age-, sex-, and region-matched controls for the pre-diagnosis and post-diagnosis time points were also evaluated. Biomarkers associated with duration and/or severity of neurodegenerative disease (specifically: monocyte chemoattractant protein (MCP)-1 and -2, interferon-gamma induced protein (IP)-10, interleukin-8, TARC, eotaxin-1 and RANTES) were evaluated in serum specimens via Quansys immunoassay. These biomarkers have been validated for stability in archived frozen human sera.

MCP-2 is elevated in post vs. pre-ALS-onset specimens ($p=0.015$), and between post-onset ALS and PD specimens ($p=0.007$). MCP-2 is marginally significant in post-onset ALS vs. control specimens ($p=0.068$). RANTES is marginally significant in post vs. pre-ALS-onset specimens ($p=0.089$) and pre-ALS-onset vs. controls ($p=0.076$). IP-10 is marginally significant in post vs. pre-PD-onset specimens ($p=0.08$) and in pre-onset PD patients vs. controls ($P=0.09$). Findings suggest neurodegenerative diseases have an inflammatory component across diverse environments.

This study was funded by Binghamton University URA and Harpur Edge.

Seasonal variation in day length and its implications for interpretation of activity budgets of chacma baboons in the Cape Peninsula, South Africa

SHAHRINA CHOWDHURY^{1,3,4} and LARISSA SWEDELL^{2,3,4}

¹Anthropology and Archaeology, Brooklyn College, CUNY, ²Anthropology, Queens College, CUNY, ³Anthropology, Graduate Center, CUNY, ⁴New York Consortium in Evolutionary Primatology (NYCEP)

For primates living outside the tropics, seasonal differences in day length can pose challenges, causing animals to condense their daily routine into dramatically reduced daylight hours and leading to seasonal differences in activity budgets. Methods of analyzing activity budgets also become important in these situations as simple calculations of activities performed as a percentage of total observation time do not consider the differences in hours available to conduct those activities. Here we present data from two troops of chacma baboons (*Papio ursinus*) inhabiting one of the most southerly habitats occupied by a primate, the Cape Peninsula of South Africa, with differences of nearly five hours of daylight between summer and winter. Activity budgets differed between seasons, the interpretation of which requires the use of multiple methods of analysis. As a proportion of observation time, both troops spent more time feeding ($p=0.043$, 0.003 each troop) and less time socializing ($p=0.068$, 0.001) in the winter. Number of hours spent feeding, however, did not differ across seasons in either troop; rather, in winter both troops simply reduced their hours spent in other

activities, such as resting and socializing. These seasonal shifts suggest that food is a constraint for this population: when fewer hours were available, they maintained their foraging effort at the expense of socializing, an essential behavior for this highly social species. This study highlights both the significance of day length for primate activity budgets and the importance of analyzing activity budgets in multiple ways to take seasonal daylight differences into account.

Funded by National Science Foundation BCS-0824590, LSB Leakey Foundation and New York Consortium in Evolutionary Primatology

Caucasian, Negroid, Mongolian, Indian, or Malayan: Racial categorization of living and dead servicemembers in the Korean War

ALEXANDER F. CHRISTENSEN

Scientific Analysis, Defense POW/MIA Accounting Agency

According to one tabulation of Korean War casualties, 80% were White, while 8.4% were Black. Sources disagree on the classification of the others. One publicly available database uses a five-part racial categorization adopted by the Department of Defense in 1950: "Caucasian," "Negroid," "Mongolian" (i.e., Northeast Asian), (American) "Indian," or "Malayan" (i.e., Southeast Asian or Pacific Islander), adding an "Other" category for those that the coder was uncertain about. Records of casualties identified at the US Army Central Identification Unit (CIU) in Kokura, Japan, during the Korean War, provide a data set to compare different antemortem and postmortem classifications. As an example, 37 Filipino-Americans are classified in the database as Malayan (27), Caucasian (9), and Other (1). Similarly, 47 Puerto Ricans are classified as Malayan (35), Caucasian (9), and Negroid (3). In the CIU, anthropologists described remains as Caucasoid, Negroid, or Mongoloid. These categories did not always neatly match those recorded on casualty records. In the CIU, the 37 Filipino-Americans were described as Mongoloid (20), Caucasoid (13), and admixed (4); the 47 Puerto Ricans as Caucasoid (38), Negroid (6), and admixed (3). CIU anthropologists recognized the imperfect fit between these categories, stating in one case that a mixture of traits "is common in racially marginal areas, such as the West Indies, Hawaii, the Philippines, and Polynesia in general." This recognition that observed human variation does not always fit well into any categorical model is one of the reasons that anthropology has now moved beyond this racialist perspective.

A Proposed Method for Studying Allometric Relationships without Stature

ELAINE Y. CHU and KYRA E. STULL
Anthropology, University of Nevada, Reno

ABSTRACTS

Limb bone allometry is used to explore hominin evolution, secular change in body size, and variation in modern humans. Previous research has proven stature as a universal scaling factor to standardize for size. However, often incomplete skeletal remains present a challenge in allometry research, as there is usually insufficient data to estimate stature. Alternative scaling factors allow for more allometry research to be conducted without the limitation of complete skeletons or known stature. A modern sample of subadults (n=329) between the ages of 0 and 13 years with known height is used to explore which alternative long bone measurements provide the closest proxy for height as a scaling factor. Ratios are calculated by dividing diaphyseal length by stature and other available diaphyseal breadths, resulting in a total of twelve alternative scaling factors. Visual assessment of change in limb allometry by age led to the use of cubic splines to create equations for height as the scaling factor for each length. Knots were chosen at 3 years and 7 years as threshold ages between life history stages. Additional equations are created using four breadths that were visually selected as resembling the slope created using height. Comparing slope distances of each alternative scaling factor from height returns humerus distal breadth as the closest proxy, with the smallest average coefficient distance. The current study minimizes potentially spurious results in allometric research by removing confounding error through stature estimation and offers a skeletal dimension that yields comparable results.

This research uses data collected for a project funded by one federal grant (NIJ 2015-DN-BX-K409).

The Application of 3D Geometric Morphometrics to Subadult Dentition: Exploring Tooth Development and Eruption Through Alternative Methods

LAURA E. CIRILLO and KYRA E. STULL
Anthropology, University of Nevada, Reno

Dental age estimation is considered the most accurate method for subadults, but some imprecision in the age estimates may be due to the level of measurement. Documenting biological processes through continuous, interconnected data, rather than ordinal (development) or dichotomous data (eruption) may increase precision. The goal of this research is to compare the performance of variables evaluated with alternate levels of measurements.

A sample of 110 computed tomography scans from individuals between 3.0 and 8.0 years was used to collect 66 3D landmarks on the mandibular dentition. Landmarks were placed on the midline of each tooth at either two or three points: 1) crown apex, 2) maximum crown development

up to crown complete, 3) maximum root length up to complete root. Interlandmark distances provided tooth length and relative position to alveolar bone.

The deciduous incisors had the lowest coefficients of variation (CV) (11.4%) and the second molar and fourth premolar had the highest CV (34.7% and 48.2%, respectively), which is likely linked to inconsistent crown initiation for M2 and P4 (~50% were absent in 3 year olds). Significant ($p < 0.05$) right-left asymmetry was found in the deciduous canine and central incisor. Visual analysis in 3D space and principal component analysis demonstrated that delayed development and the direction of growth accounted for 37% of variance after Procrustes alignment. Continuous data yielded more precise estimates than ordinal data using a mixed cumulative probit. Results indicate that alternative methods for development and eruption can improve the precision of dental age estimations.

Alloparental carrying and wound care in wild chimpanzees at Ngogo, Kibale National Park, Uganda

ISABELLE R. CLARK¹, RACHNA B. REDDY², AARON A. SANDEL¹ and KEVIN E. LANGERGRABER³

¹Department of Anthropology, University of Texas at Austin, ²Department of Anthropology, University of Michigan, ³School of Human Evolution and Social Change, Arizona State University

Altruistic behavior in social mammals is often explained by reciprocity or kin selection theory. We report an exceptional case of altruistic behaviors among maternally unrelated chimpanzees at Ngogo, Kibale National Park, Uganda. After a juvenile whose mother was temporarily absent was wounded by a groupmate, an adolescent male briefly carried her ventrally, and another "leaf-dabbed" the wound. We contextualize these behaviors by summarizing related observations recorded between 2014 and 2019. While juvenile-carrying and wound care of others is rare, altruistic behavior toward non-kin may not be as exceptional at Ngogo as kin selection theory would suggest. Alloparental carrying included ventral or dorsal carrying during travel or play (N = 54). All individuals carried were infants. In 53.7% of occurrences, the carrier was an older sibling. Wound care included grooming, licking, or leaf-dabbing of one's own or another's wounds (N = 41). Most wound care was self-directed (90.2%), and 14 of 37 occurrences involved leaf-dabbing. 2 of 4 other-directed occurrences were between maternal kin, and one occurrence of leaf-dabbing was observed between non-kin. We discuss potential costs of these behaviors which, given their rarity, are unlikely to be outweighed by reciprocity benefits. Our findings contribute to a growing number of accounts of altruistic behavior in chimpanzees and other social mammals. We should no longer be asking *if* nonhuman primates

have the capacity for altruistic behavior beyond the scope of reciprocity and kin selection theory, but *how* and *why* underlying mechanisms of altruism toward non-kin differ from that of humans.

Objective and subjective measures of stress in Latinx immigrants before and after the 2016 presidential election: hair cortisol, epigenetics, and mental health

ELIZABETH S. CLAUSING¹, KIMBERLY D'ANNA-HERNANDEZ² and AMY L. NON¹

¹Department of Anthropology, University of California, San Diego, ²Department of Psychology, California State University, San Marcos

Immigrants have faced high burdens of stress since long before the current administration's anti-immigrant policies. This study is an investigation of how immigration-related stress may impact the biology and health of Latinx immigrant mothers and children, considering recent increases in divisive rhetoric and anti-immigrant policies in the U.S. We compared hair cortisol and DNA methylation at stress-related candidate genes in mothers and children with interview data in Nashville, TN from two time points spanning the recent presidential election. Structured interviews were conducted with 82 immigrant mothers and their children (aged 5-13) between 2015 and 2016 and again in 2018. Using mixed-methods, we analyze perceived stressors, mental health, and buffering factors from mothers and children in relation to hair cortisol and bisulfite pyrosequencing at two stress-related genes. Mothers report high levels of depressive symptoms (24.3%), anxiety symptoms (35.1%), and moderate perceived stress (86.5%) as well as significantly decreased levels of optimism over time (mean difference = -3.4; p -value < 0.001). Before the 2016 election, we find (log) children's hair cortisol negatively associated with mother's year's in US (β = -0.07; p -value = 0.04), and children's worry over parent's deportation (β = -0.31; p -value = 0.069), suggesting a blunting effect on stress response. We see similar results following the election. We also see longitudinal epigenetic changes in *FKBP5* (ρ = 0.42; p -value = 0.05) in the mothers but no changes in the children. Increased stress over time can lead to biological and health consequences across the lifespan, especially for these already vulnerable families.

Funds provided by the Chancellors Research in Excellence Scholars at UCSD (Application # 4-G021) and Foundation for Child Development (VU-14).

1932 to 2019: Representation of (Bi)Racial Identity in Biological Anthropology

CHAUNESEY M.J. CLEMMONS
Anthropology, Texas State University

This presentation will discuss two theses completed, nearly nine decades apart, by two mixed/Biracial women in anthropology.

ABSTRACTS

Caroline Bond Day and the presenter. There are multiple parallels between the two including the studied samples of Negro-White and/or Biracial individuals.

Earnest A. Hooton described Day as “an approximate mulatto, having about half Negro and half White blood” in his foreword for Day’s 1932 thesis: *A study of some Negro-White families in the United States*. Day, being mixed herself, was uniquely positioned to seek out individuals of mixed blood (Mulattoes, 5/8 Whites, Quadroons, Octoroons, etc.). Her thesis is a work of anthropological observations including health, mortality, longevity, personal appearance, and anthropometric measurements.

The presenter has performed research for the thesis titled: *Ancestry estimation of Biracial individuals using dental morphological traits*. Which used current dental morphological quantitative methods (Edgar (2013), rASUDAS, and biodistance analysis) to estimate ancestry of a sample of Biracial (Black/White) individuals.

Conclusions made by Day in 1932 state “in every category of mixture some individuals are much closer to the Negro type...others...Whites, and a majority fall between.” Results in 2019, similarly, demonstrated disagreement between self-reported social identifiers and ancestry estimates.

Decades of time facilitated adjustments in terminology and advanced anthropological methods while highlighting the need to broaden how identity is understood. Race, a social construct, continues to impact the identity of individuals on biological, personal, and public levels. This is made clear by examining the discordance between the complex identity factors of socio-cultural labels and anthropological observations throughout time.

Anticipatory behavior in captive male western lowland gorillas (*Gorilla gorilla gorilla*)

SIERRA J. CLEVELAND¹, PAIGE BARNES², JENNIFER TOBEY³ and MEGAN OWEN³

¹Primate Osteology Lab, Department of Anthropology, University of Oregon, ²Department of Zoology, Michigan State University, ³Population Sustainability Team, San Diego Zoo Institute for Conservation Research

The primary goal of this study was to explore behaviors considered undesirable in captive populations of western lowland gorillas (*Gorilla gorilla gorilla*). We were particularly interested in anticipatory behaviors surrounding the end-of-day transition into off-exhibit holding and the impact of this anticipation on social proximity and space use. Subjects were three male gorillas in the San Diego Zoo troop and two males in the San Diego Zoo Safari Park troop. We conducted 124.5 hours of live behavioral observations over a six-week period between June 11 and July 20, 2018, using the Behavioral Observation Research Interactive

Software (BORIS) Application. We used continuous sampling to record behavior, social proximity, and location within the exhibit. We used ANOVAs to test differences in behavioral rates between individuals, and regressions to test linear correlations with time. Two of the focal males showed an increase in self-grooming throughout the day (F-test=7.59, p<0.01; F-test=8.26, p<0.01), three of the focal males showed increased spatial selectivity (F-test=84.97, p<0.0001; F-test=12.79, p<0.001; F-test=10.58, p<0.01), and one male increased his rate of aggressive events as time progressed (F-test=8.38, p<0.01). Overall, all five focal animals demonstrated a significant change in undesirable behavior as the time to transition to off-exhibit holding approached. Introducing new husbandry practices that foster predictability, such as reliable auditory cues during nightly recall, may be useful in mitigating undesirable anticipatory behaviors, but further research is necessary.

This study was funded by Patricia Beckman and the J.W. Sefton Foundation as part of a summer research fellowship at the San Diego Zoo Institute for Conservation Research.

SAFE and sound: How the AZA’s SAFE program is working to save chimpanzees (*Pan troglodytes* ssp.)

CHRISTINA CLOUTIER BARBOUR^{1,2}, ANDREW R. HALLORAN⁵, KEVIN LANGERGRABER⁴, JOHN MITANI³ and DAVID MORGAN⁶

¹Conservation & Research, Lion Country Safari, ²Department of Anthropology, University of Utah, ³Department of Anthropology, University of Michigan, ⁴School of Human Evolution and Social Change, Arizona State University, ⁵Chimpanzee Care, Save the Chimps, ⁶Lester E. Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo

Chimpanzees (*Pan troglodytes*) are well represented in the academic literature, contributing countless data in our efforts to better understand ourselves. They are also under threat across the entirety of their natural range and may be extinct in the wild within 30 years. Concerted, unified action is required to address the threats to the species. This will require more than direct intervention; it also necessitates largescale educational outreach and stakeholder engagement. The Association of Zoos and Aquariums (AZA) has developed a highly collaborative platform through which we may achieve this goal. The AZA receives more annual visitors than all major sports team attendance combined, and engages many more millions through their social media platforms. We have the opportunity to harness the tremendous power of the organization to encourage effective conservation action through the Saving Animals from Extinction (SAFE) program. Though young, the program has already seen measurable results. For instance, the initial five species represented by the program saw a 355% increase in conservation spending in AZA in two years. Chimpanzees are

one of the latest species to be nominated as an AZA SAFE flagship animal, and already has the support of four notable field partners—Goulougo Triangle Ape Project, Ngogo Chimpanzee Project, Tonkolili Chimpanzee Project, and Wildlife Conservation Society of Nigeria—as well as seven institutional partnerships across the US. We present details regarding the Chimpanzee SAFE program here, and the ambitious new plan that hopes to save chimpanzees from extinction.

Tomb 2 at Las Huacas, Chinchá Valley: The demographic profile and mortuary practices of a Late Horizon commingled tomb

EMILIE M. COBB¹, JORDAN A. DALTON² and JULIANA G. MEJÍA³

¹Anthropology, University of North Carolina at Charlotte, ²Anthropology, University of Michigan, ³Antropología y Sociología, Universidad de Caldas, Colombia

The site of Las Huacas is a 105-hectare agricultural center located in the Chinchá Valley of Peru. Excavations by the Proyecto de Investigación Arqueológica Las Huacas (PIALH) of Complex N1 found evidence for major transformations to the complex while it was a part of the Inca Empire (Late Horizon, AD 1470-1534) and multiple mortuary features where at least 76 individuals were buried. These individuals were buried following distinct mortuary practices and burial styles, including four subterranean tombs containing commingled human remains and associated artifacts. This paper presents bioarchaeological data from one of these sealed subterranean tombs, Tomb 2. An inventory of the remains was recorded and, when possible, sex and age were estimated. We also recorded data on taphonomy, pathology, and body modifications. Our results found evidence of cranial modifications and that individuals of various ages and both sexes were buried in the tomb. Red pigment was also found on the crania and long bone diaphyses. We conclude by establishing that these secondary burials are possibly family tombs based on the range of ages (fetal development to older adults) and presence of numerous septal apertures. We also compare Tomb 2 to other mortuary assemblages from Las Huacas, the Chinchá Valley and the Andean region during the Late Horizon. The data from Tomb 2 provide important new information about the variety of body manipulations and mortuary practices that were used in the Late Horizon and about the health and life histories of the individuals that were buried in it.

Virtual estimates of brain size in the Krapina hominins

ZACHARY COFRAN, MADELEINE BOONE and MARISA PETTICORD
Anthropology, Vassar College

ABSTRACTS

The Krapina hominins comprise a relatively large assemblage of early Neandertals. Endocranial volume (ECV, a measure of brain size) has been estimated for some of these individuals, but the sample has not been treated with “virtual” reconstruction methods. We use geometric morphometrics to reconstruct endocrania and estimate ECV of five crania in this sample, including the Krapina 2 juvenile for which this metric has not been assessed. We created multiple reconstructions of each individual based on different reference crania, providing us with a measure of uncertainty due to missing data. Validating our approach, our reconstructed ECV for the Spy II Neandertal (1525 cm³) is nearly identical to published manual and virtual reconstructions. Our estimates for the relatively complete adults Krapina 3 and 6, averaging 1250 and 1160 cm³, respectively, are similar to previous manual reconstructions. Estimates for the juvenile Krapina 1 range from 1408–1428, much larger than previous that used linear regression. There is great uncertainty in the highly fragmentary Krapina 5 adult, with estimates ranging from 1357–1469 cm³ using human references, or 1496 cm³ using Spy II as a reference. Estimates for Krapina 2 range from 1282–1301 cm³. Brain size at Krapina is similar to other pre-Würm Neandertals, within the range of but lower than the average of later Neandertals. The Krapina juveniles show adult-like sizes, suggesting human-like brain size growth.

This work was supported by the Joan E. Morgenthau Hirschhorn '45-44 Fund, and the Joseph H. and Florence A. Roblee Foundation, funding undergraduates in Vassar's URSI program.

Parasites in free-ranging *M. fascicularis*

ELIZABETH M.C. COGGESHALL

Primate Behavior and Ecology, Central Washington University

As deforestation rates increase, primate habitats become altered or lost entirely, which results in an increased rate of human-alloprimate conflict. Previous research has shown that parasite dynamics can correspond with host population size in fragmented forests, and that parasite prevalence and richness is directly related to habitat fragmentation, especially those with frequent anthropogenic activity. Additionally, zoonotic disease transmission becomes extremely likely with frequent human contact. In this study, I examine the parasite load and diversity in adult female and infant long-tailed macaques (*Macaca fascicularis*). I hypothesized that (1) nematodes will be the most prevalent parasite and (2) infants will have heavier parasitic loads and a greater diversity of parasites compared to adult females. This study was performed at Don Chao Poo Forest, Phana, Thailand from July-August 2019. This forest experiences high amounts of anthropogenic activity and is protected by a Buddhist monastery. The four *M. fascicularis* groups are

sporadically provisioned by visitors who make offerings to the local deity. In total, 42 fecal samples were collected from four groups of *M. fascicularis*. Our preliminary results show that offspring samples carried 1608 parasites, adult females carried 424 parasites, and 1877 nematodes were identified. In total 2032 parasites were identified consisting of Trichuris eggs, Strongyloid ovas (morulated and larvated), L1-L3 worms, protozoa, and others.

Estimation of among-landmark covariances: not always, but sometimes

THEODORE M. COLE III¹, SUBHASH R. LELE², LIANGYUAN HU³, PETER SOLYMOS⁴ and JOAN T. RICHTSMEIER⁵

¹Dept. of Biomedical Sciences, University of Missouri-Kansas City, ²Dept. of Mathematical and Statistical Sciences, University of Alberta, ³Dept. of Population Health Science and Policy, Icahn School of Medicine at Mount Sinai, ⁴Dept. of Biological Sciences, University of Alberta, ⁵Dept. of Anthropology, Pennsylvania State University

One of the most important remaining challenges in landmark-based morphometrics is the estimation of among-landmark variance-covariance (VCV) matrices. These matrices define patterns of morphological integration and modularity and serve as the foundation for studies of quantitative genetics. We have previously shown that, due to the presence of nuisance parameters (unknown rotations and translations), estimation of general VCV matrices is impossible for most landmark data sets. We have also shown that residuals from superimposition methods cannot accurately recover VCV structure, a result that is becoming more widely recognized.

Although a general VCV matrix is non-estimable, we show that if one imposes certain constraints on the VCV structure, estimation may be possible. A constrained matrix is one where some covariances must be assumed to be zero *a priori*. We propose a method-of-moments estimator of the constrained VCV matrix, although, unfortunately, not all constrained matrices are estimable. We illustrate a few commonly-used models for VCV structure where the matrix is estimable (e.g., diagonal and block-diagonal matrices); we then describe some conditions where it is not. We introduce an R package that conducts the estimation of constrained VCV matrices for landmark data, and we provide some examples, using simulated data, where estimation is possible.

Three-dimensional cortical pore networks are morphologically optimized for localized mechanical strain in the human femoral neck and rib

MARY E. COLE¹, SAMUEL D. STOUT¹ and AMANDA M. AGNEW^{1,2}

¹Anthropology, The Ohio State University, ²Skeletal Biology Research Lab, The Ohio State University

Bone remodeling produces a complex, highly interconnected network of cortical pores that transmit vasculature. Stochastic remodeling renews bone under low strain, while targeted remodeling repairs microdamage under high strain. With age, senescing bone cells become uncoupled from these mechanical stimuli, increasing cortical porosity. We describe a novel model for strain-sensitive pore morphometry that persists over the lifespan.

Matched right-side femoral neck and midshaft fourth rib segments were collected from a cadaveric age-series, with one male and one female per decade from 20's to 90's. Whole cross-sections were scanned along a 10 mm length in a HeliScan micro-CT (6.4097 μm voxels, 60 kV, 80 uA, exposure = 0.4 s). Three-dimensional pore systems were extracted automatically with custom macros (ImageJ, CT-Analyser).

The femoral neck was significantly more porous than the rib throughout the lifespan, apparently due to more permissive and uniform endosteal resorption, which the rib suppresses in its pleural cortex. Regional pore morphometry was contrasted along the increasing superior-to-inferior strain gradient in the femoral neck cortex and between opposing strain modes of the pleural and cutaneous rib cortex. High-strain regions of the femoral neck and rib displayed significantly lower pore density, lower percent porosity, lower connectivity and convergence, and increased longitudinal orientation. Microdamage can propagate into fracture through interconnected pore networks. These isolated, disconnected pore systems appear optimized for frequently damaged high-strain regions. This regional patterning is maintained even as aging increases porosity, excepting 1) significant pore convergence and 2) extensive pore coalescence in the superior-anterior female femoral neck.

This work was supported by National Institute of Justice award #2017-MU-CX-0009. The opinions expressed are those of the authors and do not necessarily reflect those of the Department of Justice.

Healthy blood lipid profiles in wild-born chimpanzees (*Pan troglodytes*) are associated with low adiposity and inflammation

MEGAN F. COLE^{1,3}, MELISSA EMERY THOMPSON³, JOSHUA RUKUNDO⁴, SOFIA

ABSTRACTS

FERNANDEZ-NAVARRO⁵, REBECCA ATENCIA⁵, TONY L. GOLDBERG⁶ and ALEXANDRA G. ROSATI^{1,2}

¹Department of Psychology, University of Michigan,

²Department of Anthropology, University of

Michigan, ³Department of Anthropology, University

of New Mexico, ⁴Chimpanzee Sanctuary and

Wildlife Trust, ⁵Jane Goodall Institute Congo,

⁶Department of Pathobiological Sciences, University of Wisconsin

Aging processes in chimpanzees (*Pan troglodytes*), one of our closest living relatives, are crucial to contextualize the evolution of human health and longevity. Cardiovascular disease is a major source of mortality in humans, and therefore a key issue for comparative research. Current data indicates that compared to humans, chimpanzees have high blood lipids—an important risk factor for heart disease in humans. However, most work to date on cardiac health in chimpanzees has examined laboratory populations, and lifestyle is an important factor shaping cardiac health in humans. We therefore examined wild-born chimpanzees living in two African sanctuaries, as these populations consume a more naturalistic diet, range in large forested enclosures, and experience species-typical social groups. We measured body weight and blood lipids in these sanctuary-living chimpanzees (N=75) and compared them to data from laboratory-living chimpanzees (N=471, from the Primate Aging Database). We found that semi-free-ranging chimpanzees exhibited lower body weight (linear mixed models account for age and sex: $n=9117$ observations, $X^2=77.11$, $p<0.0001$), total cholesterol ($n=5586$, $X^2=52.81$, $p<0.0001$), and triglycerides ($n=5360$, $X^2=12.11$, $p<0.001$). We further investigated body fat (skinfold thickness) and inflammation (hsCRP and IL-6) in the sanctuary chimpanzees and found these measures to be lower than previously published values from laboratory-living populations. As in human groups characterized by high levels of physical activity, chimpanzees from African sanctuaries maintained healthy cardiovascular profiles across the lifespan. Our findings support the hypothesis that lifestyle can shape health indices in chimpanzees during aging and provide a new evolutionary framework for understanding human cardiovascular health.

This study was funded by the National Institute on Aging of the National Institutes of Health (Award 1R01AG049395-01).

Quantifying the emergence of sexually dimorphic traits using Walker (2008) and evaluating method performance in subadult sex estimation

STEPHANIE J. COLE and KYRA E. STULL

Anthropology, University of Nevada, Reno

At present, little is known regarding the ontogeny of the five traits used in the Walker (2008) method or at what age the method can be reliably applied. The aim of the current study is to evaluate the

performance of Walker (2008) in 301 modern subadults ($f=136$; $m=165$) aged 8 to 21 years using MSCT postmortem scans. Significant differences in trait score frequencies between subadult males and subadult females were first detected by 13 years. With few exceptions, trait score frequencies for subadult males were similar to those observed in adult males by 17 years, suggesting skull “masculinization” is complete by this age. Classification accuracies for all six Walker (2008) equations showed a strong female sex bias in the youngest individuals. As age increased, accuracies changed to favor male classification, which is consistent with validation studies using adults. Recalibration of the equations using the subadult sample improved classification accuracies, however strong sex biases towards female classification in the youngest subadults and towards male classification in the older subadults remained. The results of this research illustrate that sex differences in trait expression are present and trait frequencies comparable to those of adults are reached prior to adulthood. Subsequently, cranial traits commonly used in adult sex estimation could be applied with confidence in forensic and bioarchaeological situations involving subadults of specific ages. This study refutes the claim that distinctive sexually dimorphic features are absent in subadults and demonstrates their potential contribution to, and subsequent improvement of, the subadult biological profile.

This research was funded in part by NIJ grant 2015-DN-BX-K409: Development of Modern Subadult Standards: Improved Age and Sex Estimation in US Forensic Practice.

Climate change and conflict: patterns, processes, prospects

MARK COLLARD¹ and CHRIS CARLETON²

¹Archaeology, Simon Fraser University, ²Extreme Events, Max Planck Society for Chemical Ecology

Concern is growing among policy-makers that the current bout of anthropogenic climate change will increase conflict within and among human societies. For example, the European Commission recently advised that climate change will intensify social and political tensions, leading to more conflict. Similar statements have been issued by the United Nation's Intergovernmental Panel on Climate Change and the US Department of Defense in the last few years. But how well supported is the hypothesis that climate change increases conflict levels? In this paper, we review research on the relationship between climate change and conflict that has been published over the last two decades. We show that the situation is considerably more complex than the aforementioned warnings suggest. To begin with, it appears that key climatic variables can impact conflict levels in opposing ways. For example, there is evidence that increasing temperature

fuels conflict but increasing aridity suppresses conflict. A further complexity is that the impact of climatic variables on conflict is mediated by region such that a given variable can have a significant impact in one region but not in another. Lastly, there is reason to think that even in cases where a particular climatic variable appears to have increased conflict in more than one region, the “linking mechanisms” are not the same. In the final section of the paper, we outline what we think are the implications of these findings for policy and for future research on the topic.

We are supported by the Canada Research Chairs Program, the Canada Foundation for Innovation, the British Columbia Knowledge Development Fund, Simon Fraser University, and the Max Planck Society.

A geometric morphometric comparison of shape and integration indices in captive and wild *Macaca fascicularis* postcrania

MARK A. CONAWAY, BRITTANY KENYON-FLATT and NOREEN VON CRAMON-TAUBADEL

Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo

The effects of captivity, particularly diet in captivity, on the craniofacial structure of primates and other mammals is well documented. However, relatively few studies have examined the effects of captivity on the postcranium. Here, we perform postcranial shape analyses and evaluate indices of integration in samples of wild-caught and captive biomedical *Macaca fascicularis*. Anatomical landmark data were collected on 3D surface scans of the femur, os coxa, tibia, scapula, humerus, and radius. After Procrustes superimposition, standard shape analyses (Principal Components, Canonical Variates and Discriminant Function Analysis) were performed. Integration was quantified using the Integration Coefficient of Variation (ICV), and distributions of ICV values were generated via a resampling protocol. Statistical comparison between ICV distributions for captive and wild individuals were performed using a Mann-Whitney U test with Bonferroni correction.

Apart from the humerus, all skeletal elements present significantly different integration values in wild vs. biomedical samples, pointing to differences in covariance structure between the two groups. In particular, captive individuals tended to be more integrated than wild. Further, all shape analyses showed significant distinctions between captive and wild individuals. While still significant, the least effective morphological distinction was, likewise, with the humerus. Overall, however, these results suggest that captive and wild individuals can indeed present significant differences in morphology and integration, and that caution should be used when constructing samples of

ABSTRACTS

either or both. Further study is required, however, to assess what systematic effects captivity has on skeletal covariance structure in non-human primates.

This research is supported by a National Science Foundation Grant (NSF BCS-1830745), a Leakey Foundation Grant, as well as the University at Buffalo Mark Diamond Research Fund.

Exploring age related changes in cortical bone in individuals over 50 using radiographs

JACOB M. COOK M.A. and NICHOLAS P. HERRMANN PH.D.

Anthropology, Texas State University

Accurate age estimation is an important tool in both reducing the candidate pool for individual identification and for reconstructing the demographic parameters of past populations. In this study, we explored the relationship between the bone volume ratio (MV:BV) using linear measures of medullary cavity breadth and cortical bone thickness at three areas of the femoral shaft as a proxy for age. In addition, we document changes in shaft shape with age using a Generalized Procrustes Analysis (GPA). Digital radiographs of 164 non-pathological left femora from the Texas State University Donated Skeletal Collection (TXSTDSC) were taken and analyzed. The results of this study indicate that the overall MV:BV is moderately correlated with age ($r=0.38$) and that this relationship is stronger in females ($r=0.49$) versus males ($r=0.28$). The GPA revealed that there is site specific bone remodeling with consistent rates of cortical bone loss throughout the aging process with slightly different patterns for males and females. The most significant changes in shape are along the anterior and posterior sides of the bone at midshaft. These results reinforce previous findings that cortical bone thinning is correlated with age and that there are areas of the femur that are more affected by this process than others. The findings of this study have the potential to be applied in both forensic and bioarchaeological settings for individual identification and paleodemographic reconstructions, respectively.

Annular binding in a cranium from Mississippi County, Arkansas: what does this practice tell us about identity?

DELLA C. COOK

Anthropology, Indiana University

Shawnee Village is a Late Prehistoric site with little published archaeological information. A single adult male skull from the site was acquired by Thomas Gilcrease (1890-1962) and was part of his collection when it became the nucleus of the Thomas Gilcrease Institute in Tulsa, Oklahoma. This adult male may have served to illustrate a rare intentional modification of vault shape.

Parallelo-fronto-occipital, annular, and, more recently, pseudocircular binding are not well-differentiated in the literature, and they are difficult to quantify using standard craniometric techniques.

Parasagittal contours of the cranium and the endocast are constructed using a cubic cranio-phor. This skull is remarkably symmetrical in the concave modification of the frontal and the flattened, elevated nuchal region. Suture closure and complexity in this example are not unusual. There is periosteal reaction between the temporal lines, and there are several small destructive lesions in this tissue that suggest trauma or infection. Dental wear is light given the sutural age, reflecting extensive caries and tooth loss. Another unusual feature is a mandibular supernumerary premolar.

Annular binding deformation is unusual in the context of other crania from the Southeast, and it is one of the features that links the Southeast to Mesoamerica. A brief review of this literature is presented.

Socioecological Predictors of Health Profiles in Western Lowland Gorillas

KRISTENA E. COOKSEY¹, CRICKETTE SANZ^{1,2}, JEAN MARIE MASSAMBA², THIERRY FABRICE EBOMBI², PROSPÈRE TEBERD², ESPOIR MAGEMBA², GASTON ABEA², GAETON MBÉBOUTI², JUAN SALVADOR ORTEGA PERALEJO², IVONNE KIENAST², COLLEEN STEPHENS¹ and DAVID MORGAN³

¹Department of Anthropology, Washington University in St. Louis, ²Congo Program, Wildlife Conservation Society, ³Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo

Socioecological factors are linked to health outcomes, overall health profiles, and disease transmission in primates. Due to their close phylogenetic relatedness to humans, great apes are particularly susceptible to anthropogenic disease infection. Infectious diseases have been documented in wild gorilla populations that have manifested varying patterns of disease prevalence potentially attributable to differences in social groupings and patterns of intergroup contact. We assessed a suite of potential socioecological predictors of health incidences across four groups of western lowland gorilla (*Gorilla gorilla gorilla*) in the northern Republic of Congo. A total 17,951 observational health assessments were conducted during daily follows in the Goulougo and Djeko Triangles from August 2015 to July 2019. While overall presence of disease was relatively low, we detected several respiratory episodes and chronic health issues within the focal population. We observed an average of 9.81 incidences/month (2.6% of total observation days) for respiratory illness and an average of 21.29 incidences/month (5.7% of total observation days) for other incidences associated with declining health profiles across all groups. We suggest there is a correlation between the presence of respiratory illness with other indications

of altered health profiles. Based on the observed dynamics of disease spread, we discuss probable mechanisms of transmission within and between groups. Further, we suggest that identification of the specific predictors and modes of disease transmission can be used to mitigate some specific health risks. Recommendations for best practices and management protocols are presented as they relate to improving health profiles in gorillas.

Arcus Foundation, Cincinnati Zoo, Indianapolis Zoo, Houston Zoo, Columbus Zoological Park, Nouabale-Ndoki Foundation, U.S. Fish and Wildlife Service

Hormonal correlates of biparental care in owl monkeys (*Aotus azarae*)

MARGARET K. CORLEY¹, JUAN PABLO PEREA-RODRIGUEZ², CLAUDIA VALEGGIA¹ and EDUARDO FERNANDEZ-DUQUE¹

¹Anthropology, Yale University, ²Project Conservémonos, Project Conservémonos

This study utilizes a pair-living and sexually monogamous primate, the owl monkey (*Aotus azarae*), as a model to increase our understanding of the role of males and females in societies that are characterized by pair-bonding and biparental care. We quantified variation in hormones across three distinct reproductive periods (mating, gestation, and infant care) to examine physiological mechanisms owl monkeys may have evolved to facilitate high levels of paternal care and mating competition in both sexes. Specifically, we utilized fecal cortisol as a proxy for evaluating energetic demands during reproductive periods, and fecal androgens to evaluate a potential trade-off in investment between mating and parenting effort. We collected ~1150 fecal samples from 26 identified wild adult owl monkeys (13 males, 13 females) in 2011-2015 at the Owl Monkey Project site in Formosa, Argentina. Enzyme immunoassays indicated that females' mean cortisol concentrations during the gestation period (221 ± 51 ng) were double those of the infant care period (98 ± 25 ng), and almost triple those of males' during the gestation period (78 ± 18 ng). Males and females had similar levels in the two other reproductive periods. Males' mean fecal androgen concentrations were similar to, or lower than, females' in all three reproductive periods. The largest difference was during the infant care period when males' levels were a third of those of females (126 ± 68 vs. 403 ± 180 ng; Wilcoxon test: $W=2$, $p=0.005$), tentatively indicating a trade-off between mating and parenting effort in males.

NSF-BCS-1503753, 0621020, 1219368, 1232349, and 1540255

ABSTRACTS

Life histories in the study of ancient rare diseases

AVIVA A. CORMIER¹, JANE E. BUIKSTRA² and AMANDA WISSLER²

¹Department of Anthropology, Brown University, ²School of Human Evolution and Social Change, Arizona State University

The study of individuals with Rare Diseases from archaeological contexts is increasingly an avenue of interest for bioarchaeologists and paleopathologists as new methodologies and the integration of molecular biology allow for the elucidation of unusual differential diagnoses and the publication of the resulting case studies. A Rare Disease is defined in the US as a condition that affects fewer than 200,000 people and in the EU as a condition that affects fewer than 1 in 2,000 people. Using clinical signs and symptoms attained from the Genetic and Rare Diseases Information Center (GARD) of the NIH and the Orphanet Rare Disease database, we have identified 576 rare diseases with skeletal expressions and we present clusters of symptoms that correspond to activity and social limitations. Here we offer a framework for evaluating the skeletal expressions of rare diseases that integrates anthropological theories of disability, the life course, osteobiography, and the bioarchaeology of care, with the standard paleopathological texts, modern clinical literature, and the disease databases. We demonstrate how the analyses can extend beyond the differential diagnosis and general conclusions of physical difference to include the impact of the disease on the life experiences of the individuals and the resulting societal perceptions and attitudes. This approach allows for the understanding of the effect of the condition on the individual, the advancement of contemporary perspectives on impairment and disability, and the raising of awareness about Rare Diseases in past and present contexts.

Sub-adult Aging Method Selection (SAMS): an online decisional tool for standardized method selection and evaluation

LOUISE K. CORRON^{1,3}, DAVID NAVEGA², SILVANA CONDEMI³, FRANCOIS MARCHAL³ and PASCAL ADALIAN³

¹Anthropology, University of Nevada, Reno, ²Laboratory of Forensic Anthropology, Department of Life Sciences, University of Coimbra, ³UMR 7268 ADES - EFS - CNRS, Aix-Marseille Université

Several hundreds of publications are available to biological anthropologists for subadult age estimation. The applicability of these methods mainly depends on the context of study (e.g. forensic or bioarchaeological) and the type of skeletal or dental material available and its case or study-dependent. However, the relevance and methodological strength of these publications can be objectively assessed by comparing their sampling and statistical parameters. This paper

presents SAMS (<http://osteomics.com/SAMS>), an online decisional tool developed to objectively evaluate and provide a means to compare over 260 sub-adult age estimation publications based on standardized methodological parameters. These parameters are based on previously published recommendations for sub-adult age estimation in forensic anthropology. With SAMS, users can choose up to three selective parameters to filter the database according to the material available for their study and up to twenty descriptive parameters to be displayed with the results. The resulting query then presents the selected descriptive parameters and two means of publication evaluation, namely the Validity score and the Relevance score, calculated using a simple classification algorithm. Validity represents the percentage of compliance of a publication with valid methodological criteria. Relevance represents how well the publication matches with the users' query. SAMS can easily and quite extensively assist users in choosing sub-adult age estimation methods by providing them with the necessary information for evaluating protocol validity and other practical details on their applicability. The database will be gradually updated and implemented with new sub-adult age estimation publications as they are made available.

NA

The ontogeny of nest building behavior in captive aye-ayes (*Daubentonia madagascariensis*)

SAMANTHA E. COTHERN, KAITLYN A. TIFFANY, DAVID Q. WATTS and LISA M. PACIULLI
Department of Biological Sciences, North Carolina State University

Many animals build nests and use them for a variety of reasons such as avoiding predators and parasites, thermoregulation and protection from the elements, sleeping / resting, and/or infant care. Several primate species build nests including chimpanzees (*Pan troglodytes schweinfurthii*), who as they age, build sturdier nests in more suitable locations (Goodall 1968). This suggests that individuals learn to build better nests over time. Aye-ayes (*Daubentonia madagascariensis*) build oval-shaped enclosed nests 10-15m above ground with small branches and vines, and a 15cm opening (Petter & Peyrieras 1970, Quinn & Wilson 2004). Almost no data have been published on the construction or ontogeny of aye-aye nests. Therefore, we examined a juvenile aye-aye nest, and hypothesized that it would differ from adult nests in at least one key feature and show improvement over time. Duke Lemur Center aye-aye, Agatha, was two-years-old when she was observed making her first nest. Measurements were taken on the nest including length, width, height, and volume. The nest was constructed from wood wool, two fleece blankets, and other items. It was 61cm wide, 42cm long, 39cm tall,

9450cm³ in total volume, and had two openings. As hypothesized, Agatha's nest differed from adult nests in having an additional hole, which could allow in inclement weather and/or a predator. This suggests that over time, aye-ayes learn to construct better and safer nests. Additional nests are being measured to provide information on the average nest, as well as the ontogeny of aye-aye nest construction.

Funding generously provided by NCSU's Biological Sciences Support for Undergraduate Research Experiences and the Office of Undergraduate Research.

Heel strike and the metabolic cost of human walking

CLARA C. COUSINS¹, MATTHEW C. O'NEILL², W. ÉAMON CALLISON¹ and NICHOLAS B. HOLOWKA^{1,3}
¹Human Evolutionary Biology, Harvard University, ²Anatomy, Midwestern University, ³Anthropology, University at Buffalo

Humans are plantigrade like many other animals, but walk with an unusual form of heel-first foot strike that is facilitated by dorsiflexing the ankle prior to touchdown. In contrast, chimpanzees are also plantigrade, but often do not heel strike when walking bipedally, and typically touchdown with plantarflexed ankle joints. Fossils and footprints have been used to reconstruct the presence/absence of heel strikes in the bipedal gaits of early hominins, but the adaptive advantage of this walking style is not fully understood. Previous research suggested that heel strike plantigrade reduces energy costs in human walking, but the magnitude and joint-specific determinants of this effect have not been quantified. Here we used respirometry to measure the metabolic cost of transport in eight human participants who walked with heel strike and non-heel strike plantigrade foot postures on a forceplate-instrumented treadmill, controlling for speed and stride frequency. We also used 3-D motion capture and inverse dynamics to estimate power at the hip, knee and ankle. When walking without heel strikes and using chimpanzee-like ankle angles at foot contact, all participants displayed considerably higher net costs of transport, on average 35±10% greater, than when walking with normal heel strikes. These cost differences appeared to be driven in part by much greater ankle joint work, as well as smaller increases in hip joint work. Our results suggest that avoiding heel strike, due to the possession of a gracile calcaneus for instance, would have likely entailed high metabolic walking costs in early hominins.

ABSTRACTS

Hand anthropometry may be an indicator of skin thickness at various hand locations and postures

MEGAN COYNE¹, SARAH E. CAMERON¹, PAOLA A. D'ANGELO², MARGARET AUERBACH² and JOHN W. RAMSAY¹

¹Biomechanics & Engineering, US Army CCDC Soldier Center, ²Emerging Materials & Development, US Army CCDC Soldier Center

The amount of required hand protection is considered to be the same across hand sizes. However, variations in hand size and skin thickness across hand locations and grip posture may be essential in the development of thermal protective gear. The objective of this study was to determine whether variations in hand anthropometrics correlated with changes in skin layer thickness measurements during different hand postures. Superficial ultrasound images of seventeen male military personnel were obtained using a 22MHz linear probe in natural and clenched positions. Images were taken from both postures at the second, third, fourth and fifth intermediate phalanges, and also centered over the third metacarpal. Anthropometric measures included: hand length, breadth, circumference, and palm length. A step-wise linear regression was performed with each anthropometric measure as the independent variable and the different skin layer thicknesses as the dependent variables. Greater hand length was significantly correlated with thicker dermis layers (clenched and unclenched) at the second ($p=0.005$, $p=0.004$) and fifth ($p=0.016$, $p=0.011$) intermediate phalanges and at third metacarpal ($p=0.028$, $p=0.043$) as well as with thicker epidermis at the third intermediate phalange ($p<0.001$). Similarly, greater hand breadth positively correlates epidermis (clenched) on the second intermediate phalange ($p=0.025$). Longer palm length also positively correlates with thicker epidermis at the second intermediate phalange in the clenched position ($p<0.001$). No correlation ($p>0.05$) was found between hand circumference and skin layer thickness at any location. Correlations between hand anthropometry and skin thickness imply that smaller hand sizes may require specialized protection from thermal injury.

The Chronostratigraphic and Depositional History of the FxJ20 Site Complex, Northern Kenya

CAITLIN CRAIG¹, SILINDOKUHLE MAVUSO², SARAH HLUBIK³, SHANNON WARREN⁴, WENDY KHUMALO⁵, DAVID BRAUN⁶ and EMMANUEL NDIEMA⁷

¹Department of Anthropology, University of Victoria, ²School of Geosciences, University of the Witwatersrand, ³Department of Anthropology, Rutgers University, ⁴Department of Geology, University of Kansas, ⁵Department of Geological Sciences, University of Cape Town, ⁶Department of Anthropology, The George Washington University, ⁷Archaeology Section, National Museums Kenya

The Koobi Fora Formation, in northern Kenya's Turkana Basin, documents an extensive Plio-Pleistocene hominin record. Previous research has documented evidence of combustion features at the FxJ20 site complex that may be associated with hominin behaviour. Despite the extensive research on these archaeological finds, the area has seen minimal lithostratigraphic and sedimentological investigation, and its broader environmental context is not as clear. Initial studies describe a series of floodplain deposits associated with a nearby fluvial channel, but a channel feature was never located. Furthermore, there has been contention on the stratigraphic relationship between the site complex and the Morotut Tuff (1.6 Ma). Thus, this study adopted a geological investigation into contributing to this site complex through comprehensive lithostratigraphic and sedimentological investigations. The stratigraphic sequence has been revised to include an underlying Okote Tuff deposit (1.64 Ma) and an overlying Morotut Tuff deposit, comfortably placing the site between 1.64 Ma and 1.6 Ma. Additionally, a nearby channel was documented with facies associations indicating the presence of either a braided stream, or a small fluvial channel draining into a larger fluvial system (potentially the paleo-Omo River). The excavation areas comprise sequences of floodplain deposits which would have provided hominins with a stable landscape containing fresh water and associated resources. Ultimately, this investigation clarifies the geological succession of the FxJ20 site complex and provides an environmental context that is critical to understanding the stimulus behind novel hominin adaptations, such as pyrotechnology.

This research was funded in part by NSF Archaeology grant #1624398 and REU #1930719.

Women's Intimate Apparel as Subtle Sexual Signaling in Heterosexual Relationships

LYNDESEY K. CRAIG

Anthropology, University of Nevada, Las Vegas

Current literature on women's sexual signaling focuses on modes of attracting potential, new sexual partners, but limited literature examines women's subtle sexual signals in committed, romantic relationships. Subtle sexual signals are inherently private and are only visible to the intended audience; a woman might use these signals to elicit or accept a sexual response from her partner or to increase her overall attractiveness, or attractivity. No studies examine women's use of and attitudes about intimate apparel – i.e., sexy underwear – as subtle sexual signals in romantic relationships. In this study, I sought to identify women's use of intimate apparel as a proceptive or receptive behavior as well as the effects of relative mate value, relationship commitment, relationship satisfaction, and

sexual functioning. A total of $N = 353$ women in the United States aged 25-45 who were in committed, heterosexual relationships completed the survey; 88.7% of the sample indicated wearing or having worn sexy underwear. Results indicate that women who report higher mate value tend to wear sexier underwear, despite their sexual activity in their current relationship. Therefore, intimate apparel may not be a form of proceptivity but a method of increasing attractivity and relationship maintenance, which might be termed underlying receptivity. Findings suggest that these women use intimate apparel to feel sexy, desired, aroused, and to prepare for sex with their partners. This study is the first to examine intimate apparel in relationships and as a subtle sexual signal of proceptivity and receptivity.

Participant recruitment costs provided by the Angela Peterson Scholarship for Spring 2019.

An exploratory study of pica in Sierra Leone

JENNIFER DANZY CRAMER^{1,5}, PAPANIE BAI SESAY², PAULA PEBSWORTH³, JOSHUA D. MILLER⁴ and SERA L. YOUNG⁵

¹Sociology, Anthropology, General Studies, American Public University System, ²Conservation Society-Sierra Leone, Sierra Leone, ³National Institute of Advanced Studies, Bangalore, India, ⁴Department of Anthropology, Northwestern University, ⁵Department of Anthropology & Institute for Policy Research, Northwestern University

Geophagy, the deliberate consumption of earth, is a type of pica, which is common among vulnerable populations (e.g., children, pregnant women). Some studies suggest that earth-eating is an adaptive behavior that protects the gastrointestinal tract and supplements micronutrients. Other studies have concluded that geophagy is a non-adaptive behavior. Despite years of scientific inquiry, its causes and consequences remain unknown. Most studies have been conducted in Central and East Africa. We, therefore, sought to fill this knowledge gap by studying geophagy in West Africa. We aimed to characterize the types of substances that are consumed, document perceived motivators for the behavior, and identify cultural practices or beliefs about pica, especially geophagy. We conducted 18 semi-structured interviews with adults in 4 villages in a larger partnership and study focused on community conservation. Participants were 23 to 65 years old; 16 women and two men. Participants reported eating a variety of substances: charcoal, ash, clay, and termite mounds. Most participants (94%) identified health factors, such as pregnancy, hunger, or illness, as the reason they engaged in geophagy. Consumable clay was most frequently purchased at the market, though two women reported traditional collection, and multi-step preparation that includes the mixing-in of herbs before selling at the market. Another type

ABSTRACTS

of clay was identified as inedible but used topically for skin infections and rashes. Participant responses support the medicament hypothesis about the etiology of geophagy. Our next steps are to analyze the consumed earth chemically and mineralogically to assess whether it provides protection and/or micronutrients.

This project was supported by a faculty research grant from the American Public University System.

Exploring Mesolithic diet through dental calculus in the central Balkans (SE Europe)

EMANUELA CRISTIANI¹, ANITA RADINI², ANDREA ZUPANCICH¹ and DUSAN BORIC³

¹Department of Oral and Maxillo-Facial Sciences, Sapienza University of Rome, ²Department of Archaeology and Physics, University of York, ³The Italian Academy for Advanced Studies in America, Columbia University

Analysis of microfossils trapped in dental calculus has become a powerful method to uncover direct evidence of human-plant interactions for dietary and other everyday purposes. In this paper we use dental calculus to explore forager familiarity with plant foods over a period of almost four millennia in the Mesolithic population of the Danube Gorges in the Central Balkans (SE Europe) before the acceptance of domesticated crops and agriculture. While macrobotanical remains are scanty in the region, faunal and isotope data have highlighted a dietary reliance on freshwater resources and main game animals for the local Mesolithic population. In this scenario, plant debris recovered in dental calculus constitute the only reliable line of evidence that can be linked to deliberate consumption of plants by local foragers. We have analyzed dental calculus of 52 individuals from a Mesolithic population found at five different sites along the River Danube in the area known as the Danube Gorges. All the individuals analyzed for this paper had micro-debris entombed in their calculus matrix. Overall, our results indicate that from the beginning of the tenth millennium, local foragers acquired and developed familiarity with important tribes of starchy plants: *Triticea*, *Avena/Poaceae*, *Fabaceae*, *Panicaceae* and *Fagaceae*. This conclusion challenges the hitherto prevailing view of the forager Mesolithic diet in this region dominated by animal protein food. We also suggest that such a familiarity might have played an important role in the process of introducing domesticated plants into the region in the second half seventh millennium BC.

European Research Council (ERC Starting Grant Project HIDDEN FOODS, G.A. no. 639286)

The misuse of "hunter-gatherers" as a discreet unit in population studies

ALYSSA N. CRITTENDEN and TREVOR R. POLLOM
Anthropology, University of Nevada, Las Vegas

Research among the world's few remaining hunting and gathering populations is seeing a resurgence across many disciplines, where such communities are regularly employed as ancestral models in psychology, public health, evolutionary medicine, and biological anthropology. Despite widespread variation in population size, ecology, diet composition, political history, and market integration, "hunter-gatherers" are often considered nearly identical units at the population level. Increasingly, large scale comparative studies cluster dozens of populations under the generic umbrella "hunter-gatherer" without any inclusion or exclusion criteria or any discussion of ecology. This acts to disassociate people from the environmental processes that influence behavior, biology, and health outcomes. For example, climate change and political ecology impact biodiversity, which influences carrying capacity, population density, subsistence, residence patterns, and levels of food and water insecurity. Without taking population differences into consideration, "hunter-gatherers" as a classification becomes amorphous and useless in our efforts to better understand adaptation and variation. Here, we discuss the inappropriateness of using "hunter-gatherers" as a discreet unit of study in population studies. Rather, we suggest that explicitly considering the demography, ecology, and political history of populations under study will only strengthen biological science.

Assessment of the relationship between ecto-endocranial shape and cranial symmetry in 6-8.0 year old humans

JESSICA M. CRONIN¹, JANE VANNAHEUANG², ANA SHAUGHNESSY³, CORTNEY M. CONNOR¹, LAURA E. CIRILLO⁴, GARY D. RICHARDS⁵ and REBECCA S. JABBOUR⁶

¹Department of Integrative Biology, University of California, Berkeley, ²Department of Public Health, University of California, Berkeley, ³Department of Molecular and Cell Biology, University of California, Berkeley, ⁴Department of Anthropology, University of Nevada, Reno, ⁵Department of Biomedical Sciences, A.A. Dugoni School of Dentistry, University of the Pacific, ⁶Department of Biology, Saint Mary's College of California

A relationship exists between ectocranial, endocranial, and brain shape. Although endocranial surfaces are covered by dura mater and maintain a direct relationship with the brain, they are separated by CSF. In the same way, ectocranial and endocranial surfaces are separated by variably thick regions of diploic bone. Given these relationships, a question arises as to the degree of correlation between endocranial and ectocranial shape. Here we examine the relationship between these two shapes in modern human juveniles.

We CT-scanned a sample of 5.8-7.9 year old juveniles ($n=38$). We collected, 1) 33 3D coordinates from isosurface reconstructions of the

endocranium and 2) 160 3D coordinates from the ectocranium with a Microscribe. Developmental ages are based on assessment of the calcification patterns and comparisons to the Schour and Massler aging system. Shape analysis for both the ecto/endocranial shape and cranial asymmetry, employed Morphologika to perform a principal components analysis on Procrustes-aligned shape variables.

The shape change between -PC1 and +PC1 is dolichocephaly- brachiocephaly while that between -PC2 and +PC2 describes shortening and height increase. All individuals showing similarity between the two shapes express right/left symmetry of their cranial base flexion and antero-posterior fronto-occipital expansion (symmetry 1) and/or skull shortening and height increase (symmetry 2). Individuals whose endocranium and cranial vault are similar on PC1 expressed symmetry 1.

Individuals expressing similarity between ecto-endocranial shape also express more right/left ectocranial symmetry. This suggests that deviations from symmetry are impacting the relationship between external and internal morphology of the cranial vault.

Funding provided by Undergraduate Opportunity Fund Grants, University of California, Berkeley to Jessica M. Cronin, Jane Vannaheuang, and Ana Shaughnessy.

B3GET: an agent-based model for growing virtual socioecologies

KRISTIN N. CROUSE
Anthropology, University of Minnesota

Agent-based models are useful in describing and making explicit how proximate mechanisms result in ultimate outcomes. Despite this, many models that are designed to answer evolutionary or 'ultimate' questions do not include these important features: (1) spatially explicit coordinates and agent interactions that happen locally, (2) agents that reproduce and imperfectly pass on their genes, thus simulating population evolution, (3) allowance for competing strategies to invade populations, (4) decentralized processes for agent reproduction and death, (5) imposed costs for every agent behavior, and (6) agent phenotypes that emerge from the interaction of their genotypes and their environment. Here, I present B3GET, an agent-based model that includes those features and is designed to answer a range of 'ultimate' questions in biology. The model simulates several factors considered important in socioecology, including life history trade-offs, investment in fighting ability and aggression, sperm competition, infanticide, and competition over access to food and mates. B3GET calculates each agent's decision-vectors from its diploid chromosomes and current environmental context. These decision-vectors dictate movement, body growth, desire to mate and eat, and other agent actions.

ABSTRACTS

Chromosomes are modified during recombination and mutation, resulting in behavioral strategies that evolve over generations. Rather than impose model parameters based on *a priori* assumptions, I used an experimental evolution procedure to evolve traits that enabled populations to persist. Initial populations crashed within a single generation. Seeding a succession of populations with the longest surviving genotype from each run resulted in the evolution of populations that persisted indefinitely, after only four iterations.

Petrosal morphology of Paleocene *Zanycteris paleocenus* and the relationship of picrodontids to plesiadapiforms

JORDAN W. CROWELL^{1,2}, JOHN R. WIBLE³ and STEPHEN G. B. CHESTER^{1,2,4}

¹Department of Anthropology, The Graduate Center, City University of New York, ²New York Consortium in Evolutionary Primatology, ³Section of Mammals, Carnegie Museum of Natural History, ⁴Department of Anthropology and Archaeology, Brooklyn College, City University of New York

Plesiadapiforms are Paleogene mammals that are supported as stem primates or stem primatomorphans (Primates + Dermoptera) by recent phylogenetic analyses. The Picrodontidae from the middle Paleocene of North America are enigmatic due to their highly derived dentitions but are generally considered closely related to palaechthonid and paromyid plesiadapiforms based on reputed dental synapomorphies. The only known non-dental fossil of a picrodontid consists of a palate and an associated basicranium of *Zanycteris paleocenus* (AMNH 17180), which were embedded in plaster following their discovery a century ago. We micro-CT scanned the embedded palate and basicranium and found that they fit together and preserve previously unknown cranial anatomy including both petrosals. Petrosals of *Z. paleocenus* exhibit a unique combination of a large continuous epitympanic wing and rostral tympanic process that form a "dish-like" extension to the apex of the promontorium, and a caudal tympanic process posterior to the fenestra cochleae. *Z. paleocenus* differs from all known non-microsomyid plesiadapiforms in lacking a posterior septum that "shields" the fenestra cochleae and additional septa originating from the promontorium. The petrosal of *Z. paleocenus* exhibits both an open sulcus for the facial nerve and a posteromedial entrance into the middle ear for an unreduced internal carotid artery, which are also present in known Paleogene microsomyids, apatemyids, and nyctitheriids, and are thought to be primitive for eutherian mammals. These observations either suggest that picrodontids are plesiadapiforms

that exhibit a unique combination of primitive petrosal and highly derived dental morphology or that picrodontids might not be plesiadapiforms after all.

This study was funded by NSF grant DEB-1456826 and a PSC CUNY Award jointly funded by The Professional Staff Congress and The City University of New York

Strontium isotopes support low mobility for Lemuriformes

BROOKE E. CROWLEY¹ and LAURIE R. GODFREY²

¹Anthropology and Geology, University of Cincinnati, ²Anthropology, University of Massachusetts, Amherst

Among mammals, including anthropoid primates, the primary factors that affect mobility are body size (larger-bodied species move more than smaller ones), diet (frugivores and trophic omnivores are more mobile than folivores), and habit (terrestrial taxa have larger home ranges than arboreal ones). If similar factors hold for lemurs, we would expect the large-bodied (particularly frugivorous) extinct species to have been more mobile than smaller-bodied (particularly folivorous) extant ones. Yet multiple lines of evidence (e.g., low Retzius Periodicities, small semicircular canal size, small relative brain size) suggest that extinct lemurs were relatively inactive. If so, they may have had relatively small home-ranges, perhaps on par with smaller-bodied extant lemurs. We used strontium isotopes (⁸⁷Sr/⁸⁶Sr), which vary primarily as a function of geology, to compare mobility for four extant and four extinct lemur genera at two sites, Ankilitelo/Mikoboka and Ampasambazimba. Within each, we expected more mobile taxa to have more variable ⁸⁷Sr/⁸⁶Sr. We found no differences in median ⁸⁷Sr/⁸⁶Sr or variance between extinct and extant lemurs at either site (Wilcoxon and Bartlett $p > 0.05$ for all comparisons). There were apparent but insignificant differences among individual genera (Kruskal-Wallis and Bartlett $p > 0.05$). These results support low mobility for extinct lemurs, and suggest that extinct as well as extant Lemuriformes differ from anthropoids in having reduced activity levels. Unfortunately, small home ranges also make lemurs more vulnerable to extinction. It is imperative that remaining cover be protected and that connectivity among fragments be improved.

This project was supported by the National Science Foundation [BCS-1750598 to LRG and BCS-1749676 to BEC].

Cribriforma in Hellenistic to Early Christian burial samples from Ayio Omoloyites in Lefkosia, Cyprus

KRYSTEN A. CRUZ¹, NICHOLAS P. HERRMANN¹, DESPO PILIDES² and YIANNIS VIOLARIS²

¹Department of Anthropology, Texas State University, ²Cyprus Museum, Department of Antiquities, Republic of Cyprus

Cribriforma is a porous lesion on the anterior femoral neck. While its etiology has been debated, it is currently thought to be associated with genetic anemias rather than nutritional anemias. Beta-thalassemia is a genetic anemia endemic to the Mediterranean and has continued to thrive due to the presence of malaria in the region. Similar to sickle-cell anemia, beta-thalassemia is a hemoglobin disorder that has a relationship with malaria which allows a heterozygous individual to survive without contracting malaria. Due to this relationship, the presence of cribriforma in a population may indicate the presence of beta-thalassemia. The Ayio Omoloyites Bioarchaeological Project focuses on the analysis of three Hellenistic to Early Christian rock-cut tombs excavated south of the old city walls of Lefkosia, Cyprus. The burial samples from Tombs 47 and 48 are limited and commingled, and have been radiocarbon dated to the Hellenistic period. These tombs likely represent kin-based mortuary facilities. Tomb 49 contained a large commingled burial ossuary, much larger than Tombs 47 and 48. The tomb has been dated to the Early Christian period. Only 2/4 adult elements from Tombs 47 and 48 displayed cribriforma, and only 2/4 subadult elements displayed the lesion. Cribriforma was present in 55/116 adult elements, and 53/93 subadult elements in Tomb 49. Unfortunately, many elements were damaged and the area of interest was not observable. The presence of cribriforma in all tombs is important because it may indicate the antiquity of beta-thalassemia in Cyprus.

This project is supported through a Cyprus American Archaeological Research Institute (CAARI)/Council of American Overseas Research Centers (CAORC) Research Fellowship 2019-20 (NPH).

Dental morphological affinities among Prehispanic human groups around the Caribbean region: from Yucatan to Venezuela

ANDREA CUCINA¹, MICHAELA LUCCI^{2,4}, CARLOS SIVOLI³ and ALFREDO COPPA⁴

¹School of Anthropological Sciences, Universidad Autonoma de Yucatan, ²PIN Polo Prato, University of Florence, Italy, ³Facultad de Odontologia, Universidad de los Andes, Venezuela, ⁴Department of Environmental Sciences, University of Rome Sapienza, Italy

Recent analyses highlighted morphological affinities among coastal populations in the Yucatan peninsula (Mexico) in Prehispanic Classic (AD200-1000) and Postclassic (AD 1000-1521)

ABSTRACTS

Maya times, related to the maritime coastal trade routes from the Gulf of Mexico to Honduras. This paper expands the analysis to Central America and Colombia and Venezuela in order to better understand population dynamics from south-eastern Mesoamerica to northern South America through time. Twenty-four dental morphological traits, recorded following the ASUDAS system have been analyzed in nine groups. Three Maya groups from the Yucatan peninsula date to the Classic and Postclassic period; Copan (Honduras) belongs to the Classic period; Panama is formed by various sites dated to the first millennium AD; Colombia is represented by a Muisca Group (1000-1600 AD), and Venezuela consists of an archaic group (pre-AD), a Saladoid (until AD 800) and a Late Ceramic one (from AD 800 on). UPGMA, Ward's cluster analyses, PCA and MDS analyses indicate morphological similarity among the Mesoamerican groups. Archaic and recent Venezuelans consistently gather together, same as Saladoids and recent Colombians, though these two small clusters never manifest reciprocal relationships. Results suggest that southeastern Mesoamerica is characterized by a morphological cohesiveness and continuity through time, likely the result of intense population dynamics in particular long the coasts. Panama always separates from all the other groups. No consistent patterns of affinities are evident between Meso and South America, suggesting isolation-by-distance. South Americans manifest indefinite geographical and chronological affinities among each other, suggesting in particular discontinuity in the peopling of Venezuela.

Research has been supported respectively by CONACyT CB-2017-A1-S-10037 project and by the H2020 Programme ARIADNEplus Project, contract n. H2020-INFRAIA-2018-1-823914. Authors' opinions do not necessarily reflect those of the European Commission.

Ancestry catches up to modern times: A new technique evaluating morphological traits using 3D technology

ELISABETH CUERRIER-RICHER¹ and TRACY L. ROGERS²

¹Department of Anthropology, University of Toronto, ²Forensic Science Program, University of Toronto Mississauga

In forensic anthropology, ancestry assessment describes population affinity using morphological and metric analyses. However, morphological analyses are particularly difficult to reproduce and standardize, since they strongly depend on an anthropologist's subjectivity, based on their experience with human variation. The purpose of this research was to improve the rigour of morphological analyses of ancestry by using three-dimensional (3D) technology to quantify relevant features on the human skull. The sample consisted of 50 European-American, 24 Canadian Inuit and 13 African-American adult female

crania, for a total sample size of 87 individuals. The samples were imaged using photogrammetry, the 3D models were constructed in 3DF Zephyr, and the shape analysis was performed in 3DS Max. The data were statistically analysed using a non-parametric multivariate analysis of variance (PERMANOVA), a linear discriminant function analysis (LDA) and a principal component analysis (PCA). Results showed that major differences between groups were clearest when 3D measurements were combined. Overall, European-Americans were statistically different from the other two groups, while Canadian Inuit and African-American individuals were harder to distinguish statistically. The current method was satisfactory in presenting a classification rate of 87.36% (jackknifed: 80.46%) and an average repeatability of 97%. Nonetheless, this project had some limitations. Future research should evaluate the technique with a larger sample size, more diverse populations, other ancestry-related cranial traits (e.g., oval window), and other 3D measurements (e.g., volume). Despite its few limitations, this new and simple method of 3D shape analysis shows promise for the future of ancestry assessment via 3D technology.

This research was supported by the Social Sciences and Humanities Research Council of Canada (SSHRC).

Geographic distance from central slave trade ports as a measure of cranial morphological similarity between Barbados and the United States

ANDREANA S. CUNNINGHAM

Anthropology, University of Florida

The Atlantic crossing refers to the slave trade route that displaced millions of Africans to the Americas. Following arrival, local trade networks of intra-American slave re-exportation prospered. Specifically, slaves in Caribbean regions were frequently re-exported to American colonies. This study utilized a 3D landmark geometric morphometric approach to quantify relationships between geographical and morphological distances in African descendants from the United States and Barbados. This study included crania from 62 individuals, including 54 post-emancipation individuals from the Smithsonian's Robert J. Terry Anatomical Skeletal Collection and 8 virtually reconstructed laser surface scans of pre-emancipation individuals from the Newton Plantation, Barbados, slave burial site. Geographic coordinates for Terry Collection were based on documented state of birth.

Fixed landmark and sliding semilandmark data were collected from crania using a MicroScribe for physical crania, and Amira software for laser surface scans. Data were aligned with a generalized Procrustes superimposition, and coordinates were tested with PCA, redundancy, and permutation analyses to assess morphological distribution

and the magnitude of geographical structure. PCs 1-6 accounted for approximately half of the cranial variation. There was a significant relationship between country and shape on PC1, but not PC2. The calculated variances in the Barbados and U.S. samples were very similar. The redundancy tests showed significant positive correlations between morphological distance and geographic distance. Further, some central U.S. port cities correlated closely with the Barbados sample. However, morphological and geographic distance matrices were not directly linear, suggesting that increasing distance alone does not account for the observed cranial distribution.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship under Grant No. DGE-1315138 and DGE-1842473.

Human Cadaver Bacterial Succession Comparison in Two Depositions: Surface vs Shallow Burial

SARAH L. CUNNINGHAM¹ and KRITHIVASAN SANKARANARAYANAN²

¹Anthropology Department, Binghamton University, ²Department of Microbiology and Plant Biology, University of Oklahoma

Decomposition is a dynamic environment populated by a complex network of communities including: mammalian, insect, and microorganism species that inhabit the death environment and prey upon the remains and each other. An emerging avenue of research has endeavored to use the bacteria inside a decomposing body, formerly the microbiome, and soil bacterial from the surrounding grave soil to connect the patterns of microbial succession with decomposition in an effort to estimate the Postmortem Interval. Previous research has found bacterial succession patterns in surface deposited human cadavers. However, perpetrators may attempt to hide victim remains in shallow, clandestine burials. The differences in bacterial composition and succession patterns in a burial context is, as yet, unknown. This research compares the succession patterns in human cadaver decomposition in two deposition contexts; surface and shallow burial.

Four donated human cadavers were placed in the Texas State Forensic Anthropology Research Field located in San Marcos, Texas in spring 2017. Two cadavers were buried in shallow graves (45.72 cm and 40.64 cm) and two deposited on the soil surface. Using alpha diversity evenness, two general trends were observed. First, the buried cadavers exhibited one major period of more uniform bacterial composition. Second, the surface cadavers exhibited two such events.

ABSTRACTS

While the surface cadavers displayed similar patterns of bacterial succession to one another, the buried subjects exhibited greater variation in time between cadavers.

This material is based upon work supported by the National Institute of Justice Graduate Research Fellowship in Science, Engineering, and Mathematics (2016-DN-BX-0010).

Human induced threats to a nonhuman primate of "Least Concern" (*Otolemur crassicaudatus*, Primates: Galagidae) in northern South Africa

FRANK CUOZZO¹, ALI HALAJIAN², MICHELLE L. SAUTHER³, BIBI LINDEN^{1,4}, JABU LINDEN^{1,4}, JAMES MILLETTE III⁵ and DOMENIC ROMANELLO⁵

¹Nocturnal Primate Biology Project, Lajuma Research Centre, ²Department of Biodiversity, University of Limpopo, ³Department of Anthropology, University of Colorado, ⁴Department of Zoology, University of Venda, ⁵Department of Anthropology, University of Texas, Austin

We present unique data on human-induced threats to the thick-tailed galago (bushbaby), *Otolemur crassicaudatus*, in northern Limpopo Province, South Africa. Threats include: road kills, kills by domestic dogs, and electrocutions. We have recorded 21 *Otolemur* human-related deaths since 2014 (road kills $n = 10$; dog kills $n = 6$; electrocutions $n = 5$). In and around Louis Trichardt (Makhado), vehicle traffic is frequently responsible for the deaths of individuals. This is especially clear based on our map of deaths on primary roads. Roadkill remains often disappear within only a day or two after the event, thus numbers reported here likely represent a fraction of the actual number of vehicle deaths. The use of dogs is necessary in both urban and more rural areas. However, this comes at a cost to endemic animals. Efforts to mitigate the impact of dogs are needed, especially given false perceptions among some about this species. Electric fences and power lines are known to cause death among many organisms. These data illustrate that this threat includes a large, nocturnal primate. Our data likely represent a portion of the actual human impact on this species. We suggest *Otolemur crassicaudatus*, which has received limited attention compared to other strepsirrhines (e.g. Madagascar's lemurs) and better-known primate taxa, such as African apes, should more accurately be listed as a "data deficient" species by the International Union for Conservation of Nature (IUCN), rather than "least concern". New surveys are clearly required to assess this species' current distribution and demography.

National Science Foundation BCS Biological Anthropology #1638833

Dietary correlates of mandibular premolar form in haplorrhine primates

E. SUSANNE DALY^{1,2} and GARY T. SCHWARTZ^{1,2}

¹School of Human Evolution and Social Change, Arizona State University, ²Institute of Human Origins, Arizona State University

Premolar form varies considerably across living and extinct primates, and some have suggested this is related to dietary differences. Previous work has focused primarily on premolar size and concluded that in some taxa enlarged premolars facilitate processing mechanically challenging (i.e., hard or tough) foods. Here we use a broad comparative sample to further probe the relationship between diet and other important aspects of premolar form, specifically 3D occlusal anatomy and the degree of talonid expansion. Measures of P₄ occlusal topography (surface complexity, relief, sharpness) and relative talonid expansion were taken from 3D surface meshes acquired using structured blue light scans of 428 P₄s from 20 haplorrhine species. Statistical analyses, focused on pairwise comparisons of closely related taxa whose diets differ in their material properties, were used to assess the relationship between diet and these functional aspects of premolar form.

Taxa with more mechanically challenging diets tend to have significantly expanded talonids. Furthermore, taxa with harder diets tend to possess more complex premolars with low crown relief, while those with tougher diets have sharper premolars with higher relief. Additionally, some frugivorous taxa relying on tougher, non-preferred foods have premolars with higher relief in comparison to hard-object feeders.

Our results clarify the relationship between dietary proclivities and premolar form in primates, and highlight the role of premolar form as an additional tool for interpreting dietary adaptations in the fossil record.

This research was funded by the School of Human Evolution and Social Change and the Graduate and Professional Student Association of Arizona State University.

In quest of a non-invasive measure of acute stress response: Time-matched fecal glucocorticoids in wild female white-faced capuchin monkeys (*Cebus capucinus*)

JULIANE DAMM^{1,3} and COLLEEN M. GAULT^{2,3}

¹Instituto de Neuroetologia, Universidad Veracruzana, ²Data Management, Lomas Barbudal Monkey Project, ³Department of Primatology, Max Planck Institute for Evolutionary Anthropology

For many arboreal primates, non-invasive collection of endocrinological data is limited to obtaining fecal samples. The quantification of immunoreactive glucocorticoid metabolite concentrations in feces (ifGCM) is a well-established method

to map stress levels, but, due to the integrative nature of fecal samples, there have been few studies investigating ifGCM levels in relation to acute stressors.

White-faced capuchin monkeys (*Cebus capucinus*) have a short gut-transit time of only two to three hours, making them an optimal model species for investigating the effects of acute stressors on ifGCM levels. Pinpointing acute stress responses could allow disentanglement of chronic from acute stress to determine how individuals' reactivity to immediate stressors changes under different environmental and social conditions.

We assessed ifGCM concentrations in 269 fecal samples of 11 wild female white-faced capuchin monkeys on 41 focal follow days using an enzyme immunoassay. We identified all intergroup encounters and severe intragroup aggression, assuming both would reliably elicit an acute stress response. The relationship between the stressors and the ifGCM levels was analyzed via a general linear mixed model. There was a non-significant increase of ifGCM between 1.5 and 2 hours after onset of intergroup encounters. There was no significant increase of ifGCM concentrations after within-group conflict, regardless of whether the focal animal was the victim or the initiator of aggression ($p=0.217$).

Short-scale variation in ifGCM concentrations may be insufficiently specific to document impacts of acute, social stress events in primates with high frequencies of social interactions even if defecation rates are high.

S. Pery support: NSF (BCS-0613226), Leakey Foundation, National Geographic Society (#8671-09), UCLA; C. Gault support: Leakey Foundation, DAAD, GWIS, NSF graduate fellowship, Emory University, MPI-EVAN.

Measuring frailty in a Mississippi asylum sample

SHAMSI DANESHVARI BERRY¹, ALEXIS O'DONNELL² and AMY W. FARNBACH PEARSON³

¹Health Informatics and Information Management, University of Mississippi Medical Center, ²Department of Anthropology, University of Mississippi, ³Center for Bioarchaeological Research, Arizona State University

Skeletal indicators of early stress have been associated with increased morbidity and mortality. However, there also appears to be a survival advantage for those who survive the stressor and heal skeletal lesions. This study focuses on indicators of skeletal stress in individuals interred in the Mississippi State Asylum (MSA) between 1855 and 1935. Sixty-six skeletons have been excavated to date of an estimated 5000 to 7000 interred at the site. Death records estimate that roughly 70% of people who died at the asylum were African American. We collected data on two porous cranial lesions indicative of developmental

ABSTRACTS

stress, porotic hyperostosis (PH) and cribra orbitalia (CO). African Americans (N=26) were compared to European Americans (N=4) through odds ratios and Fisher's exact analyses. The results did not find associations between PH ($p=0.36$) or CO ($p=0.23$) and African ancestry, estimated by dental morphology. This suggests multiple possible explanations. Regardless of race, recorded professions for those sent to the asylum indicated relatively low socioeconomic status for most patients. The lack of difference in frailty indicators in those with African ancestry in this sample might suggest that the nutritional or pathological insults causing these lesions and survival thereof were similar across races for the asylum population, despite severe structural racism in the south. It could also suggest that these insults were similar across races for individuals who were institutionalized, either before or after entering the asylum, as their length of residence in the asylum is unknown.

Body proportion and somatotype of young male weightlifters from Merida, Mexico

SUDIP DATTA BANIK

HUMAN ECOLOGY, CINVESTAV-IPN

The power capacity of weightlifting athletes (WA) depends on muscular force; short leg length and high arm muscle are (AMA) may help.

Objective: To record anthropometric characteristics, to evaluate somatotype of young male WA from Merida, Mexico, and to compare with other studies from Mexico and abroad.

Methods: A cross-sectional study was carried out in August 2019. Young adult male WA ($n=25$) from the Sports Institute of Yucatan who participated in the international level championships in the recent years were selected in the weight categories between 67 kg and 81 kg, following International Weightlifting Federation guideline. Anthropometric measurements included height, sitting height (SH), weight, skinfolds (biceps, triceps, subscapular, iliac crest, supraspinale, medial calf), girths (flexed and relaxed mid-upper arm, calf) and breadths (bi-epicondylar humerus and femur). Subischial leg length (SLL) is the difference between height and SH. Body fat (%), AMA, height-weight-ratio and somatotype (endomorphism, mesomorphy, ectomorphy) were calculated.

Results: Mean values (standard deviation) of age, body weight, height, SH, and SLL were 21.87 (3.59) years, 73.28 (8.25) kg, 165.72 (5.95) cm, 84.25 (4.53) cm, and 81.38 (3.70) cm respectively. Height-weight-ratio and body fat (%) were 39.72 and 12.44%. The athletes were endomorphic mesomorph; mean values of somatotype were 3.23 (0.93) – 5.98 (2.36) – 0.79 (0.47) (endomorphism – mesomorphy – ectomorphy). Mesomorphy shows significant correlation ($p<0.05$) with SLL ($r=-0.472$) and AMA ($r=0.751$).

Conclusion: In comparison with reported data from the USA and other Latin American countries, the WA from Yucatan show higher endomorphy, mesomorphy, and lower ectomorphy.

Not applicable

Collective decision-making, social organization, and group foraging in capuchin and spider monkeys

GRACE H. DAVIS^{1,2,3,4} and MARGARET C. CROFOOT^{1,2,3,4,5}

¹Anthropology, University of California, Davis,

²Tropical Ecology, Smithsonian Tropical Research Institute, Panama, ³Biology, University of Konstanz,

Germany, ⁴Ecology of Animal Societies, Max Planck Institute of Animal Behavior, Konstanz, Germany, ⁵Animal Behavior Graduate Group, University of California, Davis

How do groups of individuals decide where to go and what to do? Collective decisions like these are a primary challenge of group-living, and how social species reach consensus is central to understanding the evolution of complex social systems like our own. How collective decisions about group foraging choices are reached, and which group members have influence, likely depends on groups' social organization. This study investigates how social organization impacts collective decision making in two group-foraging primate species: white-faced capuchins (*Cebus capucinus*) and black-handed spider monkeys (*Ateles geoffroyi*) living on Barro Colorado Island, Panama. Capuchins and spider monkeys importantly differ in the cohesiveness of their social groups and the strength of their dominance relationships. Using the focal tree method on group feedings on *Dipteryx oleifera* trees, we calculated detailed individual feeding rates for focal individuals in each tree (>180 total trees across 9 months). These feeding rates generate individual foraging gain curves that predict optimal leaving times from the focal tree using the marginal value theorem. Preliminary results indicate that in groups with fixed-membership like capuchins, influential dominant individuals more often exert disproportionate control over decisions. In fission-fusion groups like spider monkeys, members share group decisions and mitigate decision costs by splitting into subgroups when conflicts of interest arise. Together, this captures important elements of group decision-making in social primates: when to go and who decides.

This research was funded by National Geographic, The Leakey Foundation, NSF DDRIG BCS-1751750, NSF GRIP, NSF GRFP, UC Davis, Smithsonian Tropical Research Institute, Animal Behavior Society, and The Explorer's Club.

Something Fishy in Denmark? An Analysis of Freshwater and Marine Fish Consumption in Medieval Denmark

ASHLEY C. DAWSON and CASSADY Y. URISTA
Anthropological Sciences, Radford University

Previous examinations of diet using stable carbon and nitrogen isotope ($\delta^{15}\text{N}$ and $\delta^{13}\text{C}$) analysis on a cross-section of Danish society at the medieval site of øm Kloster found differences in a comparison of peasants, elites and the monastic community throughout the medieval period. Specifically, this research found that in the middle period (1300-1375 AD) the monastic sample showed a sharp increase in their $\delta^{15}\text{N}$ ratios, surpassing that of even the elites. However, there was no shift in the $\delta^{13}\text{C}_{\text{coll}}-\delta^{13}\text{C}_{\text{ap}}$ value, nor in the $\delta^{13}\text{C}$ ratios from either carbonate or collagen from the monastic sample. These results suggest

ABSTRACTS

that freshwater fish may have had an increased role in the diet of the monastic community in the middle period. Considering this, the current research aims to examine the role of freshwater fish resources in the diets of monastic, elite and peasant populations interred at øm Kloster using the analysis of the stable isotopes of sulfur ($\delta^{34}\text{S}$). Interestingly, the preliminary $\delta^{34}\text{S}$ results instead suggest a fairly strong marine component to the diet. These results are explored and put into context in this paper.

Bio-molecular characterization of Ancient Romans: a powerful tool for the biological dissection of the widest city of Ancient World

FLAVIO DE ANGELIS¹, CRISTINA MARTÁNEZ-LABARGA¹, ANDREA BATTISTINI², STEFANIA DI GIANNANTONIO², WALTER PANTANO², SARA VARANO¹, VIRGINIA VELTRE¹, FEDERICA ZAVARONI², PAOLA CATALANO², TULLIA DI CORCIA¹, MARCO ROMBONI¹, STEFANIA ZINGALE¹ and OLGA RICKARDS¹

¹Centre of Molecular Anthropology for Ancient DNA Studies, University of Rome Tor Vergata,

²Anthropology service, Soprintendenza Speciale Archeologia Belle Arti e Paesaggio di Roma, Rome, Italy

Imperial Rome was by far one of the largest city in Antiquity and despite the plentiful cultural records, the biological profiles of Imperial Age Romans (1st-3rd centuries CE) is still a partially unmatched issue. The outstanding developments in bio-molecular research make the skeletal remains a terrific source of knowledge to reconstruct the biology of the Romans. One of the main topics to be addressed by molecular assessment is the nutritional habits through isotopic analysis: the data pertaining more than 300 people buried in the Suburbium are consistent with a heterogeneous landscape where each community seems to be featured by private foodstuff exploitation, even though Roman authorities started to step in food supply of the City since the mid-Republican period. As the center of the Empire, Rome appealed to people into its walls to gain better life conditions. Imperial Rome should have had a dense population and at least moderate migration rates that helped to combat the extremely high mortality rates: the oxygen isotopes analysis performed in more than 100 samples seems to confirm this moderate migration rate at least in the commoners, with an average value of 10% newcomers in several necropolises. Genomic evaluation of ancient Romans has been mandatory to gain information on population stratification. Whole genome sequencing approach has been performed on 50 samples: the analysis are starting to shed light on people origin

and this genomic approach stands for a valuable tool in the differential diagnosis of specific genetic-related disorders some people suffered from in Ancient Rome.

This research is funded by MIUR PRIN2015 Prot. 2015PJ7H3K.

Sociosexual responses to the simulated presence of solitary individuals in pair bonded owl monkeys (*Aotus Azarae*)

ALBA DE LA CHICA GARCIA¹, DAVID WOOD² and EDUARDO FERNANDEZ-DUQUE²

¹Anthropology, University of Barcelona (Spain),
²Anthropology, Yale University

The role of solitary floaters has not been properly evaluated when considering reproductive strategies of pair-living and sexually monogamous species. Our goal was to evaluate the role that reproductive competition between solitary and resident adults has in regulating owl monkey pair-living. Owl monkeys (*Aotus azarae*) live in groups of one pair of reproducing adults and 1-4 younger, non-reproducing individuals. Individuals disperse from their natal groups around 3 years old, becoming floaters while attempting to evict a resident same-sex adult. During the playing back of unfamiliar male (graff) and female (tonal) loud calls and a control stimulus from the center and border of three group's home ranges, we collected data on sociosexual behavior for 20 min before, 20 min during, and 40 min after the playback. When graff or tonal calls were reproduced, only adult pairs reacted (N=12). During and after the playbacks, both sexes scent marked more following graff than tonal hoots (males 0.240±0.228 vs 0.005±0.012; females 0.107±.119 vs 0.077±0.105). They also scent marked their partner (males: 0.222±0.204, females: 0.072±0.111 per hour) and urine washed (males: 0.038±0.083, females: 0.040±0.045 per hour) after graff calls but not tonal ones. The increased rates of these behaviors, by males and females, in response to graff (male) calls suggest that males may be mate guarding their partners. More examination of sex roles which considers competition and parenting by both sexes is still needed in primatological research.

NSF-BCS-1503753, 0621020, 1232349, 1540255

Reclaiming lost identities: Ethical engagement with the unclaimed dead in anatomical collections

CARLINA M. DE LA COVA

Anthropology, University of South Carolina

Since their inception the Hamann-Todd, Robert J. Terry, and William Montague Cobb anatomical collections have been instrumental to the development and methodological advancement of bioarchaeology and forensic anthropology. Each series has contributed new knowledge

to the discipline in regard to aging, sexing, and paleopathological identification. However, the anatomical legislation responsible for the amassment of these collections was structurally violent, targeting the unclaimed poor and marginalized for nonconsensual dissection. This presentation will examine the demographic composition of these collections and illustrate how structural violence at legislative and societal levels resulted in the dissection and curation of the individuals that comprise these collections. Focus will be placed on how to ethically engage with the Hamann-Todd, Robert J. Terry, and William Montague Cobb anatomical collections in a manner that acknowledges who the individuals that comprised these collections were, how they ended up in these collections, and how we, as bioarchaeologists, can break the cycle of structural violence that plagued these persons in life and continue to do so in death.

This research was made possible thanks to funds from the University of South Carolina, the University of North Carolina at Greensboro, and Indiana University.

Characterizing the human genomic diversity of the Incan Capacocha ceremony in Chile and Argentina

CONSTANZA DE LA FUENTE^{1,2}, MAANASA RAGHAVAN¹, MARIO CASTRO DOMINGUEZ⁴, RICARDO VERDUGO² and MAURICIO MORAGA^{2,3}

¹Human Genetics, University of Chicago,

²Programa de Genética Humana, ICBM, Facultad de Medicina, Universidad de Chile, ³Departamento de Antropología, Facultad de Ciencias Sociales, Universidad de Chile, ⁴Sistema Nacional de Museos Servicio Nacional del Patrimonio Cultural, Ministerio de las Culturas, las Artes y el Patrimonio, Gobierno de Chile

The Inca Empire was established in the 13th century CE, spreading from its capital, Cuzco, to southern Colombia and Central Chile. The study of mummies buried on mountain summits along the Andes in Peru, Chile, and Argentina have been suggested to be associated with the Inca ceremony Capacocha. As part of the ceremony, one or more individuals, mainly children, were sacrificed and buried with Inca-style offerings. This ceremony likely served as a public manifestation of the Inca power, and several questions about the social status and origins of these individuals have arisen and remain unclear. Our research aims to evaluate the genetic diversity of individuals associated with the Capacocha ceremony, in order to explore their origins. Using ancient genomic tools, we analyzed three individuals: two newly-produced genomes from *El Plomo* Mt. (Chile) and *El Toro* Mt. (Argentina) and one previously-published genome from Argentina (*Aconcagua* Mt.). After evaluating the genetic affinity of the ancient individuals with several present-day populations from South America, we observed a clear affinity between Quechua and Aymara speakers and the individuals from *El Plomo* and *Aconcagua*.

ABSTRACTS

The individual from *El Toro*, however, although geographically closer to the Quechua and Aymara speakers, did not have a closer affinity with them, showing instead a proximity with southern groups. Interestingly, the association of this individual with the ceremony has been questioned before. Our analysis may support the Central Andean origin of at least two individuals from the capacocha rite, contributing to our understanding of the social dynamics of this ceremony.

FOUNDERCYT #1181889; University of Chicago; Instituto de Investigaciones Arqueológicas y Museo "Prof. Mariano Gambier" (FFHA UNSJ); Catalina Teresa Michieli.

The Relationship Between Soft Tissue Anatomy and Skeletal Sexual Dimorphism in the Cranium and Clavicle

JADE S. DE LA PAZ¹, STEPHANIE WOODLEY¹, NAWAPORN TECHATAWEEWAN², HALLIE BUCKLEY¹ and SIÂN HALCROW¹

¹Anatomy, University of Otago, ²Anatomy, Khon Kaen University

The aim of this research is to establish accurate metric sex estimation methods from the cranium and clavicle, through the dissection and analysis of skeletal and soft tissue sexual dimorphism. Accurate methods are important to help with identification in modern forensic cases and to understand the structure of past populations and metric methods can limit the subjectivity and expertise required with morphological methods.

This presentation focuses on the dissection phase of this project and the relationship of soft tissue to three sexually dimorphic skeletal landmarks: the nuchal crest and mastoid processes of the cranium, and the rhomboid fossa of the clavicle.

A total of 20 bequeathed cadavers from modern European New Zealand and Thai populations (ethical approval granted) were dissected for this project. Muscles were dissected to calculate physiological cross sectional area, or overall size. These data were compared with the metric and morphological size of the relevant skeletal landmarks to identify the sexually dimorphic relationship between the two.

Preliminary results indicate that males show generally larger muscles than females, with some exceptions. Following standard methodology, the individuals are consistent with the male and female skeletal morphology. Even some muscularly robust females show standard female characteristics, skeletally. The implications for this muscular data can provide further insight into human sexual dimorphism in these skeletal landmarks, in addition to the sexual dimorphism of the neck muscles. Future development of a population-specific metric sex estimation method from these data will contribute to improving accuracy of sex estimation from the cranium and clavicle.

Is human brain organization economical? Brain region metabolic rates in relation to size changes in evolution and life history

ALEXANDRA A. DE SOUSA¹, ORLIN S. TODOROV² and MICHAEL J. PROULX³

¹Centre for Health and Environment, Bath Spa University, ²School of Biological Sciences, University of Queensland, ³Department of Psychology, University of Bath

The human brain is responsible for 20% of the resting metabolic rate of the body. It has more than tripled in weight since the human and chimpanzee lineages diverged. This relatively recent increase in maintenance costs must have been met by either a reduction in energy expenditure by other costly functions such as digestion, or by an increase in energy turnover due to dietary shifts such as animal consumption and cooking. However, just as different organs consume energy at different rates, structures within the brain also vary in energy expenditure. The metabolic cost per unit brain tissue decreases as brains get larger because larger brains have a greater fraction of white matter to gray matter, and white matter has a lower metabolic rate than gray matter. Further, it might be possible for two brains of the same size to have different energy requirements if they are organized differently. For 13 brain regions, we examined whether there was a relationship between human cerebral glucose metabolic rate and the extent to which they changed in size in human evolution, based on nonhuman primate phylogenetic predictions of brain structure volumes. We did not find a significant relationship in our dataset. We further examined whether brain region metabolic rates influenced changes in brain organization that occur during human life history. We found no significant relationships between brain region metabolic rates and changes in volumes during development and ageing. Our findings suggest that brain organization is not constrained by variation in brain region metabolic costs.

Mortuary Contexts in Palenque, Mexico: Bone needles as indirect evidence for the presence of mortuary dress in poorly preserved Prehispanic Maya burials

MIRKO DE TOMASSI

Interdisciplinary Humanities, School of Social Sciences, Humanities, and Arts, UC Merced

Bone needles found in Prehispanic Maya mortuary contexts are frequently interpreted according to the sex of the associated individual. If the individual is female, there is typically a gender-related interpretation focused on activities carried out in life. If the individual is male, then bone needles are generally associated with practices of self-sacrifice or bloodletting. Although these interpretations may be valid, preliminary results from two recently excavated domestic burials (burial 1, infant; burial

23, middle-aged woman) and two previously reported contexts (ruler Pakal and his wife) from Palenque, Mexico, show how bone needles could have had a different function in some funerary contexts. These individuals were buried with bone needles in the neck area. In Pakal's burial, where preservation was good because of the elaborate funerary context, there is direct evidence of textiles and a needle that closely resembles a pin. Additional iconographic data demonstrates that the royal individuals were covered by a funerary cape and these needles may have served to grasp the textile. Burial 1 presents anatomical evidence of a funerary bundle wrapping the individual ("verticalization" of the right clavicle, transposition of the right radius and ulna). Burial 23, like the royal contexts, presents no evidence of body constriction, perhaps indicating a cape rather than a funerary bundle. Although further evidence is needed, I suggest bone needles found in the neck area could be evidence for the presence of funerary cape or a practice of bundling the dead and merits exploration in contexts presenting this characteristic.

Dental topographic evolution of African rodents from the Eocene into the Miocene - a parallel for African primate diversification?

DORIEN DE VRIES¹, JEROEN B. SMAERS² and ERIK R. SEIFFERT³

¹Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, ²Department of Anthropology, Stony Brook University, ³Department of Cell and Neurobiology, University of Southern California

The direction and timing of anomaluroid and hystricognath rodent dispersals into Afro-Arabia roughly parallel those of strepsirrhine and anthropoid primates. Anthropoids and hystricognaths evidently dispersed to Afro-Arabia after strepsirrhines and anomaluroids did, but the former two groups ultimately came to dominate Oligocene and Miocene faunas. This study aims to quantify molar topography in African anomaluroids and hystricognaths and analyze topographic diversification relative to major ecological events (e.g. competition, climate change) within a phylogenetic context provided by Bayesian tip-dating analyses of both clades.

Dental topographic diversification was quantified using multiple variables (ariaDNE, RFI, OPCR, and surface area) calculated on the lower m2 crowns of 41 fossil rodent species ranging in age from Eocene to early Miocene. A principal components analysis was run on the four topographic variables, and ancestral trait values were calculated throughout the anomaluroid and hystricognath phylogenies at each 1-million-year interval using a multi-variance BM model that allows for different rates of evolution.

ABSTRACTS

Our results reveal that anomaluroids and hystricognaths show considerable overlap in dental topographic values, suggesting similar capacities for breakdown of foods. Differences in the groups' respective diversification patterns are therefore more likely to be due to behavioral characteristics other than feeding performance (e.g., substrate preference, activity pattern, temperature tolerance). Eocene anomaluroids show higher average dental disparity than Eocene hystricognaths, but this pattern reverses in the Oligocene. Hystricognath dental diversity increased in the late Eocene, dropped in the early Oligocene, and then peaked in the early Miocene, mirroring changes in lineage diversity and global temperature.

Funding from the National Science Foundation (BCS-0416164, BCS-0819186, BCS-1231288, BCS-1824745), the Leakey Foundation, and Sigma Xi.

New insights into ape and human evolution from a (mediocre) suspensory platyrrhine: The muscle-tendon architecture of *Lagothrix lagotricha* and the origins of anthropoid suspension

ANDREW S. DEANE¹, JASON ORGAN¹, EVIE VEREECKE², MAGDALENA N. MUCHLINSKI³ and TIMOTHY BUTTERFIELD⁴

¹Anatomy, Cell Biology & Physiology, Indiana University School of Medicine, ²Faculty of Medicine, University of Leuven, ³Department of Anatomical Sciences, Oregon Health and Science University, ⁴Department of Rehabilitation Science, University of Kentucky College of Health Sciences

Humboldt's woolly monkey (*Lagothrix lagotricha*) is a 'tail-assisted' platyrrhine brachiator that infrequently engages in suspension (~11% of locomotion) and prefers non-suspensory forms of locomotion (i.e. quadrupedal climbing). Although morphologically most similar to suspensory anthropoids, *Lagothrix* limbs are typically less derived and many skeletal characters are intermediate with non-suspensory anthropoids. Relatively little is known about the comparative and functional morphology of *Lagothrix* appendicular musculature. This study examines morphological variation in anthropoid muscle-tendon architecture (relative muscle mass and relative physiological cross section area; PCSA) to gain insight into the role of muscular variation in suspensory adaptations and the origins of this specialized locomotor adaptation. *Lagothrix* (n=7) forelimb and hindlimb muscle-tendon architecture data (relative muscle mass, relative physiological cross-sectional area; PCSA) was compared with similar data for ten anthropoids with varying locomotor adaptations (n=19 fore-/17hind-limb). Although *Lagothrix* hindlimb musculature resembles other non-suspensory anthropoids, its forelimb musculature is most similar to committed suspensory anthropoids (i.e. *Hyllobates*) despite infrequent suspension. These results confirm that anthropoid muscle-tendon

architecture varies with respect to locomotion and that *Lagothrix* forelimb musculature is, at least in part, a functional response to the minimum biomechanical demands of suspension. Likewise, they suggest that forelimb muscular adaptations are relatively uniform across distantly related lineages of anthropoids. This is significant for understanding the origins of crown hominoids and is consistent with the interpretation that suspension has multiple independent origins in several anthropoid groups. *Lagothrix* represents a compelling comparator for musculoskeletal adaptations in early anthropoid adopters of suspensory postures and locomotion (i.e. *Pierolapithecus*, *Morotopithecus*).

Lemurs Smell Better than Catarrhines

REBECCA M. DECAMP, STEPHANIE A. POINDEXTER, CHRISTOPHER A. SCHMITT and EVA C. GARRETT

Anthropology, Boston University

The primate sense of smell evolved in a complex manner. Like most other mammals, the primate sense of smell is divided into two systems: The Main Olfactory System (MOS) which detects volatile odorants and the Vomeronasal System (VNS) which detects non-volatile pheromones. The MOS expresses proteins which are coded for by the Olfactory Receptor (OR) gene family. The VNS expresses proteins coded for by the Vomeronasal Receptor 1 (V1R) gene family. Most catarrhines have high percentages of OR and V1R pseudogenes and have lost neuroanatomical components of the VNS. Conversely, there is speculation that strepsirrhines retained the ancestral olfactory state. Here, we made inferences about how olfactory capabilities changed throughout the primate lineage by reconstructing the functional repertoire of OR and V1R genes in ancestral primates using morphological proxies. We used Maximum Likelihood analysis as well as a phylogenetic least squares regression to reconstruct OR and V1R repertoires both for ancestral nodes of the primate lineage by including fossil species. We found that strepsirrhines, specifically lemuroids, may be derived in their olfactory capabilities. The Functional V1R repertoire in the LCA of all primates was estimated at ~40%, while the functional V1R repertoire for lemuriforms (excluding Chiromyiformes) was estimated at ~66.5%. Additionally, the percentage of functional OR repertoire in the last common ancestor of primates was estimated at 55% while the last common ancestor of lemuriforms was estimated to have 67% functional OR genes. These results may have implications for the ecological challenges ancient lemurs encountered when they rafted to Madagascar.

Sex-biased gene expression in the rhesus macaque brain

ALEX R. DECASIE^{1,2}, KENNETH L. CHIOU^{3,4}, MICHAEL J. MONTAGUE⁵, CHET C. SHERWOOD⁶, MICHAEL L. PLATT^{5,7,8}, MELWEEN I. MARTINEZ⁹, SAMUEL E. BAUMAN⁹, OLGA GONZÁLEZ¹⁰, NOAH SNYDER-MACKLER^{11,3,4} and JAMES P. HIGHAM^{1,2}

¹Department of Anthropology, New York University, ²New York Consortium in Evolutionary Primatology, ³Department of Psychology, University of Washington, ⁴Nathan Shock Center of Excellence in the Basic Biology of Aging, University of Washington, ⁵Department of Neuroscience, University of Pennsylvania, ⁶Department of Anthropology, The George Washington University, ⁷Department of Psychology, University of Pennsylvania, ⁸Department of Marketing, University of Pennsylvania, ⁹Caribbean Primate Research Center, University of Puerto Rico, ¹⁰Southwest National Primate Research Center, Texas Biomedical Research Institute, ¹¹Center for Studies in Demography & Ecology, University of Washington

Humans exhibit sex differences in the prevalence of some psychiatric and neurodevelopmental disorders, including autism and schizophrenia, which are thought to be driven by differences in neuroanatomy and gene expression. However, the evolutionary pressures that may have contributed to these differences remain unknown due to a dearth of comparative studies and a limited understanding of brain sex differences in nonhuman primates. To address this gap, we quantified sex-differences in brain gene expression in a cross-sectional sample of 20 (10M/10F) semi-free ranging adult rhesus macaques and compared these differences to those observed in humans. We focused on 8 brain regions that are involved in various cognitive and sensorimotor functions that show sex differences in primates. As in humans, the anterior cingulate cortex (ACC) was the most dimorphic region, with 6.7% of genes differentially expressed between males and females (compared to <1% for other regions). Cell-type deconvolution analyses suggest this may be due to sex differences in cell-type proportions, with relatively higher proportions of oligodendrocytes in males (p=0.036). Notably, the ACC is involved in social valuation, a cognitive process that is likely to be subject to different selection pressures in each sex. In addition, male-biased genes in the cortex were enriched for autism-related genes (odds ratio=2.47; p=0.002), similar to findings in humans. This work will expand our understanding of sexual dimorphism in the primate brain by demonstrating the unique and shared characteristics of sex-biased brain gene expression among humans and rhesus macaques.

This material is based on work supported by the National Science Foundation Doctoral Dissertation Research Improvement Grant (grant no. BCS-1752393).

ABSTRACTS

An examination of pelvic and overall body growth velocity in growing girls from the United Kingdom.

SARAH-LOUISE DECAUSAZ¹, JANE E. WILLIAMS², MARY S. FEWTRELL³, JAY T. STOCK² and JONATHAN C. WELLS³

¹Anthropology, University of Victoria,

²Anthropology, Western University, ³, UCL Great Ormond Street Institute of Child Health

The growth pattern of the female pelvis is unclear, making it difficult to quantify possible causes for compromised obstetric capacity. The pelvis may be affected by puberty and changing soft tissue dimensions. Previous work shows that soft tissue accumulation during puberty funds gestation and lactation. Scholars have also noted varied relationships between the onset of menses and changing fat deposits throughout the bodies of growing girls. This study examines growth patterns of pelvic breadth alongside changes in soft tissue dimensions. Body composition data and pelvic dimensions were collected from dual energy x-ray absorptiometry (DEXA) scans from 286 girls and women living in London and south-east England today between the ages of 4 and 22 years. Measures of body composition collected include lean mass and fat mass by the four-component model, height and weight. Outcome pelvic dimensions collected from DEXA scans were bi-iliac breadth, mediolateral inlet breadth and biacetabular breadth. Variables were converted to age-adjusted z-scores to enable accurate comparison between adults and growing children. Growth velocity charts for pelvic breadth and body dimensions were created using the LMS method. Mediolateral inlet breadth and biacetabular breadth have an increased growth velocity between 9 and 14 years of age and bi-iliac breadth increases steadily from 6 years of age onwards. Growth velocity of fat mass, lean mass and weight increases slightly between 10 and 13 years. These results suggest that investment in the pelvis slightly precedes investment in the tissues that are going to fund gestation (lean mass) and fat mass (lactation).

Funding for this project was provided by a Small Grant Fund from the Parkes Foundation.

The peopling of South America: insights from genetic markers

CRISTINA B. DEJEAN^{1,2}, CRISTIAN M. CRESPO¹, VALERIA ARENCIBIA^{2,3}, DARÃO CARDOZO^{2,3}, MARÁA B. POSTILLONE² and SERGIO A. AVENA^{1,2,3}

¹Ciencias Antropológicas, Universidad de Buenos Aires, ²CEBBAD, Universidad Maimónides,

³CONICET, Secretaría de ciencia, tecnología e innovación productiva, ⁴Ciencias Biológicas, Universidad de Buenos Aires

The earliest human occupation of South America has been dated to at least 14000 years BP. Several lines of evidence suggest that these early settlers may have moved south along the Pacific and/

or Atlantic coast, but it seems clear that in their southward advance the earliest South American settlers adapted to contrasting landscapes and underwent different evolutionary trajectories, a process that is reflected in genetic markers.

The aim of this work was to analyze and compare maternal genetic diversity in two Argentine regions in the broader context of South America. A total of 117 individuals were included in our sample, 51 from Northwestern Argentina (NWA) and 66 from Patagonia, dated between 3000 and 300 years BP. Mitochondrial hypervariable region 1 was analyzed and consensus sequences were obtained from at least two independent extractions.

The most frequent lineage detected in NWA was A2, followed by B2, D1 and C1, while in Patagonia C1 was the most often represented, followed by D1, D4h3, B2 and A2. The number of haplotypes detected were similar in both regions: 35 in NWA and 33 in Patagonia, where D1g was the most diverse. Despite having arisen from a single population, the diverse cultural evolutionary trajectories followed by the human groups in each region resulted in different haplotype compositions, probably due to founder effects and genetic drift. Most lineages found in our sample have been reported in other South American past and contemporary native groups, probably with a Pacific origin.

UBACyT 20020170200363BA, PICT 2014-3012, Fundación Científica Felipe Fiorellino

Predictors of chest redness in dominant male geladas

PATRICIA M. DELACEY¹, THORE J. BERGMAN^{1,2} and JACINTA C. BEEHNER^{1,3}

¹Psychology, University of Michigan, ²Ecology and Evolutionary Biology, University of Michigan, ³Anthropology, University of Michigan

Sexual selection produces badges of status that communicate signaler strength to nearby rivals. Skin pigmentation is one such badge of status where the intensity of color is associated with competitive ability. For example, male geladas (*Theropithecus gelada*) have a chest patch that is thought to ward off challenges from rival bachelor males. Previously, we reported that chest redness increases with internal metabolic activity. Here, we additionally examine whether male chest redness is associated with variables directly related to male reproductive success (number of females, testosterone levels, and male tenure length). We used digital photos, calibrated with a color standard, to measure redness (red:green ratio) in male chest patches (N=15 males; 120 photos) across the first year of each male's tenure. We only included males whose full tenures were known. We then matched each photo to the number of unit females and recent fecal testosterone samples (within 7 days). We found that redder chests were associated with (1) more

unit females (LMM: $\beta=0.01$, $SE=0.007$, $df=21.09$, $t=1.87$, $P=0.076$), and (2) higher testosterone (LMM: $\beta=0.07$, $SE=0.03$, $df=115$, $t=2.39$, $p=0.018$). Contrary to predictions, we found that redder chests were associated with (3) shorter tenures for these males (LMM: $\beta=-0.002$, $SE=0.0008$, $df=12.26$, $t=-2.53$, $P=0.0257$). These results suggest that the reddest males employ a short, but possibly productive, reproductive strategy by targeting and maintaining access to the largest units. Testing whether this strategy is indeed an optimal one will require genetic paternity data.

The National Science Foundation (BCS-0715179, BCS-1723228, IOS-1255974, IOS-1854359); Leakey Foundation (multiple awards); National Geographic Society (#NGS-8100-06, #NGS-8989-11, #NGS-50409R-18); Fulbright; University of Michigan

Shape of the prespheno-septal synchondrosis predicts facial reduction

VALERIE B. DELEON¹ and TIMOTHY D. SMITH^{2,3}

¹Department of Anthropology, University of Florida, ²School of Physical Therapy, Slippery Rock University, ³Department of Anthropology, University of Pittsburgh

Facial reduction is observed to varying degrees across primates. Most strepsirrhines and some haplorhines show the ancestral, rostrally-elongated snout. Other haplorhines show a reduced snout, often with the face positioned inferiorly. Humans fall at the latter end of the spectrum, and facial reduction is important in studies of hominin evolution. Many hypotheses have been presented over the years to account for how and why facial reduction occurs. Midline cranial base synchondroses are of particular interest. Recently, we described differences in the shape of the prespheno-septal synchondrosis among primates. Strepsirrhines have a unidirectional synchondrosis allowing rostral growth. Most anthropoids, including *Macaca*, have a radially-directed synchondrosis allowing rostral and ventral growth. Here, we tested the hypothesis that shape of the prespheno-septal synchondrosis predicts the degree of facial reduction.

We used shape data collected from CT images of a representative sample of primate heads. Snout length and relative position of the face were estimated using 3D coordinate data for landmarks on the cranial base and face. Shape of the prespheno-septal synchondrosis was estimated separately using 2D semilandmark coordinates in the midsagittal plane. The relationship of these shape variables was tested using regression analyses.

Results indicated a significant relationship between shape of the prespheno-septal synchondrosis and facial reduction. As expected, a coronally oriented prespheno-septal synchondrosis is associated with a rostrally-elongated snout. A radially-oriented synchondrosis is

ABSTRACTS

associated with facial reduction and the inferior displacement of the dental arcade. This study indicates the importance of understanding growth processes in evolutionary and comparative interpretations of phenotypic differences.

The authors gratefully acknowledge funding from the National Science Foundation (NSF BCS-1830894, BCS-1830919, BCS-1231717, BCS-1231350, BCS-1728263; BCS-0959438).

Changes in the index of sexual dimorphism over time and the relationship with female pelvic size

HILLARY DELPRETE

History and Anthropology, Monmouth University

It has been demonstrated that larger body size is correlated with higher levels of dimorphism, and levels of dimorphism may change over time. The aim of this study was to determine if the degree of pelvic sexual dimorphism in six skeletal populations changed over time and if these changes were related to pelvic size. Data on 23 pelvic measures were collected from 668 individuals from the Hamann-Todd, Terry, Spitalfields, and Coimbra Collections. To determine the degree of sexual dimorphism, an index value was computed for each measure, separated by collection, by taking the female mean and multiplying it by 100, and then dividing that value by the male mean. In addition, a geometric mean (GM) was computed for each individual as a proxy for pelvic size; within collections, these GM values were averaged to compute an overall pelvic size for males and females. Each collection was then divided into time cohorts and tested for change over time in index values using MANOVA. According to the results, each collection had at least two index values that significantly changed over time. Interestingly, populations with a larger overall GM for female pelvic size had more significant changes in index values, and number of changes corresponded with pelvic size in females; the larger the GM value, the higher the number of significant changes over time. This trend was not observed in males. Perhaps in populations where females have a larger pelvic size there is reduced constraint due to reproduction, therefore morphology is more flexible.

No funding to declare

An activity based five-day professional development workshop for pre-college educators: incorporating evolution and biological anthropology into middle- and high-school curricula

LILY J. D. DEMARS¹, AMERICA M. GUERRA¹, JOSHUA M. WISOR¹, MARGARITA HERNANDEZ¹, TAYLOR S. WOOD², AMBER CESARE², KATHLEEN HILL² and TIMOTHY M. RYAN¹

¹Anthropology, Penn State University, ²Center for Science and the Schools, Penn State University

In July 2019, Penn State Anthropology faculty and graduate students collaborated with the Penn State Center for Science and the Schools to host a five-day professional development workshop for middle- and high-school educators. The workshop was developed as part of a broader impacts initiative with a goal of making our research more accessible and interesting to pre-college educators and their students within the context of the Next Generation Science Standards. The workshop content focused on the relationship between skeletal biology and behavior in the context of primate and human evolution. However, many other topics were incorporated into activities throughout the week including: primate locomotion, functional morphology, biomechanics, osteology, the history of anthropology and anthropological discoveries, and data visualization. Teachers engaged in activities based on relevant scientific practices that apply systems thinking to the design and implementation of research projects using the Modeling Authentic STEM Research (MASTER) Model as a framework. The goal of this exercise was to prepare teachers to engage their students in biological anthropology-related classroom research projects. Workshop content included hands-on activities, discussion, and presentations. Educators then developed an overarching research question with 3-4 sub-questions to implement in their classrooms. Post-workshop educator evaluations were very positive. On a scale of 1-5 (1 = strongly disagree; 5 = strongly agree), the average response for "My understanding of this topic has been enhanced" was 5 (SD=0). And for "I will be able to apply what I learned into my classroom instruction" the average response was 4.86 (SD=0.49).

NSF BCS-1719187; NSF GRFP No. DGE1255832 (LJDD & MH)

Evaluating bilateral asymmetry in femoral neck shaft angle and femoral head diameter in *Homo sapiens*, *Pan troglodytes*, and *Papio sp*

LEANNE E. DEMAY¹, CALEY M. ORR^{1,2}, ANNA G. WARRENER² and MARY SHIRLEY MITCHELL²

¹Department of Cell and Developmental Biology, University of Colorado School of Medicine, ²Department of Anthropology, University of Colorado Denver

Laterality has been frequently examined to address the evolution of brain organization and cerebral asymmetries that may relate to language, symbolic thinking, and tool use in hominins. Identifying skeletal asymmetries may assist in tracking the evolution of such laterality in the fossil record. Most studies have focused on handedness and less is known about asymmetries of the lower limb. In particular, plasticity in proximal femoral morphology (e.g., in neck-shaft angle: NSA) has been correlated with population mobility, suggesting that it may reflect loading

mechanics at the hip. Thus, lower limb skeletal asymmetry may indicate left-right differences in hip joint loading possibly related to limb dominance ("footedness") or other factors influencing gait asymmetry. In the current study, three-dimensional polygon models of right and left femora from humans, chimpanzees, and baboons were collected using an Artec Space Spider scanner and NSA and femoral head diameter (FHD) were measured. The 3D data does not reveal significant right-left asymmetry in NSA in any of the sampled taxa. Similarly, neither humans nor baboons show a significant left-right difference in FHD, but the chimpanzee sample is significantly asymmetric in FHD. These results provide no evidence of substantial asymmetry in the forces acting on the hip in humans and baboons. The observed bilateral asymmetry in FHD of chimpanzees may be due to their unusual mode of knuckle-walking locomotion. Future research will focus on examining asymmetry in other aspects of femoral morphology along with the underlying biomechanics.

Modern Human Anatomy program, University of Colorado School of Medicine

Stable isotope analysis of dental calculus and dietary change in the North Carolina Piedmont, AD 800 – 1710

SOPHIA C. DENT¹, DALE L. HUTCHINSON¹, MATTHEW A. FORT^{2,3}, KRISTIN M. HEDMAN³ and STANLEY H. AMBROSE²

¹Anthropology, University of North Carolina at Chapel Hill, ²Anthropology, University of Illinois Urbana-Champaign, ³Program on Ancient Technologies and Archaeological Materials, Illinois State Archaeological Survey

Dietary reconstruction uses destructive analysis of skeletal elements, which is often opposed by descendant populations. Dental calculus has been proposed as an alternative analytical material, but studies have yet to establish a firm relationship between calculus and bone stable isotope ratios. To assess calculus as a dietary proxy, we applied logistic regression models to paired bone and calculus samples (n = 29). The beta-coefficients and standard error of the regression models are: mineral $\delta^{13}\text{C}$ [1.192 (0.009)], organic $\delta^{13}\text{C}$ [0.979(0.113)], and $\delta^{15}\text{N}$ [0.839(0.086)]. All are significant at alpha = 0.001. The strength of these correlations indicates that calculus is an effective proxy for bone and useful for reconstructing diet. We applied these regression models to the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of calculus samples from Piedmont North Carolina, AD 800 – 1710 (n = 25). We compared calculus $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ to an interpretive baseline of 87 local plants and animals using Bayesian isotope mixing models. Sampled individuals are from three temporal groups: Early (AD 800 – 1200), Protohistoric (AD 1200 – 1600), and Colonial (AD 1600 – 1710). Our results indicate that Colonial groups consumed more fish

ABSTRACTS

than other groups, and maize consumption fluctuated across time. Estimated dietary proportions of fish are: $26.6 \pm 14.5\%$ (Early), $24.9 \pm 15.5\%$ (Protohistoric), and $43.8 \pm 8.8\%$ (Colonial). Dietary proportions of maize are: $20.6 \pm 13.9\%$ (Early), $12.7 \pm 9.7\%$ (Protohistoric), and $23.6 \pm 6.8\%$ (Colonial). Results from paleoethnobotanical and zooarchaeological studies corroborate that Piedmont groups shifted their dietary and socioeconomic practices to creatively negotiate colonial-attendant environmental change.

This research was supported by NSF grant BCS 1450633.

Getting to the root of the problem: World frequencies of three-rooted lower first and second molars

LARESA L. DERN, SHAUN B. JOSEPH, HEATHER J. NESBITT, MACKENZIE R. SULLIVAN and G. RICHARD SCOTT

Anthropology, University of Nevada-Reno

Typically, lower molars have one mesial and one distal root. Some lower molars exhibit an accessory distolingual root, making the tooth three-rooted. Geographic variation of three-rooted lower first molars is well known, but no data are available for three-rooted lower second molars. Our global sample consists of 18,156 individuals from 13 regions ($k=173$) for the first molar and 13,644 individuals from 12 regions ($k=159$) for the second molar. All data came from the Christy G. Turner II database except for African samples published by J.D. Irish. For three-rooted first molars, the global frequency is 9.5%. The highest frequencies are found in Circumpolar populations (27.4%) and East Asians (22.3%), with intermediate frequencies in Northwest Coast Natives (14.3%) and Southeast Asians (12.6%). All other regions show low frequencies (0.5-7.6%), with near absence in Europe and Africa. Three-rooted lower second molar frequencies are dramatically lower with a global frequency of 0.5%. The highest frequency is for Polynesia (1.1%) while East Asia and Melanesia show above-average frequencies (0.06-0.07%). Frequencies of less than 0.1% were observed in Central Asians and Native North Americans while the trait is completely absent in North African samples. All other regions have intermediate frequencies (0.1-0.5%). The presence of a third root on the first lower molar shows a weak positive correlation with presence on the second molar ($r=0.255$). Given the reduced morphological stability of the second molar, lower three-rooted frequencies are expected for this tooth, but the significance of regional variation requires further investigation.

Genetic analysis of the South American Macushi population

KATE L. DEROSA, CASSANDRA A. KOCH and D. ANDREW MERRIWETHER

Anthropology, Binghamton University

The Macushi are a Carib-speaking population indigenous to the Roraima state of northern Brazil. Their kinship system follows a bifurcate-merging pattern with preferential cross-cousin marriage. The Macushi share territories with the Wapishana and have established trade routes with the Yeukana and have had regular contact with non-indigenous cattle ranchers since the 19th century. Mitochondrial DNA (mtDNA) analysis of 94 maternally unrelated individuals was performed using the d-loop region (15,938-429) to assess the genetic diversity of the population. Y-chromosome analysis was performed on 50 paternally unrelated individuals using *DYS385a&b*, *DYS389I&II*, *DYS390*, *DYS391*, *DYS392*, *DYS393*, *DYS437*, *DYS438*, *DYS439*, and *DYS448*. The Macushi population consists of mtDNA haplogroups A ($n=2$), B ($n=47$), C ($n=18$), and D ($n=27$), as expected for indigenous South American (SA) groups. These data were compared with previously published mtDNA data from SA, indicating female migration is greatest with Amazon and Andean populations. AMOVA was used to determine the relationship between geography, language, and genetic distance, finding that geography and language were significantly positively correlated with genetic distance. Y-STR analysis revealed haplogroup Q was the dominant lineage in the Macushi as previously observed in SA. Y-chromosome data was further compared to previously published data, indicating widespread male migration throughout SA. AMOVA of the Y-chromosome data found a significant positive correlation between genetic distance, geography, and language. While this study indicates differing migration patterns for males and females of the Macushi population, autosomal markers are needed in order to better assess patterns of gene flow.

Do chimpanzees of Gombe National Park, Tanzania have community-specific dialects?

NISARG P. DESAI¹ and MICHAEL L. WILSON^{1,2}

¹Anthropology, University of Minnesota, ²Ecology, Evolution, and Behavior, University of Minnesota

Chimpanzees provide important comparative data for understanding the evolution of human language. One key component of spoken language is vocal learning: the ability to voluntarily modify the acoustic structure of vocalizations. While common in taxa such as songbirds and whales, vocal learning capacities of nonhuman primates appear more limited, raising questions about how and why this capacity evolved in the human lineage. Intriguingly, evidence for vocal learning has been reported in the form of regional variation ('dialects') in the 'pant-hoot' calls of chimpanzees, suggesting that some capacity for vocal learning may be an ancient feature of the *Pan-Homo* clade. Nonetheless, reported differences have been subtle, with between-community

variation representing only a small portion of total acoustic variation. To gain further insights into the extent of regional variation in chimpanzee vocalizations, we performed a preliminary analysis of pant-hoots from chimpanzees in two neighboring communities at Gombe National Park, Tanzania. We tested for group differences in acoustic parameters using acoustical analysis techniques that involve (i) statistical hypothesis testing on manually coded acoustic features, and (ii) machine learning techniques on automated acoustic features. The first approach, using a binomial GLMM, revealed no statistically significant difference between the communities in any acoustic parameter. Two machine learning techniques, random forests and artificial neural networks, had classification accuracy of 80% and 60% respectively, which is no better than chance (binomial exact test, $p=0.11$ and 0.75 , respectively). Thus, we did not find evidence of dialects in this population, suggesting that extensive vocal learning emerged only in hominins.

Funding for recording chimpanzee vocalizations at Gombe National Park was provided through a Talle Faculty Research Award to Dr. Michael Wilson from the College of Liberal Arts, University of Minnesota.

Rediscovery of original site A bipedal footprints at Laetoli, Tanzania

JEREMY M. DESILVA¹, CATHERINE MILLER^{1,2}, ANDREW S. DEANE³, KALLISTI FABIAN⁴, LUKE FANNIN^{1,2}, JOSEPHAT GURTU⁴, ELLIE GUSTAFSON⁵, KEVIN G. HATALA⁶, AUSTIN C. HILL¹, SAID KALLINDO⁴, BLAINE MALEY⁷, ELLISON J. MCNUTT⁸, ANJALI PRABHAT¹, SHIRLEY RUBIN⁹, REBECA THORNBERG⁵ and CHARLES MUSIBA⁵

¹Anthropology, Dartmouth College, ²Ecology, Evolution, Environment and Society, Dartmouth College, ³Anatomy, Cell Biology & Physiology, Indiana University School of Medicine, ⁴Department of Cultural Heritage, Ngorongoro Conservation Area Authority, ⁵Anthropology, University of Colorado, Denver, ⁶Biology, Chatham University, ⁷Anatomy, Idaho College of Osteopathic Medicine, ⁸Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ⁹Anthropology, Napa Valley College

The 3.66 Ma bipedal trackways discovered in 1978 at Laetoli, Tanzania site G still represent the oldest unequivocal evidence for human-like bipedalism. Two years before the discovery of Laetoli site G, a set of 5 bipedal prints was unearthed at site A. These unusual prints were originally attributed to a hominin, but soon after hypothesized to have been made by an ursid. This hypothesis that has recently been challenged by our team, but such an evaluation would benefit from re-examination of the original site A trackway. In 2019, we relocated this trackway, excavated the original 5 prints, and extended the excavation. While no additional bipedal prints were found, we were able to digitally archive and scan the trackway using photogrammetry, and a portable 3d laser scanner

ABSTRACTS

(Creaform GoSCAN 50). The third footprint in the sequence was the best preserved, with a clear imprint of the hallux and the scalloped impression of the second digit. Identification of the hallux on this print supports the hypothesis that this was a small, possibly juvenile, cross-stepping hominin rather than an ursid. However, foot proportions, gait parameters, and preliminary examination of the footprint contour maps of the site A trackway differ from the records at Laetoli site G or S. Whether these differences can be explained ontogenetically or taxonomically remain unclear.

Hominin dietary implications of plant nutritional properties from the southern African Lowveld

EMMA J. DEVEREUX^{1,2}, OLIVER C.C. PAINE², CHRISTINA RYDER², CORLI WIGLEY-COETSEE^{3,4}, JACQUELINE CODRON⁵, DARYL CODRON^{5,6}, MATT SPONHEIMER² and AMANDA G. HENRY¹

¹Faculty of Archaeology, Leiden University, The Netherlands, ²Department of Anthropology, University of Colorado Boulder, ³School of Natural Resource Management, Nelson Mandela University, George, South Africa, ⁴Scientific Services, SANParks Kruger National Park, Skukuza, South Africa, ⁵Florisbad Quaternary Research Department, National Museum, South Africa, ⁶Centre for Environmental Management, University of the Free State, Bloemfontein, South Africa

Dental microwear and stable carbon isotope analyses have enhanced our understanding of early hominin dietary behavior and called into question many previously held assumptions. For example, the pronounced craniodental robusticity of *Paranthropus* was originally interpreted as an adaptation to a diet of hard-object foods such as nuts and seeds—an interpretation supported by studies of the southern African species, *Paranthropus robustus*. However, dental microwear and isotopic studies reveal that its eastern African congener, *Paranthropus boisei*, focused its diet on tough C4 plant foods, such as grasses and/or sedges.

We are now faced with the possibility that paranthropine morphology allowed for some degree of dietary flexibility and that food choice was dictated as much by the nutritional properties and spatiotemporal availability of wild plant foods as much as by masticatory adaptations. As such, an understanding of how wild plant foods in modern African savannas vary across habitat and season may shed light on the dietary differences we see between early hominin species living in eastern and southern Africa. At present, empirical data on the nutritional properties of wild plant foods growing in modern African savanna habitats are relatively scant.

Here we present measures of crude protein and dietary fiber for plants collected from savanna habitats in SANParks Kruger National Park, South

Africa. We find that significant variation exists within habitats and plant categories, and that C4 grasses and sedges, in particular, can be highly variable.

Project funded by the European Research Council, EU Horizon 2020 research and innovation programme, grant number STG-677576 ("HARVEST").

Multiple developmental stress events and mortality outcomes in the context of medieval English famines

SHARON N. DEWITTE

Anthropology, University of South Carolina

Research in living and past populations has revealed associations between the experience of physiological stress early in life and negative health outcomes later in life, but further work is needed to assess the context-specific nature of these associations. This study builds on previous work assessing the developmental origins of health outcomes in the context of crisis events (plague and famine) in medieval England. This study uses a sample of $n = 276$ individuals from the St. Mary Spital cemetery, London (SRP98, c. CE 1120-1540) who were interred in mass burials associated with periods of famine. The effects of multiple stress events during childhood (as indicated by macroscopic linear enamel hypoplasia, or LEH) on risks of mortality during periods of famine are assessed with a Cox proportional hazards model. Given previous findings of increasing risks of mortality with adult age during medieval famine, estimated negative effects of enamel hypoplasia on risk of mortality would suggest there is a detrimental effect of developmental stress on later mortality outcomes given that younger adults are otherwise expected to be at lower risks of mortality. The results of this study indicate that the presence/absence of LEH is not significantly associated with odds of dying. However, increasing numbers of LEH are positively associated with odds of dying, i.e., the risk of mortality increases with an increasing number of defects. These findings suggest a mortality cost, at least in the context of famine, associated with the experience (and survival) of multiple stress events during childhood.

Funding was provided by NSF (BCS-0406252), the Wenner-Gren Foundation (#8247).

Differences in development of the deciduous dentition between *Gorilla gorilla* and *Gorilla beringei*

RACHEL R. DICKERSON¹ and EMILY E. HAMMERL²

¹Anthropology, University of Pennsylvania,

²Anthropology, University of Nebraska-Lincoln

Primate dental development can be used to both determine age in individuals and estimate life history patterns in past species. An understanding of the differences in dental development

between primate species is imperative for reliable research in these areas. The aims of this study are to compare the development of deciduous teeth between *Gorilla gorilla* and *Gorilla beringei*. Most research into primate dental ontogeny focuses on chimpanzees, while few studies concentrate on gorillas. Even fewer comparative studies of *Gorilla gorilla* and *Gorilla beringei* have been undertaken. Moreover, previous research on primate dental development largely examines the development of permanent teeth, which is more strongly influenced by environmental stressors than deciduous teeth. To address these gaps in the current literature, this study examines the development of deciduous teeth and permanent teeth, drawing comparisons between *G. gorilla* and *G. beringei*. Radiographic images from the mandibles of 44 nonadult individuals from museum collections are scored using a dental age method adapted by Hammerl (2013) from Kuykendall's (1996) method of age-scoring permanent dentition. Age for stage and stage for age statistics, which describe the average age at a given stage (including midpoint age at attainment values) and average stage for a given age, respectively, are determined. Results show a greater interspecies difference in rates of deciduous than permanent dental development. These results elucidate the need for expanded research into deciduous teeth of primates for purposes of measuring differences in ontogeny between extant primate species and better estimating the ontogeny in extinct primates and hominids.

Myological specializations within the hyper-derived forelimb of *Perodicticus potto*

EDWIN DICKINSON¹, MARISSA L. BOETTCHER^{1,2}, KAITLYN C. LEONARD¹, ANTHONY HERREL³ and ADAM HARTSTONE-ROSE¹

¹Biological Sciences, North Carolina State University, ²College of Medicine, Medical University of South Carolina, ³Departement Adaptations du Vivant, C.N.R.S./M.N.H.N, Paris

The forelimb of the African lorid, *Perodicticus potto*, has undergone several bizarre anatomical specializations, including the substantial reduction of the second digit, the hyper-abduction of the pollex, and the presence of a specialized vascular bundle (the retia mirabilia) within the wrist. The resultant pincer-like morphology has been interpreted to reflect a specialization towards extraordinary grip strength, which historical behavioral accounts of this taxon also note. However, this claim of extraordinary grip strength has not been empirically substantiated. Here, we present detailed dissection data, enabling us to quantify the myology of the forearm and hand musculature of *P. potto*. These data are compared with those from a broad primate sample, including several similarly sized strepsirrhines. Contrary to expectation, we found that

ABSTRACTS

potto's actually have relatively below-average digital flexor physiological cross-sectional area, raising questions as to the 'extraordinary' nature of the potto's previously described gripping ability. We also identified several unexpected myological characteristics in the forelimb of *P. potto*, including the largest *M. brachioradialis* (an elbow flexor) among our primate sample. Additionally, despite the potto having only a vestigial second digit, we observed an independent *M. extensor indicis* that is otherwise absent in almost a quarter of the other primate taxa in our sample – all of whom have more substantial second digits than that of the potto. Collectively, these findings emphasize the unusual nature of the potto's antebrachial musculature, but suggest that the nature of their grip may owe more to their capacity for endurance than an increase in myological force.

This work was funded, in part, by the National Science Foundation (IOS-15-57125 and BCS-14-40599)

Wild Bornean Orangutans (*Pongo pygmaeus wurmbii*) Navigate to Non-Fruit Foods

ANDREA L. DIGIORGIO^{1,2}, TRIWAHYU SUSANTO³ and CHERYL D. KNOTT^{2,3}

¹Princeton Writing Program, Princeton University, ²Department of Anthropology, Boston University, ³Department of Biology, Universitas Nasional

Wild primates have foraging goals beyond energy maximization. These foraging goals are often met by less energy dense, and more reliable, non-fruit foods. Are they able to meet these goals by navigating to high-energy fruit resources and consuming non-fruit (lower-energy) foods along the way, or do they navigate to non-fruit foods as well? Here we address this question in wild Bornean orangutans, a species known for consuming ripe fruit when it is available. Our research suggests that orangutans maintain a ratio of non-protein energy to protein and choose to consume non-fruit foods when in proximity to fruit foods. Using the movement ecology paradigm, we examine sequences of feeding bouts where an orangutan travels from one fruit patch to another, stopping at one or two non-fruit foods along the way ($n = 54$). By asking whether the direct path length between the two fruit patches is the same as, or less than, the actual travelled path length, we can determine whether the orangutans deviate from a fruit-to-fruit path and navigate to non-fruit foods. We find that orangutans do deviate from the direct fruit-to-fruit path by an average additional 18% of path length (range 8% - 84%; $p = 6.819e^{-07}$). This is not impacted by fruit availability. This research suggests that orangutans are navigating to more constant non-fruit

foods as well as the temporally and spatially patchy fruit resources. We discuss this in terms of which types of foods orangutans are navigating toward.

National Science Foundation; National Geographic Society; LSB Leakey Foundation; Wenner Gren Foundation; US Fish and Wildlife Service; Disney Conservation Fund; Woodland Park Zoo; Nacey Maggioncalda Foundation; Primate Conservation Incorporated

My So-Called Lab: Using Social Media to Highlight Diverse Experiences of Women in STEM

HEATHER DINGWALL¹, MARIEL YOUNG¹, EVELYN JAGODA¹, KATHERINE L. BRYANT², JUSTIN PARGETER³, ANN C. KRUGER⁴, LEA ANN LEMING⁵ and ERIN E. HECHT¹

¹Human Evolutionary Biology, Harvard University, ²Donders Institute for Brain, Cognition, & Behaviour, Radboud University, ³Anthropology, Emory University, ⁴College of Education and Human Development, Georgia State University, ⁵WebMD

In STEM fields, women and members of minority groups are systemically underrepresented. Implicit environmental and social barriers, including stereotypes, gender bias, and the climate of STEM departments, hinder progress. Despite this, research shows that STEM success is associated with a growth mindset (believing intelligence is malleable rather fixed). A key component of the growth mindset is the viewpoint that STEM skill is not an innate characteristic, but is built through experience and learning. We describe the development and implementation of an outreach project promoting a growth mindset to counteract implicit biases in STEM, *My So-Called Lab (MSCL)*. The project goal is to promote and encourage women scientists by making their work accessible to broad audiences, and providing a platform for engagement and discussion. *MSCL* embraces a broad definition of research, including wet lab work, field work, data science, and more; it aims to curate a variety of STEM experiences. The project has three main components: (1) an ongoing showcase of selfies, in which women scientists submit photos and biographies of themselves doing research; (2) a podcast in which women scientists are interviewed to discuss their research, rewarding moments, challenges, and other insights about life in the lab, and (3) several linked social media platforms allowing users to share and discuss this content. As part of our poster presentation, we will introduce the website and social media accounts to the AABA community, showcase a selection of interviews and selfies, and invite further contribution.

This work is funded by a grant from the National Science Foundation (No. NCS/DRL 1631563) and a Marie Skłodowska-Curie Individual Fellowship Grant #750026.

Using socio-ecological analyses to identify determinants of Mseleni Joint Disease

ELIZABETH S. DINKELE^{1,2}, ROBEA BALLO² and VICTORIA E. GIBBON¹

¹Clinical Anatomy and Biological Anthropology, University of Cape Town, ²Cell Biology, University of Cape Town

Mseleni joint disease (MJD) is a crippling osteoarthritis that is geographically localised to a community of Bantu-language speakers in KwaZulu-Natal, South Africa. The prevalence of MJD was conservatively estimated as 5.1% in 1985, and women were 3 times more likely to be affected. Of particular concern was the incidence of MJD in adolescents, and the resultant disability and limited education, which perpetuated poverty and gender inequality. The spatial isolation of MJD is puzzling because the affected population is not genetically, or culturally isolated. This had led to the suggestion that MJD has an environmental aetiology. Socio-ecological analyses combining surveys of community members ($n=100$) and medical record reviews ($n=1080$) were used to identify disease determinants and provide an updated estimate of prevalence. Despite a higher prevalence of 10.1%, an apparent decline in incidence was noted. This was attributable to the absence of diagnoses in those under the age of 18 years, and the high prevalence in those over the age of 65 years. Women were 2.1 times more likely to have MJD ($p \leq 0.0001$) suggesting that biological differences between sexes and/or gender-based practices are causative of MJD. Improved access to sanitation, housing and food/water correlate with reduced load-bearing activities and a later age of onset. Differences in the distribution of MJD are likely attributable to regional changes in the social, economic and political landscape. More longitudinal data is required to contextualise the interactions between various socio-ecological risk factors so they can be effectively managed.

The financial assistance of the National Research Foundation (NRF) and Rare Disease Foundation (RDF) towards this research is hereby acknowledged.

The Silent Thief: Identifying Osteoporosis in Medieval Cambridge

JENNA M. DITTMAR¹, BRAM MULDER², SARAH A. INSKIP¹, PIERS D. MITCHELL², CRAIG CESSFORD^{2,3}, JAY T. STOCK⁴ and JOHN E. ROBB²

¹McDonald Institute for Archaeological Research, University of Cambridge, ²Department of Archaeology, University of Cambridge, ³Cambridge Archaeological Unit, ⁴Department of Anthropology, Western University

Osteoporosis is a metabolic disorder that is characterized by low bone mass and microarchitectural deterioration of bone tissue with a consequent increase in bone fragility and susceptibility to fractures. Osteoporosis presents a major health threat to elderly individuals, both in

ABSTRACTS

modern times and in the past. This research aims to identify osteoporosis in osteological assemblages in order to begin to untangle the factors that contributed to the presence of this condition in the past. Adult individuals with well-preserved vertebral columns ($n=79$) from three medieval burial grounds located in and around Cambridge, UK were assessed using Genant's semi-quantitative method to identify vertebral fractures. Significantly more vertebral fractures were found in old adult males (>60 years old) than in younger male individuals. However, this trend was not identified in females. This data was then compared to measures of mineral quantity of the trabecular bone in the femoral head ($n=115$), as quantified by micro-computed tomography. The micro-CT analysis of the femoral head indicated that females have greater bone loss with age than males. A subset of individuals ($n=47$) were examined to assess the relationship between the presence of vertebral fractures and bone loss. No correlation was identified between the incidence of vertebral fractures and trabecular bone loss in the femoral head in males or females. These findings highlight the difficulty of evaluating the health burden of osteoporosis by assessing fracture patterns in archaeological assemblages as low bone mass does not always result in fractures, and high bone mass does not always prevent it.

The After the Plague project is supported by the Wellcome Trust (Award no. 2000368/Z/15/Z).

Analysing the occlusal wear of the hominins of Sima de los Huesos

JESSICA AM. DOLDING-SMITH^{1,2}, ANNA F. CLEMENT³, PATRICK MAHONEY², SIMON W. HILLSON³, JUAN-LUIS ARSUAAGA⁴, JOSÉ MARÍA BERMÚDEZ DE CASTRO⁵ and MARÍA MARTINÓN-TORRES^{1,5}

¹Anthropology, UCL, ²School of Anthropology & Conservation, University of Kent, ³Institute of Archaeology, UCL, ⁴Centro de Investigación de la Evolución y Comportamiento Humanos, Universidad Complutense de Madrid, ⁵National Research Centre on Human Evolution, CENIEH

The occlusal surface of a tooth can provide evidence of past behaviour. In general terms, occlusal wear decreases through time, with industrialised modern humans having low occlusal wear because of the greater reliance upon processed foods. Neanderthals are thought to have exceptionally heavy occlusal wear, due to high mechanical loading from paramasticatory and masticatory behaviour.

Here, we compare occlusal wear of hominins from Sima de los Huesos (SH, $n=19$) to Neanderthals ($n=27$) and modern humans (Middle Palaeolithic, $n=5$; Upper/ Early Epi-Palaeolithic, $n=26$; Igloodik Inuit $n=79$; 19th-20th-century Madrileños individuals, CMH, $n=14$). The SH are thought to either be early Neanderthals or closely related to them, and

share a number of cranial and dental traits with both Neanderthals (e.g. shovel-shaped incisors) and modern humans (e.g. frequent absence of the hypoconulid).

Results deviate from the general and expected trend. The SH group had more wear on their upper I1 compared to Neanderthals ($p=0.022$), but not modern humans ($p>0.05$). We find that SH upper P3 is more worn than all other groups ($p<0.05$), except CMH ($p=0.201$), potentially pointing to masticatory behavioural differences. The mandibular dentition of the SH was significantly more worn compared to Neanderthals (C-M2, $p<0.05$), Inuit (I1-M2, $p<0.05$), and CMH (M2, $p=0.030$). It may be that SH were using their mandibular dentition less for paramasticatory activities or that the lower age range of the SH hominins used in the mandibular group meant that they generally had less wear.

Dirección General de Investigación de Spanish Ministerio de Economía y Competitividad (MINECO)/FEDER grant number: CGL2015-65387-C3-2-3-P and The Leakey Foundation (personal support of Dub Crook and Gordon Getty to author MM-T).

Sacroccocygeal fusion and its implications with age estimation and sexual dimorphism

PAULINA DOMINGUEZ ACOSTA and HANNAH N. TREVIÑO

Anthropology, Texas State University

Age and sex estimation are increasingly less accurate and precise as age increases due to degenerative changes on the skeleton. Tague (2011) uses sacroccocygeal fusion to estimate age, also to understand how sexual dimorphism affects sacroccocygeal fusion. Results provided by Tague (2011) and Passalacqua (2009) show conflicting conclusions on whether sacroccocygeal fusion is related to age. Both studies lack a large sample size for individuals over 80 years and have considerably less females than males. This research includes a preliminary examination of the methods Tague (2011) used to analyze sex and age correlation of sacroccocygeal elements. An analysis of the pelvic measurements, fusion rates between the sacrum and coccyx and the number of fused coccyx elements were conducted for this study. The individuals analyzed are from the Texas State Donated Skeletal Collection. Fisher's exact test were used to determine statistical significance.

Preliminary analysis of 30 individuals from a random sample yielded significant ($p=0.01404$) results between male, female and the sacroccocygeal fusion, but no overall significant differences in age. There is also a significant ($p=0.0001935$) relationship between sacroccocygeal fusion and the number of coccyx elements fused. We did not find any significance between age cohorts; this could be due to the small sample size that was

utilized for the preliminary analysis. The final goal of this study is to include more females, as well as individuals from different age cohorts, to analyze if age is also a contributing factor to sacroccocygeal fusion.

Age-at-death estimation from features of the first rib

ELLEN DOOLEY and SEAN D. TALLMAN

Forensic Anthropology, Boston University School of Medicine

Several techniques for estimating adult age-at-death are used in biological and forensic anthropology, including morphological changes of the ribs. However, due to human variation and taphonomic damage, it remains difficult to produce accurate and meaningful age-at-death estimations based on skeletal remains. This research further explores morphological changes to the first rib, which is easily identifiable and relatively robust, including the costal face and tubercle facet identified by Kunos' (1999) and modified by DiGangi et al. (2009). A total of 400 European American individuals ($f=200$; $m=200$) from the William M. Bass Donated Skeletal Collection at the University of Tennessee, Knoxville, were observed using modified descriptions for Kunos' (1999) five traits of the costal face and tubercle facet on an ordinal scale of 1-8. Additionally, bone quality was assessed on an ordinal scale of 1-3 and was incorporated as a variable in order to improve estimations. Spearman's correlation coefficients demonstrate that all eleven traits correlate with age at a statistically significant level, with bone quality being the most significant feature, and the tubercle facet surface topography being the least significant feature for both sexes. Further, female and male differences were found, and cross-validated ordinal logistic regression equations are presented for females, males, and pooled sex. The results of this research underscore the importance of developing age estimation methods on skeletal regions that are under researched and for those that are more resistant to taphonomic damage.

Funding for this project was provided by the program in Forensic Anthropology at the Boston University School of Medicine.

Using remote sensing and machine learning to reconstruct paleoenvironmental features in the Koobi Fora Formation

ELIZABETH R. DORANS¹, JOÃO D'OLIVEIRA COELHO^{2,3}, ROBERT L. ANEMONE⁴, RENÉ BOBE^{2,5,6}, SUSANA CARVALHO^{2,3,5,6}, FRANCES FORREST⁷ and DAVID R. BRAUN⁸

¹Biological Sciences, Vanderbilt University, USA, ²Primate Models for Behavioural Evolution Lab, Institute of Cognitive & Evolutionary Anthropology, University of Oxford, Oxford, UK, ³Centre for

ABSTRACTS

Functional Ecology, Universidade de Coimbra, Coimbra, Portugal, ⁴Department of Anthropology, University of North Carolina Greensboro, USA, ⁵Interdisciplinary Center for Archaeology and Evolution of Human Behaviour (ICAREHB), Universidade do Algarve, Portugal, ⁶Gorongosa National Park, Sofala, Mozambique, ⁷Sackler Educational Laboratory for Comparative Genomics and Human Origins, American Museum of Natural History, USA, ⁸Center for the Advanced Study of Human Paleobiology, Department of Anthropology, George Washington University, USA

Advances in Geographic Information Systems and Remote Sensing technologies have the potential to revolutionize archaeological and paleontological fieldwork. Machine learning models have been effective in identifying conditions ideal for preservation, exposure, and discovery of fossils in a range of geographic contexts. Researchers working in the Koobi Fora Formation of northern Kenya have long inquired about the geographic patterning of extinct fauna and their respective paleoenvironments. This project is the first attempt to use machine learning techniques to capture paleoecological patterns utilizing topographical and spectral variables that may be predictive of the input of aquatic components in the paleoenvironments of the Koobi Fora Formation. LANDSAT and SRTM images were used to obtain spectral and topographical variables of interest. We carried out fossil surveys to measure the relative abundance of aquatic fauna within specific points of interest that corresponded to 30x30 m pixels in the satellite data. These faunal input data were used to construct a beta regression model predicting percent aquatic faunal input based on spectral and topographic data. A prediction test for all observations using a LOOCV architecture yielded mean and median errors of 14.7% and 12%, respectively. The high predictive power of data from satellite imagery supports the application of machine learning techniques to enhance traditional fieldwork methods in the exploration of fossil localities. The preliminary results of this study encourage future extensions of these methods to address other research questions, such as the use of faunal abundance data to predict the distribution of more specific paleoenvironments.

This research was supported by: Koobi Fora Research and Training Program, funded by NSF Archaeology Program #1624398 and REU #1930719; FCT (SFRH/BD/122306/2016); and The Boise Trust Fund.

Archery's Lasting Mark: A Biomechanical Analysis of Archery

TABITHA DORSHORST¹, JOSEPH HAMILL², GILLIAN WEIR² and BRIGITTE HOLT¹

¹Anthropology, University of Massachusetts Amherst, ²Kinesiology, University of Massachusetts Amherst

The physical demands of archery involve strenuous movements that place repetitive mechanical loads on the upper body. Given that bone remodels in response to mechanical loading, it is reasonable to assume that repetitive bow and arrow use impacts upper limb bone morphology in predictable ways. The introduction and increased use of archery in subsistence hunting have been suggested to impact bilateral humeral asymmetry. This claim, however, has yet to be tested *in vivo*. This project uses kinematic and electromyographic approaches to validate claims 1) that archery places mechanical loading on the bow, or non-dominant, arm resulting in lowered asymmetry, and 2) mechanical loads in the draw, or dominant, arm are in the anterior-posterior direction while those in the bow arm are in the medial-lateral direction.

Results of EMG analysis show that some muscles (i.e. Pectoralis major and posterior Deltoid) act symmetrically on both humeri, while most muscle groups (i.e. Biceps brachii, Triceps brachii, Deltoid (lateral), and Latissimus dorsi) are activated asymmetrically on the humerus. Overall, asymmetrically acting muscle groups acting on separate arms result in similar overall directional bending. The large activation of the Triceps on the bow arm suggests more anterior-posterior directional bending, similar to the draw arm. Repeated bow use would undoubtedly induce humeral modification consistent with increased non-dominant arm robusticity, which in turn would lower asymmetry. Findings from this project thus support the hypothesis that the adoption of the bow and arrow results in decreased humeral asymmetry, but does not support morphological claims regarding the non-dominant arm.

Testing the Relationship between Histological Integrity and Protein Content in Diagenesis Using Adult and Immature Bones

KATHLEEN I. DOWNEY

Anthropology, The Ohio State University

Adult and immature bones were compared across two parameters of diagenesis: histological integrity and protein content. Increased porosity caused by microscopical focal destruction within the microstructure is a factor affecting the histological integrity of bone removed from an archaeological context. Porosity is thought to have an effect on the loss of the organic matrix, which includes the protein content mostly composed of collagen. Immature bones are naturally more porous than adult bones, and this was utilized to test the relationship between the two diagenetic parameters to simulate an overall difference in porosity. Bones were observed macroscopically and microscopically with thin sections. Statistical tests on the examinations of surface preservation, periosteal/endosteal line persistence, and the

Oxford Histological Index (OHI) were some of the features used to analyze this relationship. A new method of scoring, the birefringence scale, was developed for this research in order to estimate the percentage of birefringence still observed in the histological sample compared to the total expected from a fresh, modern bone. The results of this study found no significant difference in the preservation of the microstructure between adult and immature bones. However, between the adult and immature bone samples some significant difference in the retention of collagen between the two groups was found. Statistical analyses also found that surface preservation is a poor approximation of histological integrity. These results provide a better understanding of the interaction between histological integrity and protein content, as well as further our overall understanding of diagenesis as a process.

Grit or Groundstone? Dental microwear texture analysis of the Neolithic-Copper Age & Copper Age-Bronze Age transitions in prehistoric Croatia

JESSICA L. DROKE¹, JAMES C.M. AHERN^{1,2}, IVOR JANKOVIĆ^{1,2} and MARIO NOVAK²

¹Anthropology, University of Wyoming, ²Centre for Applied Bioanthropology, Institute for Anthropological Research, Zagreb

The chronological transitions from the Neolithic to the Copper Age and later Bronze Age in Croatia are marked by a steady intensification in the farming of domesticates as well as improvements in food processing technology. An effective way to examine these chronological shifts in both food and lifeways is through the examination of diet by dental wear. Dental microwear texture analysis (DMTA) was conducted according to standard procedures on high-resolution dental replicas from 3 sites: Neolithic Beli Manastir (n=13), Copper Age Potočani (n=37), and Bronze Age Bezdanjača (n=17). Three textural variables were included: complexity (*Asfc*), anisotropy (*epLsar*), and textural fill volume (*Tfv*). Independent sample t-tests were used to compare each of the three variables for the Neolithic-Copper Age and Copper-Age-Bronze Age transitions. For both transitions, the only significant variable is *Asfc* (p=0.036 and p<0.001). A further examination of group mean values indicates a continual drop chronologically from the Neolithic ($\bar{x} \pm 2.76$) to the Copper Age ($\bar{x} \pm 2.31$) and then to the Bronze Age ($\bar{x} \pm 1.53$). Since *Asfc* is an indicator of dietary hardness, consistently lower values show a softening of the diet through time. There are three key ways to interpret this shift: 1) as a result of purely dietary composition, 2) as a function of higher quality processing technology, or 3) as a combination of the two. We suggest that the

ABSTRACTS

third option is the most likely, while emphasizing the interaction and reflexive relationship between agricultural intensification and technological innovation.

Funding was received from the George C. Frison Institute of Archaeology & Anthropology, University of Wyoming Center for Global Studies, and partially funded by Croatian Scientific Fund grant HRZZ IP-2016-06-1450

Rhodes has fallen, but academia's ivory tower still stands: The impact of Rhodes Must Fall in archaeology and anthropology

LORIT A. DROR¹ and MICHAEL B.C. RIVERA^{2,3}

¹Anthropology, University College London,

²Archaeology, University of Cambridge,

³Archaeology & Anthropology, The Arch and Anth Podcast

Five years after the initial Rhodes Must Fall (RMF) protest movement have passed, and this paper considers the legacy of this campaign in decolonizing anthropology, archaeology and universities worldwide.

Beginning in March 2015, RMF was a protest movement campaigning for the removal of a statue of British colonialist Cecil Rhodes at the University of Cape Town, South Africa. The movement grew to include issues of decolonization in universities around the country and, ultimately, the world. News, books and journal publications have been reviewed and information was collated on decolonizing movements in the anthropological and archaeological disciplines, and academia more broadly. In the United States, there is a severe underrepresentation of black doctorate holders in biological anthropology. The situation is similar in the United Kingdom and western Europe, where under-recruitment and lack of retention of black and other minority academics remain major issues. As a discipline, anthropology has its roots in the colonial mission Rhodes was so integral in. Our academic forebears' legacies continue to dehumanize and alienate members of our institutions and societies, and we have yet to correct this heinous situation.

We argue that members of the AAPA, and anthropologists at large, should put real effort into effecting systemic culture change. We recommend being mindful of the language used in academic spaces, reframing evolutionary narratives, and strategizing on how to nurture diversity in representation. Greater freedom to think using one's diversity in experience (i.e., not stifled by colonial attitudes) will stimulate a more ethical and historically conscientious science.

Cranial evidences of violence in ancient societies from northwestern Argentina

HILTON D. DRUBE^{1,2}, SUSANA E. MARTÁNEZ¹, ELINA A. SILVERA¹, JOSÉ LOBO-GÓMEZ¹ and AGUSTÁN TOGO²

¹Facultad de Ciencias Exactas y Naturales, Universidad Nacional de Catamarca, ²Facultad de Ciencias Médicas, Universidad Nacional de Santiago del Estero

Violence has been universally defined as the deliberate use of physical force against individuals, a group of persons or against oneself, with the consequences of injury and even death on the afflicted people. Several studies have studied violence in past societies through the analysis of lesions caused by injuries on the skeleton. Such evidences include changes in the skeletal structures that imply perimortem fractures, injuries caused by different weapons, dislocation and avulsion lesions, among others. The aim of this paper is to examine markers of trauma probably caused by interpersonal violence in a sample of 59 skeletons exhumated from archaeological sites corresponding to the times of contact in the Chaco-Santiaguina plains in northwestern Argentina. Standard methods for determining age and sex were employed. Skeletal remains were examined for pathological lesions, focusing particularly on alterations caused by traumas on the cranium. Infracranial traumas were not included in this report. A significant presence of perimortem fractures as well as blunt cuts on the cranial vault are observed. Three cases of healed nasal fractures are also reported. The Chaco-Santiaguina plains in northwestern Argentina were characterized by conspicuous displacements of people both from the Andes mountains as well as from the eastern lowlands at the time of the arrival of Europeans in the region. This situation had generated conflicts that were increased by the presence of the Spaniards. These cases of cranial evidences of violence may reflect the social tensions and conflicts described by the early chronicles of the Spaniards in this particular area.

Funding support provided by FACEN-UNCa, FCM-UNSE and FHCSyS-UNSE.

"Gargle and Twargle" Vocalizations in *Cebus capucinus* to Assess Infanticide Risk

ALEXA DUCHESNEAU¹, DANIEL G. EDELBERG² and SUSAN E. PERRY³

¹Department of Anthropology, Yale University,

²Department of Mathematics, Yale University,

³Department of Anthropology, University of California at Los Angeles

Zahavi's "Bond Testing Hypothesis" (1977) states that irritating stimuli are used to elicit honest information from a social partner regarding the relationship. *C. capucinus* are known to use irritating stimuli to acquire social bond information

and may use two unexplained elements of their vocal repertoire, the "gargle" and the "twargle" (loud, raspy, broad-band close-range vocalizations), similarly. We hypothesized that gargles and twargles are stimuli used to assess the sentiments of the target toward the vocalizer. The greatest threat to *C. capucinus* infant survival, and hence to adult female reproductive success, is infanticide perpetrated by alpha males. Thus, we predicted that infants, pregnant females and females with infants would gargle/twargle at higher rates than subsets of/the entire population, and that their gargles/twargles would primarily be directed to the alpha male. Over 16 years, researchers collected gargle/twargle data via ~10-minute focal follows in 10 habituated groups in Lomas Barbudal, Costa Rica. Using chi-squared tests we found that, consistent with the "infanticide risk assessment" hypothesis, infants (< 8 months) vocalized at higher rates than the general population ($p < 0.01$). Pregnant females and females who gave birth within the last 24 months vocalized at higher rates than the adult baseline rate (≥ 60 months), ($p < 0.01$). Furthermore, individuals primarily gargled/twargled to the alpha male (both $p < 0.01$); however, there was no significant difference in rates towards sires (confirmed or presumed) versus non-sires ($p > 0.05$).

MPI-EVAN, UCLA and grants to S. Perry: NSF (1638428, 0613226, 848360), National Geographic Society (7968-06, 8671-09, 20113909, 9795-15, 45176R-18), Templeton World Charity Foundation (0208), WCF, and 5 Leakey Foundation grants

Impact of environmental tobacco smoke on immune function in urban Missouri children with elevated blood lead levels

MEGAN E. DUNCANSON¹, RACHEL E. NEAL², LINDSEY A. WOOD³, BETHANY JOHNSON², BLAKE MANION², TERRY J. WILSON⁴ and PAULA M. LUTZ^{4,5}

¹Anthropology, University of Louisville,

²Environmental and Occupational Health Sciences, University of Louisville, ³Epidemiology and Population Health, University of Louisville,

⁴Biological Sciences, Missouri University of Science and Technology, ⁵Zoology and Physiology, University of Wyoming

Lead (Pb) and environmental tobacco smoke exposure (ETS) constitute two of the most common environmental developmental toxins. Cigarettes contain heavy metals including Pb; thus, ETS exposure may be linked to increased blood lead (PbB) levels. Elevated PbB levels in children are linked to immunological, behavioral, and cognitive deficits. Children under 6 years of age are more susceptible to the effects of Pb, especially children between 12-24 months who also exhibit oral exploratory behavior resulting in higher environmental Pb exposure. In a limited number of studies focusing on children, an association of elevated PbB levels with altered immune system function has been reported, and the effects on immune function may be age-dependent. The

ABSTRACTS

current study examined the effect of elevated PbB levels in the presence/absence of ETS (Pb+ETS, Pb-only, ETS-only), on immune system function in a cohort of 523 children (aged 5 months to 12 years) from two urban centers of Missouri (St. Louis and Springfield). A blood sample was taken and PbB levels were determined by graphite furnace atomic absorption spectrophotometry. The average PbB level was 12.9 µg/dL. Cell counts, IgE levels, and sCD25+ concentrations were analyzed. The statistically significant correlation of IgE and PbB, as well as the differences in IgE between PbB risk classes reported in our earlier studies are confirmed in the complete cohort. Certain immune parameters were found to be associated with age as well. We interpret the current findings as potentially indicative of generalized Pb-exposure induced increase in lymphocyte activation of both T-cell and B-cells.

This work was supported by the National Institutes of Health [R01 ES06065, R21 DA027466, P30 ES014443, P20 RR017702, and P20 GM103453].

Holocene size reduction in Aboriginal Australians: the mandibular evidence from Roonka

ARTHUR C. DURBAND¹, ETHAN C. HILL² and KERYN WALSH³

¹Sociology, Anthropology & Social Work, Texas Tech University, ²Department of Anthropology, University of New Mexico, ³Department of Anthropology, Science Centre, South Australian Museum

Trends in the reduction of size and robusticity of the cranium have been recorded in a variety of human populations in different regions. Similar trends have been documented in Australia, with some evidence suggesting that the most significant changes occurred 10,000-7,000 years BP. Skeletal collections spanning this time range in Australia are relatively rare, so it has been difficult to analyze this transition in detail.

The site of Roonka, located along the Murray River 8 km North of Blanchetown, has yielded over 200 skeletons from excavations conducted between 1968-1977. Dating from this site suggests that it was occupied as early as 18,000 years BP, and burials date between ~8,000 years BP and the time of European contact in South Australia. While the skeletal material recovered during the excavation was extensive, most of the crania were poorly reconstructed using molding wax and thus unsuitable for metric analysis. The mandibles from this site have not received much attention, and preservation is generally better than the crania. This element can provide an opportunity to examine size reduction in Australia during the early Holocene.

This project documents changes in mandibular size and shape using a sample of 206 mandibles that range in age from ~19,000 years BP up

to European contact, including 43 complete or nearly complete mandibles from Roonka. These analyses demonstrate evidence of temporal size reduction between the older Roonka II and younger Roonka III individuals. Implications of these results for the evolution of modern Australians will be discussed.

This work was supported by the Australian-American Fulbright Commission.

Bites and chews in two sympatric lemur species in southwestern Madagascar

MARIANA DUTRA FOGAÇA¹, NINA C. FLOWERS¹ and NAYUTA YAMASHITA^{1,2}

¹Institute of Population Genetics, University of Veterinary Medicine, Vienna, ²Austrian Academy of Sciences

Jaw form has been related to loads incurred during feeding, which are determined by oral processing behaviors. In this study, we examine how foods that differ in geometry and mechanical properties affect biting and chewing in two lemur species that are sympatric in the dry forest site of Beza Mahafaly special reserve in southwestern Madagascar.

We conducted all-day focal animal follows of *Lemur catta* (Lc) and *Propithecus verreauxi* (Pv) in the dry season months of May-July. During observations, we took detailed data on feeding behaviors including pre-oral processing, ingestion location, and food intake. Foods were later collected and tested for toughness and elastic modulus in a field laboratory. Bites and chews were quantified from videos shot concurrently with observations. For this analysis, we focused on two foods that were eaten by both species, tamarind (*kily*) fruit and *mamyaho* leaves.

Lc and Pv spends 33% and 0.88% of total feeding time, respectively, on old *kily* fruit and 19% and 2% on *mamyaho* leaves. Preliminary analysis shows differences in ingestive behaviors for both species. Lc, on average, has higher chew numbers than Pv when consuming leaves, but the opposite pattern occurs for *kily* fruit. While bite numbers and chewing rates are similar across all categories, biting rates differ by food. Pv takes longer to feed on *kily* based on average sequence time. Our results show that bites and chews vary by lemur species and by food type, suggesting differences in processing related to overall food properties.

Funded by the Austrian Science Fund (FWF)

Variation in Cranial Variance: Patterns of variation in a diverse American population

ISIS DWYER¹, JOSEPH T. HEFNER² and M. KATE SPRADLEY³

¹Anthropology, University of Florida, ²Anthropology, Michigan State University, ³Anthropology, Texas State University

The socially constructed racial categories of American Black and American White represent two morphologically distinct groups within the overall distribution of human variation. As a result, both categories represent different models of migration and magnitudes of morphological and genetic diversity. This study employs a 3D landmark geometric morphometric approach and an evaluation of macromorphoscopic cranial traits to estimate the magnitude and pattern of cranial variation within samples of early 20th century Americans. This study includes 245 crania from individuals of documented American Black (N=122) and American White (N=123) descent from the Hamann-Todd Human Osteological Collection.

Thirty-five fixed three-dimensional landmarks were collected using a MicroScribe, and fifteen macromorphoscopic traits were collected using the Macromorphoscopic Software. Landmark data was adjusted using a generalized Procrustes superimposition, analyzed via PCA, with variance quantified by the sum of eigenvalues (SEV). Macromorphoscopic data was analyzed via PCA on correlation matrices, with variance quantified by the Pearson product moment correlation. Despite differences in perceived diversity of both samples based on their ancestral history, both display similar magnitudes of variation. However, each sample exhibits a distinct pattern of both landmark and macromorphoscopic variance. The results imply that unique patterns of variation may exist within morphologically distinct groups, beyond the broad macromorphoscopic variance across a diverse population often used to estimate ancestry. Further research will explore other morphologically distinct groups along the spectrum of human variance to uncover previously undocumented signatures of variation.

Assessing Hominid Femoral Variation Using Diffeomorphic Surface Matching

LESLEY H. EASON and LUCYNA A. BOWLAND
Anthropology, University of Arkansas

Due to the integral nature of the hip and thigh in bipedal locomotion, functional interpretations abound with regard to morphological variation among hominin fossil femora. While it is well known that fossil femora vary in size and shape, the degree to which variation is functionally significant is often debated. To assess significance of variation, modern studies employ three-dimensional geometric morphometrics (3D GM) to capture and compare the pattern and magnitude of shape variation. Studies using 3D GM can discriminate some species but often fail to discriminate congeneric species. To address this problem, the current study compares the discriminatory power of 3D GM to that of diffeomorphic surface matching (DSM). DSM allows for non-landmark assessment of shape deformation

ABSTRACTS

that also captures details of homologous and non-homologous features. In contrast, 3D GM cannot compare discrete traits such as the presence versus absence of a fovea capitis or gluteal tuberosity. This study tests the discriminatory power of 3D GM versus DSM using 3D surface models of hominid proximal femora. Samples include *Gorilla* (*G. gorilla* [n=15] and *G. beringei* [n=18]), *Pan* (*P. paniscus* [n=18] and *P. troglodytes* [n=39]), *Pongo pygmaeus* (n=15), and modern humans (n=37). Results demonstrate that DSM is better at discriminating congeneric hominid taxa, especially with regard to *Gorilla* species. If significant shape variation exists among hominin fossil femora, then the pattern of variation may resemble that of apes in this analysis. Future DSM analyses will incorporate additional catarrhine taxa, as well as hominin fossil femora.

Confirmation of dynamic adaptive evolutionary changes in normal human body size over time on the island of Flores, Indonesia.

ROBERT B. ECKHARDT¹ and MACIEJ HENNEBERG^{1,2}

¹Kinesiology, Pennsylvania State University, ²Biological Anthropology and Comparative Anatomy, Adelaide Medical School

Diniz-Filho, et al. (2019) revisited the adaptive evolution of body size in the human population of Flores, a topic previously addressed in detail by our group (Jacob, et al., 2006). Most earlier discussions of the skeletal material from Liang Bua Cave, Flores, focused on stature. The initial incorrect estimate of 1.06 m for LB1, was revised upward to correct for its developmental abnormality (Eckhardt, et al., 2014; Henneberg, et al., 2014). Diniz-Filho focus on body mass, a trait of salient ecological significance. Our new estimates, based on corrected LB1 stature, range from 19 kg to 31 kg. The Diniz-Filho simulation posits reduction from 45-55 kg to 25-30 kg over 2,250-10,125 years. However, earliest known (~700 ka) hominin gnathic remains from Mata Menge, Flores, are smaller than those of LB1/LB6 and similar in size to those from Luzon, Philippines (Détroit et al. 2019). Thus, if anything, there probably has been intermittent hominin size increase on Flores. Extant Flores inhabitants (Rampasasa) weigh on average 40-45 kg. Though their ancestors were on the island >10 ka ago their size did not necessarily reduce. Agreeing with us on non-isolation, Diniz-Filho postulate repeated rounds of immigration to and even recolonization of Flores over time. Regardless of non-linear trends in body size indicated by the skeletal size differences over time, plausible demographic components of both models render speciation highly improbable, and call into question attribution of Flores hominin remains to *Homo erectus* or "*Homo floresiensis*" rather than the small-bodied *Homo sapiens* still represented by current inhabitants.

Cumulative stressful events predict disease and mortality risk in gorillas

ASHLEY N. EDES

Center for Species Survival, Smithsonian Conservation Biology Institute

Over time, repeated stressful experiences can impair physiological function, increasing risk of poor health outcomes. Studies of cumulative stressors in nonhuman primates are infrequent, although recently cumulative early life adversity was shown to predict longevity in baboons. Herein, the relationship between cumulative stressful experiences and health risk in western lowland gorillas was explored. Data were collected from 63 zoo-housed gorillas (aged 6-52 years). Stressful events ($\chi=65.2$, $SD=47.4$, $range=2-233$) were defined as illnesses, immobilizations, zoo transfers, agonistic interactions with wounding, and pregnancies. Age ($\beta=1.743$, $SE=0.422$, $p=0.0001$) but not sex ($t=-0.559$, $df=61$, $p=0.578$) was significantly associated with cumulative stressful events. Risk of all-cause morbidity, cardiac disease, and mortality was analyzed using generalized linear models (GLMs) with binomial distribution and logit link; models including age and/or sex as random effects were also tested and the best fit determined using Akaike's Information Criterion (AIC). Stressful events ($\beta=0.026$, $SE=0.011$, $p=0.018$), age ($\beta=0.123$, $SE=0.041$, $p=0.003$), and sex ($\beta=2.435$, $SE=0.805$, $p=0.002$) best predicted all-cause morbidity. The primary predictor of cardiac disease was sex ($\beta=2.083$, $SE=0.618$, $p=0.0007$), but stressful events approached significance ($\beta=0.012$, $SE=0.006$, $p=0.060$) and were retained in the best fit model. Age ($\beta=0.068$, $SE=0.026$, $p=0.009$) and stressful events ($\beta=-0.002$, $SE=0.007$, $p=0.811$) best predicted mortality risk, the latter not significant but retained within the best fit model. These results further demonstrate stressful experiences have lasting effects on health. An important next step is exploring how variables such as social connectedness, early life, and behavior moderate the relationship between cumulative stressors and health outcomes.

Pathological Conditions of Subadults from the Neo Punic site of Zita, Tunisia

STACY EDINGTON¹, JESSICA I. CERESO-ROMÁN¹, GLENYS MCGOWAN², BRETT KAUFMAN³, HANS BARNARD⁴ and ALI DRINE⁵

¹Department of Anthropology, University of Oklahoma, ²School of Social Science, University of Queensland, ³Department of Classics, University of Illinois at Urbana-Champaign, ⁴Department of Near Eastern Languages and Cultures, University of California, Los Angeles, ⁵Department of Archaeology, Institut National du Patrimoine Tunisie

A *Tophet* is an urnfield with Phoenician and Punic burials that have historically been identified as a location for ritual infant sacrifice and burial. Our

research of the *tophet* site Zita near Zarzis, Tunisia dating from ~100 BCE to 50/100 CE challenges this common interpretation. Excavations in 2013-2014 recovered two dozen urns, ten of which were bioarchaeologically analyzed yielding nine individuals ranging from 4.5 months to 7.5 years old at the time of death. Data collected for the individuals at Zita include inventory of remains, pathological analysis, as well as analysis on the thermal alterations for each of the individuals. The individuals displayed pathologies such as extensive periosteal reactions, porotic hyperostosis, among others. Here we explore what diseases could be associated with the various individuals in an effort to produce a clinical diagnostic and interpret the social implications of these diseases. Preliminary results suggest that these individuals perished at different stages of healing, while the high frequency of pathology suggests systemic problems within the group and a high infant mortality not necessarily associated with infanticide or ritual sacrifice.

A 3D geometric morphometric assessment of the ASUDAS: Incisor Shoveling

DANIEL E. EHRLICH¹, SETH M. WEINBERG², MARY L. MARAZITA² and STEVEN F. MILLER^{1,3}

¹College of Graduate Studies, Midwestern University, ²School of Dental Medicine, University of Pittsburgh, ³College of Dental Medicine-Illinois, Midwestern University

The Arizona State University Dental Anthropology System (ASUDAS) consists of reference plaques, and written descriptions to aid in scoring dental non metric traits (NMT). This study focuses on one NMT, incisor shoveling, which the ASUDAS defines on a 7 grade scale. While 7 grades creates a smooth gradient of expression it also results in smaller between-grade differences, thereby increasing inter-/intra-observer error.

This study takes an empirical approach, applying geometric morphometrics (GM) to evaluate how well the ASUDAS descriptions correspond to human variation. We used 3D scans of dental casts (n=216) from 6 populations, representing 4 distinct geographic regions, in order to capture a wide degree of variation. We score incisor shoveling by ASUDAS standards and subsequently apply a semi-landmark patch (n=100) to quantify incisal form.

Following Procrustes superimposition with semi-landmark sliding, we explored morphological shape space using Principal Components Analysis and Canonical Variate Analysis. PCs 2 and 3 (13% and 12% variation) relate directly to marginal ridge projection and lingual fossa depth, i.e. shoveling. Despite some overlap, ASUDAS grades are distributed fairly uniformly and linearly across shape space. CVA found significant differences ($p < .05$) between some (though not all) of the 7 grades expression. Collapsing grades from

ABSTRACTS

7 to as few as 3 increased the explanatory power of CV1 (32.3% to 72.6%) and produced significant differences ($p < .05$) between remaining grades of expression. Our study highlights the utility of the ASUDAS grades for describing relative incisor shoveling, and also the need to reduce grades before analysis.

Testing for paternal influences on offspring telomere length in a human cohort in the Philippines

DAN T.A. EISENBERG^{1,2}, PETER H. REJ¹, PAULITA DUAZO³, DELIA CARBA³, M. GEOFFREY HAYES^{4,5,6} and CHRISTOPHER W. KUZAWA^{6,7}

¹Department of Anthropology, University of Washington, ²Center for Studies in Demography and Ecology, University of Washington, ³USC-Office of Population Studies Foundation, Inc., University of San Carlos, Cebu City, Philippines, ⁴Division of Endocrinology, Metabolism and Molecular Medicine, Department of Medicine, Northwestern University Feinberg School of Medicine, ⁵Center for Genetic Medicine, Northwestern University Feinberg School of Medicine, ⁶Department of Anthropology, Northwestern University, ⁷Institute for Policy Research, Northwestern University

Telomeres are comprised of DNA repeats located at chromosomal ends that shorten with cellular replication and with age in most human tissues, and thus are biomarkers of aging. In contrast, spermatocyte telomeres lengthen with age. These changes in telomere length (TL) appear to be heritable, as older paternal ages of conception (PAC) predict longer offspring TL. Mouse studies suggest that paternal factors like smoking, inflammation and DNA damage can influence sperm TL and thus offspring TL, pointing to possible heritable genetic effects of paternal experience. Here, we test whether similar human paternal environmental experiences predict offspring TL as well as the pace of age-related change in TL with PAC. Using data from metropolitan Cebu, the Philippines, we tested if smoking, psychosocial stressors, and/or shorter knee height (a measure of early life adversity) predicted shorter offspring TL. We also tested if these variables modified the PAC-related increase in offspring TL. While we did not find the predicted associations, we observed a trend towards fathers with shorter knee height having offspring with longer TL, and a significant interaction between knee height and PAC in predicting offspring TL. Specifically, offspring of fathers with shorter knee heights experienced a stronger positive effect of PAC on their TL. While the reasons for these associations remain uncertain, shorter knee height is characteristic of earlier puberty. Since spermatocyte TL increases with

sperm production, we speculate that individuals with earlier puberty, who therefore experienced an earlier onset of sperm production, had more time to accumulate longer sperm telomeres.

Funding from NSF (BCS-1519110 and BCS-0962282), the Wenner-Gren Foundation (Gr. 8111), and NIH (TW05596, DK078150, RR20649, ES10126, and DK056350).

The bioanthropological role in investigations of genocide

LUCIA M.M.K. ELGERUD

Anthropology, University of Tennessee Knoxville

Biological anthropology's role in investigations of human rights violations and mass atrocities has been evolving since the 1980s yet guidelines are lacking as to the types of data that should be collected and for what outcome. One of the main goals of these investigations is to support the trials of mass atrocity perpetrators, amongst other important post-conflict concerns. However, human rights violations, war crimes, and genocide are often conflated even though each crime carries different legal underpinnings. Similarly, there are few parameters to guide the biological anthropologist as to the type of data that should be collected in order to serve as evidence of these different types of crimes. Neither are there sufficient guidelines for the type of bioanthropological data that can be indicative of the two constituent features of genocide: the physical act and the requisite intent to destroy a group. This study – building upon the work by Komar (2008) and Munoz & Congram (2016) amongst others – seeks to understand the contributions that biological anthropology can make to investigations of genocide specifically by (1) reviewing convicted cases of genocide that have been supported by anthropological data and (2) providing a list of the types of bioanthropological data that should be collected within this particular type of mass atrocity context. As such, this study examines the bioanthropological role in investigations of genocide and serves as a starting point for future work examining the role of biological anthropology in a variety of mass atrocity scenarios.

What does it mean to be urban? Assessing craniodental impacts of anthropogenic environments

ANDREA R. ELLER¹, RITA M. AUSTIN^{1,2,3}, STEPHANIE CANINGTON^{1,4}, COURTNEY A. HOFMAN^{2,3} and SABRINA B. SHOLTS¹

¹Anthropology, Smithsonian Institution's National Museum of Natural History, ²Anthropology, University of Oklahoma, ³Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, ⁴Center for Functional Anatomy and Evolution, Johns Hopkins University

Urban environments can be defined by a few uniform characteristics, largely independent of time and climate. These characteristics include

flat substrates, caloric surpluses, and increased pathogen exposure; thus, heavily anthropogenic environments can exert unique pressures on permanent residents. The EMPHASIS project, an ongoing survey of the National Museum of Natural History (NMNH) skeletal collections, investigates the impacts of anthropogenic environments on humans and nonhuman primates. Here, we report data on the occurrence and severity of skeletal pathology and dental calculus from a survey of human crania ($n=1586$) from 13 locales across four countries (Egypt, Mongolia, Peru, and Switzerland). To investigate health impacts of urbanity across populations, we devised a scoring system to differentiate rural and urban populations among cranial collections at NMNH. Using geographic and archaeological information we categorized locales based on residents' likely lifetime exposure to humanmade structures and nonfamilial relatives, alongside general outlines of diet and class status. Skeletal pathologies were visually assessed for general characteristics, location, and severity on a 3-point scale; dental calculus was assessed for tooth location and abundance on a 4-point scale. Our preliminary results indicate bony pathologies in 52.5% of rural and only 12.1% of urban individuals while dental calculus was observed in 39.4% of rural and 42.6% of urban individuals. Pearson's chi-square tests indicate a significant correlation between skeletal pathologies and environment ($p < 0.005$; $a=0.05$, $df=1$), but not dental calculus ($p > 0.10$; $a=0.05$, $df=1$). These findings suggest there is utility to this approach for better understanding and operationalizing urbanity in human evolutionary studies.

Test of high-frequency GPR for identifying hominin skeletal deposits in the Rising Star Cave

MARINA C. ELLIOTT¹, BECCA PEIXOTTO^{1,2}, COREY JASKOLSKI³, KENNETH BROAD^{3,4}, DIRK VAN ROOYEN¹, MAROPENG RAMALEPA¹, MATHABELA TSIKOANE¹, KERRY W WARREN⁵, JOHN HAWKS^{1,6} and LEE R. BERGER¹

¹Evolutionary Studies Institute, University of the Witwatersrand, ²Centre for the Exploration of the Human Journey, Perot Museum of Nature and Science, ³Visualization lab, Virtual Wonders, ⁴Rosenstiel School of Marine and Atmospheric Science and Abess Centre, University of Miami, ⁵Human Evolution Research Institute, University of Cape Town, ⁶Department of Anthropology, University of Wisconsin-Madison

Ground Penetrating Radar (GPR) has been used extensively in archaeology to detect subsurface structures, including burials, for almost 30 years. However, standard GPR equipment is limited for some applications by the large size of the equipment, deep penetration depths and the inability to visualize small targets. Recently, small, high-frequency GPR units have been developed that offer better penetration and higher resolution in

ABSTRACTS

confined spaces and at shallow depths. To test whether we could use this technology to identify hominin skeletal deposits or other subsurface anomalies in the Rising Star cave, we scanned sections of the floor with a GSSI SIR 4000 GPR system with 2000MHz Palm antenna. We scanned a total of 12m² in the Dinaledi Subsystem and 2m² in the Lesedi Chamber. Six anomalous areas were identified and two of the strongest anomalies in the Dinaledi Chamber were selected for excavation. Anomalies in these areas were identified as rocks, which are uncommon in the Dinaledi sediments. Almost no hominin material was recovered from the two units. While the high frequency GPR did not lead to the identification of new hominin deposits, it did recognize subsurface geological anomalies and elucidated variations in fossil density within the cave system. This demonstrates the potential value of high-frequency GPR in cave settings.

The National Geographic Society, Lyda Hill Foundation, University of the Witwatersrand, South African Centre of Excellence in the Palaeosciences, and the South African National Research Foundation.

Genetic relatedness and association patterns among individuals in four groups of wild woolly monkeys in Amazonian Ecuador

KELSEY M. ELLIS^{1,2}, LAURA ABONDANO² and ANTHONY DI FIORE²

¹Department of Anthropology, Miami University, ²Department of Anthropology and Primate Molecular Ecology and Evolution Laboratory, University of Texas at Austin

Atelin primates – spider monkeys (*Ateles*), woolly monkeys (*Lagothrix*), and muriquis (*Brachyteles*) – are typically characterized by a high degree of male philopatry and obligate female dispersal. However, prior work on *Lagothrix* has revealed that some males may disperse from their natal groups and that many adults – males and females alike – live as adults in social groups with at least one close adult relative and often have close relatives in neighboring groups as well, creating a potential for kin-biased affiliative behavior. Using a panel of 12 polymorphic microsatellite loci, we estimated pairwise genetic relatedness among 86 individually-recognized woolly monkeys (*Lagothrix lagotricha poeppigii*) living in four social groups with contiguous or overlapping home ranges at the Tiputini Biodiversity Station in Ecuador, and examined how kinship mapped onto patterns of association among these individuals. Party composition and proximity (<5 m) data were derived from behavioral observations conducted over two four-month periods on all adults and subadults in the four groups during full-day follows. Although adult males had, on average, a greater proportion of close same-sex kin (i.e., parent-offspring, full-siblings, or half-siblings) co-residing in the same group compared to

adult females we found no significant difference in the average relatedness of same-sex dyads (mean male $R = -0.006 \pm 0.167$, mean female $R = -0.006 \pm 0.156$, $P = 0.87$) across the sampled population, suggesting that dispersal is not strongly sex-biased. Furthermore, despite having close kin available, adults did not preferentially associate with their adult relatives, and the strongest associations were among non-related opposite-sex individuals.

Funded by NSF BCS-1540403, the Leakey and Wenner-Gren Foundations, the National Geographic Society/Waite Grants Program, and the University of Texas at Austin

The Eclectic Omnivore's Dilemma: Conflict and Coexistence in an Agricultural Landscape

AMANDA L. ELLWANGER^{1,2} and JOANNA E. LAMBERT³

¹Anthropology, University of Texas at San Antonio, ²Cultural and Behavioral Sciences, Georgia State University Perimeter College, ³Program in Environmental Studies and Department of Ecology and Evolutionary Biology, University of Colorado Boulder

Human-nonhuman primate conflict is common, particularly where livelihoods present opportunities for behaviorally flexible animals to exploit concentrated, nutritionally-rich foods. As eclectic omnivores, baboons are especially capable crop-foragers. In Hemel-en-Aarde Valley, South Africa, people and chacma baboons (*Papio hamadryas ursinus*) share a complex socio-ecological landscape. We evaluate how human attitudes towards baboons are shaped by perceptions of conflict and coexistence. Between September 2015 – April 2017, we conducted interviews with 50 respondents who worked and/or lived in the valley using structured and semi-structured interviews. We used qualitative analyses to classify sentiment toward baboons and open-coding to identify emergent themes in interviews. We conducted pile sorting and multidimensional scaling to examine how respondents perceive baboons relative to other animals, including humans. We identified five main themes including conflict, coexistence, context, community, and nature. Positive sentiments were associated with seeing baboons interacting with each other in "natural" contexts. Respondents expressed pleasure at human-like characteristics observed in baboons, but the underlying association shared by respondents identifies baboons more closely with fynbos animals—not humans. Negative sentiments towards baboons were associated destructive and aggressive behaviors, which were perceived as lacking respect for human authority. Issues of context were particularly important in influencing respondent sentiment; baboon were not welcome in farms and other human areas but were often admired when in nature or in the mountains. Eclectic omnivory has made baboons

very successful but farmers view this behavior as intentional and wasteful. A perceived similarity of baboons to humans renders it problematic when baboons behave like animals.

This research was funded in part by awards from the National Science Foundation (Doctoral Dissertation Research Improvement Grant #1455675), University of Texas at San Antonio, and the Society of Ethnobiology.

Behavioral adaptation to seasonal day length variation by chacma baboons (*Papio hamadryas ursinus*) at the southern-most edge of their range

NICHOLAS W. ELLWANGER^{1,2} and THAD Q. BARTLETT¹

¹Department of Anthropology, University of Texas at San Antonio, ²Department of Geography and Anthropology, Kennesaw State University

Time is a constraining variable on the daily activity patterns of non-human primates. In temperate habitats, non-human primates experience a winter day length bottleneck that restricts the number of hours available to complete all self-maintenance and social behaviors. We investigated how chacma baboons (*Papio hamadryas ursinus*) alter patterns of time allocation across an annual cycle at the southern-most extent of the species' range (latitude= S 33° 22' 22"). Across 10 months, we calculated daily time spent in core behaviors (feeding/foraging, resting, grooming, and traveling) by all adult individuals using 10-minute continuous focal animal sampling. Because of high seasonal variance in day length (range=4.6 hours), we quantified activity budgets as total hours/day instead of percentages. There was no significant correlation between day length and hours spent feeding/foraging ($r = -0.129$, $p < 0.242$). However, there was a significant positive correlation between day length and the number of hours spent resting ($r = 0.628$, $p < 0.001$), socializing ($r = 0.464$, $p < 0.001$), and traveling ($r = 0.547$, $p < 0.001$) per day. The data suggest that day length acts as an important constraint on chacma baboon activity patterns in this high latitude temperate environment. During winter, chacma baboons must significantly reduce the number of hours spent in all non-feeding behaviors to maintain a consistent level of feeding effort across the year. We explore the role seeds from invasive trees—the most common food consumed—play in potentially reducing the plasticity of feeding time for this population and compare these data to patterns of time allocation in other primate populations that occupy habitats in temperate regions.

This research was funded by The Department of Anthropology and Education Abroad Office at The University of Texas at San Antonio

ABSTRACTS

Exploring intraspecific variation in Old World monkeys

SARAH ELTON

Anthropology, Durham University

Dennis Slice worked tirelessly to develop and promote the field of geometric morphometrics (GM). In his memory, I review how GM, including analysis in Morphueus, sheds light on Old World monkey variation, and discuss sampling challenges when relating morphology to ecology. Skull form was quantified in widespread African cercopithecids using 3D coordinates (87 landmarks). Kriging indicated that centroid size variation in *Papio* (106 sampling localities [sl]), *Ptilocolobus* (70 sl), *Chlorocebus aethiops* (128 sl) and *Cercopithecus nictitans-mitis* (91 sl) had common trends (larger in central Africa and smaller in the east). However, patterns and explanations across taxa were not identical. In *C. aethiops* and *Papio*, geography and environment explained some variance in size and shape, but much (~60 - 80%) remained unexplained. In *Ptilocolobus*, geography explained very little variance (~2% for size, ~5% for shape), but with taxonomy explained ~74% (35% of shape). *Cercopithecus nictitans-mitis* size had a strong spatial component (48% explained), but environment contributed less. Diet probably accounts for some unexplained variance but linking high resolution data to provenanced museum specimens is challenging. In *Papio*, a sample of >350 skulls was reduced to 45 with adequate dietary data. Partial least squares indicated significant correlations between skull shape and diet ($RV = 0.3303$, $p < 0.0001$), distinguishing between individuals with diets high in subterrestrial foods versus those with more fruit. Given the ecological flexibility of *Papio* and many other monkeys, more detailed data, sampled across ranges, are required to robustly interrogate the links between form, geography, ecology and behaviour.

Funded by Leverhulme Trust and Anatomical Society.

Aging of the hypothalamic-pituitary-adrenal axis in wild chimpanzees

MELISSA EMERY THOMPSON^{1,2}, STEPHANIE FOX¹, ANDREAS BERGHAENEL¹, KRIS SABBI¹, SARAH PHILLIPS-GARCIA¹, DREW K. ENIGK¹, EMILY OTALI², ZARIN P. MACHANDA^{2,3}, MARTIN N. MULLER^{1,2} and RICHARD W. WRANGHAM^{2,4}

¹Anthropology, University of New Mexico, ², Kibale Chimpanzee Project, ³Anthropology, Tufts University, ⁴Human Evolutionary Biology, Harvard University

Cortisol, a key product of the stress response, has critical influences on degenerative aging in humans. In turn, cortisol production is affected by senescence of the hypothalamic-pituitary-adrenal (HPA) axis, leading to progressive dysregulation and increased cortisol exposure. These processes have been studied extensively in industrialized

settings, but few comparative data are available from humans and closely-related species living in natural environments, where stressors are very different. Here, we examine age-related changes in urinary cortisol in a 20-year longitudinal study of wild chimpanzees (N = 60 adults) in the Kanyawara community of Kibale National Park, Uganda. We tested for three key features of HPA aging identified in many human studies: increased average levels, a blunted diurnal rhythm, and enhanced response to stressors. Using linear mixed models, we found that aging was associated with a significant linear increase in cortisol (Estimate = 0.027, $p < 0.0001$). This effect did not differ by sex and was independent of changes in dominance rank, suggesting it was driven by intrinsic factors rather than increasing exposure to stress. Chimpanzees also exhibited a human-like blunting of the diurnal rhythm. While we expected older males to exhibit enhanced cortisol responses to mating competition, and females to lactation, neither prediction was supported. Our results indicate that chimpanzees share key features of HPA aging with humans. These findings suggest that impairments of HPA regulation are intrinsic to the aging process in hominids and are neither side effects of extended human lifespan nor of atypical environments.

NIH National Institute on Aging/Office for Research on Women's Health R01AG049395, National Science Foundation BCS-1355014/0849380, Leakey Foundation, Wenner-Gren Foundation, University of New Mexico, Harvard University

Characterizing DNA Degradation in Severely Burned Human Skeletal Remains using STR Genotyping and NGS Targeted Capture Techniques

MATTHEW V. EMERY^{1,2}, KATELYN L. BOLHOFNER^{4,5,6}, STEVIE WININGEAR^{1,2}, ROBERT OLDT³, SREETHARAN KANTHASWAMY⁴, JANE E. BUIKSTRA^{1,5}, LAURA FULGINITI⁶ and ANNE C. STONE^{1,2,5}

¹School of Human Evolution and Social Change, Arizona State University, ²Center for Evolution and Medicine, Arizona State University, ³School of Life Sciences, Arizona State University, ⁴School of Math and Natural Sciences, Arizona State University, ⁵Center for Bioarchaeological Research, Arizona State University, ⁶Maricopa County Office of the Medical Examiner, City of Phoenix

The recovery and analysis of DNA from burned human remains represent some of the most challenging cases in forensic and bioarchaeological research. Low DNA yields are notoriously problematic in the most severe burned cases, resulting in STR dropout, low mtGenome and nuclear SNP coverage. In this study we compare STR, mtGenome, and nuclear SNP data generated using an ancient and forensic DNA extraction protocols sampled from fire-death victims. Over a period of two years, we obtained and documented 62 samples from 27 fire death and cremation cases

in collaboration with the Maricopa County Office of the Medical Examiner (Phoenix, Arizona). Samples were chosen with the goal of obtaining different skeletal elements showing different levels of burning (burn categories I-V). STR profiles were generated using the PowerPlex® ESX 17 Fast Systems STR kit by Promega. In addition, DNA extracts were converted into double-stranded DNA libraries and enriched for mitochondrial DNA and nuclear SNPs for next-generation sequencing. Our data show that STR profile quality, mtGenome, and SNP coverage significantly decreases at temperatures >55°C across both extraction procedures. However, partial STR profiles and low coverage mtGenomes were recovered using the ancient DNA extraction protocol, suggesting the retention of ultrashort DNA molecules at temperatures exceeding 550°C. These data confirm the difficulties in obtaining DNA from burnt skeletal material using conventional and next-generation sequencing technologies. Overall, our analyses suggest that ancient DNA methods offer an alternative to forensic techniques, especially under circumstances where traditional forensic applications have failed.

We thank the National Institute of Justice (NIJ) for funding this research (2016-DN-BX-0158).

A comparative perspective on childhood stress and survivorship among Inner Asian populations of the Iron Age

JACQUELINE T. ENG¹ and MICHELLE MACHICEK²

¹Biological Sciences, Western Michigan University, ²Institute of Intercultural and Anthropological Studies, Western Michigan University

Inner Asia has long been home to populations that varied in their modes of subsistence and in their cultural and biological trajectories. Recent studies have demonstrated that dietary regimes were varied depending on factors such as local resources and socio-economic characteristics. Discrete dietary strategies may be expected to have influenced health and well-being of these populations, particularly during the sensitive period of growth during childhood, and subsequently influenced survivorship into adulthood.

Enamel hypoplasia (EH) and cribra orbitalia (CO) data were analyzed from five Iron Age sites (c. 1200 BC-AD 370) to explore the association between multiple markers of stress within samples that are relatively contemporaneous, yet distinct in environment and subsistence. These include the pastoral sites Heigouliang (n=43) and Nileke (n=47) of Xinjiang, mixed-agropastoral Mongolia site of Egiin Gol (n=24), and agrarian Inner Mongolia sites of Lamadong (n=100) and Tuchengzi (n=45).

The EH and CO lesions only co-occur within the Egiin Gol (15.4%) and Tuchengzi (7.4%) adult samples. These two sites also demonstrate the highest rates of both markers in inter-site

ABSTRACTS

comparisons. Egiin Gol has significantly high rates of EH in the adult sample (Fisher's exact, $p < 0.001$), female adult sample ($p = 0.001$), and total sample of subadults and adults ($p < 0.001$), as well as highest CO rate among the male adult samples ($p = 0.014$). Tuchengzi female adult samples have elevated rates of EH ($p < 0.001$) and CO ($p = 0.030$). Current findings suggest that multiple factors such as occupation or status, and diet, likely influenced survivorship rates when comparisons are made across age-cohorts and site locations.

JE funding: Fulbright-Hays Doctoral Dissertation Abroad program and University of California Pacific Rim Award. MM funding: Wenner Gren Foundation for Anthropological Research and (CAORC) Smithsonian Institution.

The potential of semantic research data modeling in biological anthropology

FELIX ENGEL and STEFAN SCHLAGER

Biological Anthropology - Faculty of Medicine, University of Freiburg

Standardization of research data helps to increase their comprehensibility, traceability and reproducibility and is a prerequisite to data aggregation. Its necessity is growing with funding agencies demanding data management plans and issuing grants for building up data infrastructures.

Traditional approaches to data standardization from within biological anthropology assume the creation of relational databases to be subsequently filled with information. This implies unchangeable database models as a requirement for data compatibility.

In the life sciences at large, methods of semantic data modeling have been successfully adopted from information science. Here, knowledge domains are modeled as ontologies onto which existing database structures can be mapped. This approach follows recent trends in information technology where conceptual data models are separated from the logics of data storage.

In this contribution we assess the potential of semantic data modeling to support the creation of large research databases in biological anthropology. We review the coverage of primatology and especially human biology, evolution, behavior and pathology by existing ontologies and identify domain-specific gaps.

Biological anthropologists can draw on a broad range of biological, biomedical and biocultural ontologies to increase the accessibility and comprehensibility of their research data. These existing resources contribute to the analysis of anthropological data and help to incorporate contextual data from other disciplines (e. g. archaeology or cultural anthropology). Semantic data modeling allows for refining and aggregating

existing data and has the potential to bring about better integration of evidence from the various branches of biological anthropology, advancing the inner coherence of the discipline.

This research was funded by the German Research Foundation (Deutsche Forschungsgemeinschaft, DFG; grant reference WI 863/9-1).

Assessing Wild Bornean Orangutan (*Pongo pygmaeus wurmbii*) Populations with Drone Imagery

MADELINE M. EOR^{1,4}, ELIZABETH BARROW², VICTORIA GEHRKE², TERRI BREEDEN², ERIN E. KANE¹, TRI WAHYU SUSANTO^{2,3} and CHERYL D. KNOTT^{1,2,4}

¹Department of Anthropology, Boston University, ²Gunung Palung Orangutan Conservation Program, Indonesia, ³Department of Biology, National University, Indonesia, ⁴Department of Biology, Boston University

Wild orangutan populations are estimated to have declined by well over 50% in the last 60 years. Thus, a rapid, reliable survey method that can be used across orangutan habitat types is needed to track orangutan population density. Individual, adult orangutans build a new nest each night so orangutan populations have historically been evaluated through systematic, ground-based, nest surveys. However, orangutan nest surveys are costly, time-consuming, require some degradation of the forest, and are restricted to areas that are accessible by ground teams. In 2016-2017, we pilot-tested the use of drones to survey orangutan populations in Gunung Palung National Park, Borneo, Indonesia, determining that nests can be spotted and counted from the imagery collected. In 2018-2019, drone imagery for 50 transects was obtained and analyzed to calculate population density. Nests in the images were classified into nest degradation categories to match ground methods. On average, fewer nests were found using drone imagery analysis than ground surveys. We calculated habitat specific conversion factors for drone nest surveys, based on our ground-truthing, to estimate orangutan population densities. We compare the density values using these two methods and demonstrate the validity of using drones as an effective technique for estimating orangutan population size. Data were compared to completed phenological surveys and showed close correspondence between nest density and fruit availability. The drone imagery will allow for more rapid assessment of new or more intensive human impacts on the land, providing further insight into what conservation efforts are needed to protect orangutan populations.

US Fish and Wildlife (F15AP00812, F18AP00898); National Science Foundation (BCS-1638823); Conservation, Food and Health Foundation; Woodland Park Zoo; Disney Conservation Fund; Sea World/Busch Gardens; Ocean Park Conservation Fund; Remembering Great Apes

The effect of hand preference on human pelvic shape asymmetry

AMANDINE ERIKSEN¹ and NOREEN VON CRAMON-TAUBADEL²

¹Department of Basic Medical Sciences, University of Arizona College of Medicine-Phoenix, ²Department of Anthropology, University at Buffalo-SUNY

The study of asymmetry offers valuable insight into the biomechanical factors, such as hand preference, that influence development of the human body. Previous studies of human skeletal asymmetry often lack known handedness data and tend to presume right-handedness without specifically analyzing upper limb elements. Here, we investigate differences in individual asymmetry (IA) in the pelvis for a modern sample of 43 males and females for whom hand preference was documented. The shape of the os coxa and sacrum was quantified using landmark configurations on 3D bone models. All possible distances between landmarks were calculated for the left and right sides of each bone and were used to calculate average IA for each individual bone. The results found that IA for the two bones was not correlated ($r = -0.03$, $p = 0.85$), suggesting that more asymmetrical individuals do not necessarily display the same patterns of left or right-side dominance across the pelvis. Kruskal-Wallis and Mann-Whitney U tests found no significant differences in IA across sex or handedness groups for the sacrum but right-handed males had higher right-side dominance in the os coxa compared to all females and left-handed males, while females showed no differences between handedness groups. Thus, the results suggest that handedness can affect asymmetry in parts of the skeleton not directly linked to the upper limb. Further comparisons across skeletal regions, particularly among the upper and lower limb bones, will elucidate the relative effects of handedness in shaping human skeletal asymmetry patterns.

This was supported by funding from the Wenner-Gren Dissertation Fieldwork Grant (Grant #9641), the Mark Diamond Research Fund (SP-18-19), and the 2017 Morris E. and Lucille R. Opler Dissertation Research Scholarship.

A test of interobserver error in radiating fracture measurement techniques

ELIZABETH A. EVANGELOU¹, TESSA SOMOGYI¹, ALYSSA B. FELBERBAUM¹, MALLORY J. PETERS¹, AMOYIEN K. THOMPSON², DANIELA SANTAMARIA VARGAS¹ and ELIZABETH A. DIGANGI¹

¹Anthropology, Binghamton University, ²Biology, Binghamton University

Radiating fractures resulting from blunt force and gunshot trauma are commonly measured and analyzed in skeletal trauma analyses. Here we test three radiating fracture measurement techniques to determine which has the least amount of interobserver error: (1) Microscribe digitizer; (2) flexible measuring tape; and (3) Scale Master digital plan

ABSTRACTS

measure. Radiating fractures were the result of gunshot trauma from a larger project focusing on fracture patterns. Forty-five donated human heads were shot either anteriorly through the frontal bone or laterally through the temporal/parietal bone(s) prior to soft tissue removal. We randomly selected two radiating fractures on each cranium to measure. Measurements were recorded by practitioners with various levels of osteological experience. One-way MANOVAs assessed interobserver error for each technique with an alpha set to .05. The results indicate that there is no statistically significant difference between observers regardless of technique ($p=.777$ for the digitizer; $p=.980$ for the flexible measuring tape; and $p=.871$ for the Scale Master). However, when comparing the effect size statistics for each of the techniques, the results indicated that the flexible measuring tape measurements were the most affected by the skill of the observer, followed by the Scale Master measurements. The digitizer was the least affected by observer skill, making the digitizer the most precise technique of those tested. However, not every lab has access to a digitizer, so we recommend the use of a Scale Master as an alternative to the measuring tape when a digitizer is not available.

This project was supported by award number 2016-DN-BX-0155 from the National Institute of Justice.

Coercive takeovers and fitness in hamadryas baboons

KATARINA D. EVANS^{1,2}, SHAHRINA CHOWDHURY^{1,2,3} and LARISSA SWEDELL^{1,2,4}

¹Anthropology Program, City University of New York Graduate Center, ²New York Consortium in Evolutionary Primatology (NYCEP), ³Anthropology and Archaeology, Brooklyn College, CUNY, ⁴Anthropology, Queens College, CUNY

Hamadryas baboons (*Papio hamadryas*) are a useful model for human evolution for several reasons, including their complex multilevel social system. The most stable social unit in this system, the one-male unit (OMU) – comprising a leader male, females and sometimes follower males – is formed via successive takeovers of individual females by males. While takeovers occur via aggressive and non-aggressive mechanisms, aggressive male coercion is most common and appears important in maintaining cohesive OMUs. Here we use data from Filoha, Ethiopia to examine the relationship between aggressive takeovers and fitness in leader males. We found 1) a significant relationship between the number of aggressive takeovers and both the number of births and number of females in a male's OMU and 2) a stronger relationship between the number of aggressive, compared to non-aggressive, takeovers and the mean number of females in a male's OMU (aggressive: $F(1,60)=10.08$, $p=0.002$, non-aggressive: $F(1,60)=2.60$, $p=0.112$). The number of births, however, did not differ

between aggressive and non-aggressive takeovers (aggressive: $F(1,60)=14.55$, $p=0.0003$, non-aggressive: $F(1,60)=15.71$, $p=0.0002$). We also found a stronger relationship between the number of aggressive, compared to non-aggressive, takeovers and a male's total number of followers (aggressive: $F(1,60)=9.63$, $p=0.003$; non-aggressive: $F(1,60)=5.66$, $p=0.021$). Given previous findings showing a relationship between a male's number of followers and his fitness, these results suggest that aggressively coercive males have increased fitness for multiple reasons, including greater success in attracting followers. Our findings suggest that aggressive coercion is an effective mechanism via which leader males maintain OMUs and accrue fitness benefits.

Funding was provided by The Leakey Foundation, the Wenner-Gren Foundation, the National Geographic Society (6468-99 and 8309-07), the CUNY Graduate Center, the PSC-CUNY Award Program, and NYCEP.

Associations between genetic differentiation and craniometric interpopulation distances across North Eurasia

ANDREJ EVTEEV¹, PATRÁCIA SANTOS², SILVIA GHIROTTTO² and HUGO REYES-CENTENO³

¹Anuchin Research Institute and Museum of Anthropology, Lomonosov Moscow State University, ²Department of Life Sciences and Biotechnologies, University of Ferrara, ³DFG Center for Advanced Studies "Words, Bones, Genes, Tools", University of Tübingen

Genetic data have been extensively used to validate the role of craniometric variables as a source of information about human population history. Studies at the global level reported moderate to high correlations between the two types of data. However, recent studies have shown that the strength of association depends on a number of factors, including the type of cranial variables analyzed and the geographical scale of comparison. We explore the effect of these factors on the association between genetic *FST* and craniometric interpopulation distances across human populations in North Eurasia. We collected 42 cranial measurements for 694 male individuals representing 30 populations and paired these with genomic data of more than 50,000 loci for 2206 individuals. To test the effect of geographical scale, the total dataset was divided into 2 continental regions and 3 sub-continental regions. To test for the effect of cranial variable choice, we analyzed each variable independently and for cranial areas represented by 21 measurements of the mid-facial area, 15 of the neurocranium, and 6 of the mandible. The association of genetic and craniometric distances was assessed by Mantel tests. Our results show that the mid-face is the part of the skull showing the highest and most stable association with genetic distances ($r=0.865$, $p=0.0001$ in the total dataset). Notably, when continental or regional levels were considered,

the strength of this association decreased substantially. Nevertheless, the use of specific "phylogenetically relevant" measurements led to an increase in the degree of morphology-genetic correlation in all the studied geographical regions.

This work was supported by the German Research Foundation (DFG-FOR-2237: "Words, Bones, Genes, Tools: Tracking Linguistic, Cultural, and Biological Trajectories of the Human Past") and the RFBR (project number 18-56-15001).

The correlation between bi-iliac breadth and birth canal size in humans: implications for the obstetric dilemma

JENNIFER EYRE

Anthropology and The Center for the Study of Human Origins, New York University, Anthropology, The New York Consortium in Evolutionary Primatology

The obstetric dilemma posits that an antagonistic selection pressure prevented the modern human female pelvis from responding to selection acting to increase the size of the birth canal (BC) to decrease the incidence of obstructed labor. Selection for effective thermoregulation may be antagonistic to pressures acting to increase the size of the BC because, based on Bergmann's Rule, narrower-bodied humans should be better at dissipating heat. If humans evolved in hot climates there may have been selection to reduce body breadth and thus bi-iliac breadth (BIB). However, this hypothesis presupposes that BIB is highly correlated with birth canal capacity.

To test this, three-dimensional scans were created of adult female pelvises from skeletal collections representing geographically varied populations from a variety of climates ($n=102$). The scans were processed in Geomagic Studio. BIB and the areas of the three BC planes (inlet, midplane, and outlet) were measured in ImageJ. The correlation between the area of each plane and BIB was tested using an ordinary least squares regression analysis.

BIB and inlet area are significantly, but weakly, correlated ($r^2=0.25$, $p=0.0047$). BIB is not correlated with midplane ($r^2=0.088$, $p=0.15$) or outlet area ($r^2=0.090$, $p=0.14$). The outlet is generally the smallest of the three planes (84% of cases). Therefore, while BIB might be a factor in determining the size of the inlet, the inlet is rarely the most constrained in size. The results suggest that while selection on BIB might play a role in the obstetric dilemma, it is unlikely to play a large one.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship Program under Grant No. 1650895.

ABSTRACTS

Investigating population affinity from the Iron Age to Early Medieval period: A pilot study from Wessex, England

KATIE E. FAILLACE¹, JACQUI MULVILLE¹, RICHARD MADGWICK¹ and JOEL D. IRISH²

¹Department of Archaeology, School of History, Archaeology, and Religion, Cardiff University, ²Research Centre in Evolutionary Anthropology and Palaeoecology, School of Natural Sciences and Psychology, Liverpool John Moores University

Though bioarchaeological methods are continually improving, genetic influence of potential migrants in Roman and Early Medieval England remains unclear. This study addresses the issue by applying dental morphological methods for investigating population affinity to assemblages from the British Iron Age (600BC-AD43), Roman (AD43-410), and Early Medieval (AD410-1066) periods. Specifically, this poster presents a pilot investigation of three sites in Wessex: Iron Age Danebury (n=46), Romano-British Amesbury Down (n=77), and Early Medieval Collingbourne Ducis (n=50). Dental morphology traits (n=36) were recorded following the Arizona State University Dental Anthropology System. Traits with significant intra-observer error, or highly correlated with other traits were identified and excluded from analysis. Population affinity was analysed using the Mean Measure of Divergence (MMD).

Results indicate strong similarities between all three samples. Comparison of Danebury and Amesbury Down produced the lowest MMD of 0.0003; the MMD between Amesbury and Collingbourne Ducis was 0.0115 and between Danebury and Collingbourne Ducis was 0.0106. None of these values were statistically significant ($p=0.984, 0.440, 0.616$ respectively), therefore these populations are morphologically indistinguishable. Given the elevated MMD for comparisons with Collingbourne Ducis, it is possible that the Roman to Early Medieval transition includes greater genetic change than the Iron Age to Roman transition. However, since there is no statistical difference between the samples, the mechanisms for that change is unclear. This pilot study develops our understanding of the biological implications to selected 'cultural revolutions' in Britain, suggesting that in these populations genetic changes were relatively minor despite periods of major cultural change.

New speleothem records from southwestern Madagascar and their implications for the role of climate and humans in megafaunal extinction

PETERSON FAINA¹, STEPHEN J. BURNS², NICK SCROXTON³, DAVID MCGEE⁴, LAURIE R. GODFREY⁵ and LOVASOA RANIVOHARIMANANA¹

¹Bassins sédimentaires Evolution Conservation, Université d'Antananarivo, Madagascar, ²Department of Geosciences, University of Massachusetts Amherst, ³School of Earth

Sciences, University College Dublin, Ireland, ⁴Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology, Cambridge, ⁵Department of Anthropology, University of Massachusetts Amherst

The relative importance of climate and humans in the disappearance of the Malagasy megafauna is under debate. Data from southwestern Madagascar imply aridification contributed substantially to the late Holocene decline of the megafauna. Evidence for aridification includes tree-ring carbon isotopes, lacustrine charcoal concentrations and pollen assemblages, alongside fossil evidence for the disappearance of vertebrate indicators of more pluvial conditions. However recent archaeological research in southwest Madagascar indicates humans were present in the area at least 2000, and perhaps 3000, years ago.

In contrast speleothem records from northwestern Madagascar suggest that peak megafaunal decline and habitat change resulted primarily from human activity around 950 CE. Could there have been contrasting mechanisms of decline in different parts of Madagascar? Or are we lacking the precisely dated, high resolution records needed to fully understand the complex processes behind megafaunal decline?

Reconciling these contrasting hypotheses requires additional climate records from southwest Madagascar. We have recovered multiple stalagmites along a coastal transect from north of Tulear south to Itampolo. U-series age dating of these samples provides highly precise chronologies of past changes over the past 3000 years. Speleothem stable oxygen and carbon isotope analyses provide insight into past rainfall variability and vegetation changes respectively. Combined, these analyses allow us to test the aridification hypothesis for southwestern Madagascar.

This project was supported by the National Science Foundation [AGS-1702891 to Stephen J Burns, AGS-1702691 to David McGee, and BCS-1750598 to Laurie R Godfrey]

Testing associations between diet and premolar size in four African colobine monkeys

LUKE D. FANNIN¹, JAKE ARFT-GUAPELLI², DEBBIE GUAPELLI-STEINBERG³, NOAH T. DUNHAM⁴, ANDREA DONALDSON⁵, PAM CUNNEYWORTH⁵ and W SCOTT. MCGRAW³

¹Anthropology, Dartmouth College, ²Pacific Ridge School, ³Anthropology, Ohio State University, ⁴Cleveland Metroparks Zoo, ⁵Colobus Conservation Limited

Folivorous primates are hypothesized to have relatively larger premolars than frugivores due to the mechanical and energetic challenges of leaf consumption. Specifically, it is reasoned that as folivory increases, so do the mechanical demands of mastication, resulting in more

frequent premolar loading. Because interspecific variation in folivory and leaf material properties is extensive, a strictly linear association between folivory and premolar size is unlikely. Here, we investigate the relationship between relative premolar size and diet in four African colobines for which skeletons and feeding data are available from single source populations. The sample consists of three colobines from Ivory Coast's Tai Forest – *Colobus polykomos*, *Piliocolobus badius* and *Procolobus verus* – and one – *Colobus angolensis* – from Kenya's Diani Forest. We assessed relative premolar size using four scalars: mandibular length, M¹ area, palate area and body size. Premolar size did not consistently covary with folivory. *P. verus* (91% foliage) had the smallest relative premolar sizes, except relative to body mass. *P. badius* tended to have the largest premolars relative to palate area, despite only modest folivory (50%). Similarly, while *C. angolensis* was more folivorous (71%), *C. polykomos* (48%) had relatively larger premolars when scaled to M¹ and mandibular length. The latter result is likely explicable because of *C. polykomos*' reliance on woody *Pentaclethra macrophylla* pods. Our analysis provides little support for the notion that relative premolar size in African colobines is positively associated with folivory. Departures from expectations are interpretable in terms of food mechanical properties and/or scaling factors.

The Taiã Forest research was supported by National Science Foundation BCS 0840110, 0921770, 0922429 and Yerkes National Primate Research Center.

Maturation responses to male takeovers in immature female geladas

JACOB A. FEDER¹, JACINTA C. BEEHNER^{2,3} and AMY LU⁴

¹Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, ²Department of Anthropology, University of Michigan, ³Department of Psychology, University of Michigan, ⁴Department of Anthropology, Stony Brook University

Across primates, male immigration can greatly impact social and reproductive life. While the arrival of males is known to provoke physiological stress, it can also prompt potentially adaptive reproductive strategies in females, including spontaneous abortion, the resumption of cycling, and, possibly, the rapid sexual maturation of immature females (e.g., the Vandenberg effect). Though male effects on female maturation are well-documented in callitrichid primates, their importance in group-living species is less well-known. Here, we investigated the influence of novel males on immature female steroid hormones in geladas (*Theropithecus gelada*), a species in which male takeovers are known to trigger both spontaneous abortion and the resumption of cycling in adult females. We analyzed the effect of male takeovers (n=96) on fecal glucocorticoids (fGCs, n=1019),

ABSTRACTS

fecal estrogens (fE, $n=1506$), and maturations (i.e., first sexual swellings, $n=114$), controlling for seasonal effects. We found that immature females experienced a 10-percent increase in fGCs ($p=0.03$) and a 65-percent increase in fE ($p<0.001$) during the 30 days following takeovers. These effects held even in females who were too young to feasibly mature (i.e., <3 years of age). Additionally, fE, but not fGCs, increased during the 100 days prior to maturation ($p<0.001$). Lastly, the arrival of new males coincided with a four-fold increase ($p<0.001$) in the likelihood of female maturation. These data provide evidence for male-mediated maturation in a wild primate and identify potential endocrine mechanisms underlying this pattern.

Funding: The National Science Foundation (BCS-0715179, BCS-0824592, BCS-1723228, IOS-1255974, IOS-1854359), Leakey Foundation, National Geographic Society (8100-06, 8989-11, NGS-50409R-18), Fulbright, University of Michigan, Stony Brook University

Variation in Sexual Dimorphism Across Differing Köppen-Geiger Climate Classifications

MARIA E. FEILER^{1,2}, ERIN B. WAXENBAUM², SARAH A. SCHRADER¹, CARLA L. BURRELL^{1,3} and MENNO HOOGLAND¹

¹Laboratory for Human Osteoarchaeology, Leiden University, ²Department of Anthropology, Northwestern University, ³Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

Though skeletal sexual dimorphism is a helpful tool in archaeological and forensic contexts, evidence shows sexual dimorphism is expressed inconsistently among human populations. Cranial and pelvic nonmetric sex estimation methods have been reevaluated and recalibrated for specific ancestral groups/modern populations. Other studies show that climate can contribute to variation in sexual dimorphism as well, but little research has explored morphology shifts due to different climatic pressures.

This study aims to highlight variation across Köppen-Geiger climate classifications using a cross-population comparative study of standard nonmetric sex indicators of the cranium and pelvis. The three populations examined are a Native Alaskan sample ($n=104$), a component of the Terry Black collection ($n=99$), and a post-Medieval Dutch sample from Middenbeemster ($n=118$). These sex-balanced groups were compared for statistical significance of sexual dimorphism variation using one-way ANOVAs, Tukey-Kramer post-hoc tests, and Greene's t-test. The nonmetric traits respond to climate with little consistency. However, there is a trend toward a reduction of sexual dimorphism in populations

of colder climates for the supraorbital margin ($p=0.09$ and $p=0.04$), as well as a shift to a hyper-female morphology in the mental eminence ($p<0.05$).

Despite confounding factors such as ancestral, occupational, and nutritional differences, variation among standard nonmetric traits used in sex estimation demonstrates that further exploration of the complex relationship between climate and sexual dimorphism is warranted. Future studies will improve forensic and archaeological procedures and produce more accurate skeletal assessments tailored to climatic influence.

Personality variation in wild male chimpanzees is maintained by its changing association with rank

JOSEPH T. FELDBLUM^{1,2}, ALEXANDER WEISS^{3,4,5,6}, DREW M. ALTSCHUL^{5,6,7}, ANTHONY COLLINS⁸, SHADRACK KAMENYA⁸, DEUS MJUNGU⁸, STEFFEN FOERSTER⁹, IAN C. GILBY^{10,11}, MICHAEL L. WILSON^{12,13,14} and ANNE E. PUSEY⁹

¹Anthropology, University of Michigan, ²Society of Fellows, University of Michigan, ³Wildlife Research Center, Kyoto University, ⁴National Evolutionary Synthesis Center, ⁵Department of Psychology, School of Philosophy, Psychology and Language Sciences, The University of Edinburgh, ⁶Scottish Primate Research Group, ⁷Mental Health Data Science Scotland, ⁸Gombe Stream Research Centre, Jane Goodall Institute, ⁹Evolutionary Anthropology, Duke University, ¹⁰School of Human Evolution and Social Change, Arizona State University, ¹¹Institute of Human Origins, Arizona State University, ¹²Department of Anthropology, University of Minnesota, ¹³Department of Ecology, Evolution, and Behavior, University of Minnesota, ¹⁴Institute on the Environment, University of Minnesota

Biologists have long been interested in the mechanisms that maintain variation in heritable fitness-related traits. Recent studies in many taxa have found repeatable and heritable inter-individual differences in behavioral tendencies (i.e. "personality traits"), and associations between these traits and fitness. Adaptive explanations for the maintenance of variation in personality traits have focused on selection in heterogeneous environments, particularly temporally fluctuating social environments. Theoretical models suggest that temporally fluctuating selection is more likely to maintain genetic variance in populations when individuals are subject to age-specific selection effects, but it is not known whether personality traits are subject to such effects. Using long-term data from chimpanzees, we tested the hypothesis that personality traits play different roles in rank attainment at different times in a male chimpanzee's life. We used 37 years of behavioral data on 28 male chimpanzees in Gombe National Park, Tanzania, to examine the associations between six well-established heritable, stable, chimpanzee personality traits and dominance rank, which

is associated with reproductive success in this species. We found that the magnitude and direction of associations between three personality traits—dominance, conscientiousness, and openness—and dominance rank vary across males' lifetimes. These results highlight an important mechanism by which selection can maintain variation in heritable, fitness-related behavioral traits, namely that different personality traits appear beneficial at different life stages.

Data collection: Jane Goodall Institute and Carnegie Trust for the Universities of Scotland, long-term database construction: NSF (DBS-9021946, SBR-9319909, BCS-0452315, IIS-0431141, IOS-LTREB-1052693). Additional support: NESCent (NSF #EF-0905606), University of Edinburgh.

How HbAS and HbAC heterozygotes manifest their differences from HbAA individuals at the hemogram level.

FIONA FELKER¹, SABRINA GUIMARÃES-PAIVA², MARIA DE NAZARÉ KLAUTAU-GUIMARÃES³, SILVIENE FABIANA DE OLIVEIRA⁴ and LORENA MADRIGAL¹

¹Anthropology, University of South Florida, ²Educacion, Instituto Federal de Educação, Ciência e Tecnologia do Tocantins, Araguaína, ³Instituto de Ciências Biológicas, Universidade de Brasília, ⁴Instituto de Ciências Biológicas, Universidade de Brasília

Flansburg et al. (2019) demonstrated that sickle cell (HBAS) heterozygotes have diverse clinical expressions depending on SNPs affecting production of fetal hemoglobin (HbF) in a sample from the USA. The purpose of the current project is to determine if HbF is also associated with HBAS or HBAC phenotypes in three Afro-Brazilian communities known as *Quilombos*, each with different historical backgrounds. All of them are from the Central Brazilian states of Goiás and Tocantins. We found substantial population structure, where all HBAC heterozygotes were sampled in the third Quilombo. Unexpectedly, HbF was absent in any HBAS ($n=12$) or HBAC ($n=11$) individuals, but found in only 17 HBAA individuals, whose HbF percent ranged from 0.3 to 1.3%. Amato et al. (2012) notes that increased levels of HbF are observed in some mild β -thalassemic patients. These results may suggest that 17 HBAA individuals with elevated HbF may be thal- assemic and will now test them for it. Results of a Kruskal-Wallis-two-sided test indicated that these four hemoglobin groups (HBAA, HBAA+HbF, HBAS, HBAC) were significantly differences in their hematocrit ($\chi^2=17.58, df=3, p<0.0005$), mean cell hemoglobin ($\chi^2=15.8, df=3, p<0.001$), and mean cell hemoglobin concentration ($\chi^2=20.8519, df=3, p<0.0001$). Results of this study provide one more window into how and why some HbAS and even HbAC individuals show some clinical manifestations of their heterozygosity. We demonstrate the importance of working with human groups of different evolutionary histories.

ABSTRACTS

Not only are African-USA-derived groups different from Afro-Brazilian group, but within a region of Brazil there is population structure which affects the distribution of these alleles.

Estimating human age at death using 3-D confocal profilometry to quantify pubic symphyseal breakdown

CONNIE D. FELLMANN, MICHAEL C. PANTE, ANDREW DU and GRETCHEN CROUCH

Anthropology, Colorado State University

Forensic anthropologists use bone surface deterioration to estimate age at death. For example, the Suchey-Brooks and Todd methods classify macroscopic degeneration of the pubic symphysis into six to ten stages based on five- to twenty-year age intervals (ex. 15-24, 19-40). While generally accurate, interobserver error and subjectivity of surface trait identification are high and require the entire pubic face and rim. Our study attempts to improve age estimation methods by quantifying the microscopic breakdown of a small portion of the pubic surface in order to (1) narrow the age intervals of estimates and (2) remove subjectivity and observer error. We hypothesize that the systematic breakdown of bone at the pubic face is reflected in microscopic changes in recorded surface texture variables, such as 3-D roughness (Sa) and material volume (Vm) among other variables. To test this, we examined the pubic face of males between 18 and 90 years of age from the Hamann-Todd skeletal collection. Molds of individual pubic symphyses were taken using AccuTrans polyvinylsiloxane silicone, and then high-resolution 3-D models were created using a Sensofar S-Neox non-contact confocal profiler. Over 30 surface texture variables were measured using metrology analysis software and assessed through multivariate statistical modeling. Our initial findings suggest that pubic symphysis breakdown is quantifiable and follows age-dependent degradation for the studied variables with most measures decreasing then increasing with age (i.e., a U-shaped relationship). This relationship can potentially be used to estimate age in human skeletal samples with greater accuracy and precision than traditional qualitative methods.

Phylogenetic Analysis of extant colobines using morphological data: a reassessment

AILEEN FERNANDEZ and STEPHEN R. FROST
Anthropology, University of Oregon

To date, the phylogenetic relationships of the diverse fossil colobines of Africa and Asian remain elusive. To address this, we have been working on a morphologically-based phylogenetic analysis of extant colobines that could hopefully be applied to these fossil forms. Previous preliminary phylogenetic analysis based on a relatively small sample

of extant colobines resulted in a single most parsimonious tree with a monophyletic Presbytina, and paraphyletic Colobina. Within the Asian colobines, langurs were paraphyletic, and the Kasi were sister to Trachypithecus. Separate analyses using only males and females failed to support monophyly for either group. In this study, we report results based on a greatly expanded sample (n=426) representing all extant genera, plus 199 specimens of *Macaca* for the outgroup. We included 54 quantitative dental, 35 quantitative cranial, and 67 qualitative characters from our previous analysis. All characters were tested for the influence of allometry, and affected quantitative characters were adjusted by regression against geometric mean, and the narrow allometric method was used for qualitative characters. Quantitative characters were scored with gap-weighted coding. A monophyletic Colobina was recovered with *Colobus* (n=68) as sister taxon to a *Ptilocolobus/Procolobus* clade. Among Presbytina, langur genera were basal, and odd-nosed genera were largely grouped, except that *Pygathrix* (n=7) was nested within the langurs. The placement of *Presbytis*, however, was inconsistent with molecular and other results in that it was placed as the sister taxon to all other colobines.

Genetic diversity among indigenous South American populations reflects demographic history and environmental adaptations

CATALINA I. FERNÁNDEZ¹ and CONSTANZA DE LA FUENTE²

¹Department of Anthropology, Indiana University, ²GenSCAPE Laboratory, Department of Human Genetics, University of Chicago

Earliest indications of human migrations into southern South America date back to 15KYA, with evidence of human settlements spreading along very diverse ecological regions over the next few millennia. Along with migration and admixture, environmental adaptations could potentially explain cultural and genetic diversity among populations in this region. DNA samples, several non-communicable disease (NCD) biomarkers, dietary and physical activity data were collected for 190 individuals from two indigenous populations: the Atacamño (former agropastoralists in the Atacama Desert in northern Chile) and the Pehuenche (former hunter-gatherers in the rainforests of southern Chile). Genotyping was done using the ~800k SNP array Axiom-LAT1 and analyzed together with available data from Chilean populations and a subset from HGDP and 1KGP. In PCA, Pehuenches and Atacamños cluster together with other indigenous populations from the south and north of Chile, respectively. Ancestry analysis shows two distinct components corresponding to these populations, indicating a clear population structure along the territory. A small but consistent African

component is present among the Atacamños and absent in the Pehuenches, supporting previous findings and demographic history of admixed individuals in northern Chile. Given this clear genetic differentiation between the two populations, it is hypothesized that selective pressures associated with adaptation to contrasting environments and subsistence strategies may be partially driving these differences. Moving forward, this differentiation will be discussed in the context of the population history and adaptations of these groups, considering the peopling of the region and environmental factors that may have acted as specific selective pressures on these populations.

This research was supported by the National Science Foundation BCS #1752114 (DDIG), Wenner-Gren Foundation # 9530, and Becas-Chile, CONICYT.

Armswing dynamics in over-ground walking: The effect of velocity and footwear on armswing amplitude and asymmetry

ELEN M. FEUERRIEGEL^{1,2} and PATRICIA A. KRAMER¹

¹Department of Anthropology, University of Washington, ²Evolutionary Studies Institute, University of Witwatersrand

Bipedal walking is a whole-body process involving coordinated movements of the lower extremities, pelvis, trunk, and upper extremities. Modelling the peculiarities of lower limb motion in gait has been the focus of the bulk of biomechanics research, while the upper limb is modelled as a simple pendulum that neglects individual functional differences related to the arm's contributions to gait stabilization. Symmetry in armswing during normal gait has not been investigated systematically and those normative data that do exist on asymmetry have been collected during treadmill walking rather than overground walking.

This study investigated armswing kinematics in 20 healthy female subjects during over-ground walking while shod and unshod at three self-selected velocities: slow, normal, and fast. We hypothesized that 1) decreased armswing amplitude is associated with shorter stride lengths, and; 2) armswing asymmetry (expressed as asymmetry index) decreases with increasing walking velocity. Kinematic data from both arms and legs were compared with additional spatiotemporal gait parameters through linear regression.

The mean magnitude of asymmetry in armswing amplitude was 12.2 mm (averaged across all subjects and velocities). The mean asymmetry index was 99.8 ± 3.6 (SD), indicating a minor trend towards right armswing predominance. Walking velocity and shod condition had no significant effects on armswing asymmetry (Bonferroni corrected $p > 0.0025$). Armswing length, however, is positively correlated with stride length in both

ABSTRACTS

the shod and unshod conditions at all velocities ($p < 0.001$). The significant association of armswing amplitude and stride length may provide support of the "passive arm swing" hypothesis.

Dental non-metric morphological affinities of SE Brazilian coastal and riverine shellmound builders

DANIEL FIDALGO¹, VERONICA WESOLOWSKI¹ and MARK HUBBE^{2,3}

¹Museu de Arqueologia e Etnologia, Universidade de São Paulo, ²Department of Anthropology, The Ohio State University, ³Instituto de Arqueología y Antropología, Universidad Católica del Norte

In Southeastern Brazil, two distinct populations of shellmound builders thrived throughout the Holocene. One was mostly adapted to coastal environments, building shellmounds in ecotone areas along the meridional Atlantic coastline. The other inhabited the Atlantic forest, and built smaller shellmounds from terrestrial mollusks, in river valleys and near streams that connected the Brazilian inland plateau to the coastline. Archaeological artifacts found in riverine shellmounds indicate some degree of contact between both groups, and previous studies supported that both populations could be biologically related. However, it has also been suggested by craniometric analyses that some riverine shellmound builders share strong affinities with Early-Holocene Paleoamericans, making the biological relationship between these shellmound populations still unresolved. Here, we analyze dental non-metric traits to test the hypothesis that riverine and coastal shellmound builders share similar dental patterns, despite different geographic and environmental backgrounds, and therefore show high morphological affinities with other Sinodont Native American populations. Data on 22 dental traits from the Arizona State Dental Anthropological System (ASUDAS) were collected from 57 riverine and 98 coastal individuals from multiple sites, and compared with several worldwide reference series. Morphological affinities were analyzed through biodistance analyses, represented through Multidimensional Scaling and Cluster Analysis. Considering the available data, and the geographic scale of analysis, the results support the hypothesis of strong affinities between coastal and riverine groups. This suggests that both populations may share a common biological ancestry, and possibly maintained significant levels of contact throughout the Holocene, supporting a scenario of strong long-term gene-flow between them.

Funded by Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (Funding Code 001, November 2017 to March 2018) and Fundação de Amparo à Pesquisa do Estado de São Paulo (2017/20637-4)

Issues of representativity: Simulating the effects of kinship patterns on genetic diversity in archaeological samples

GONZALO FIGUEIRO

Departamento de Antropología Biológica, Universidad de la República, Uruguay

When working on a local level, such as in the study of the interaction of cultural processes and microevolutionary phenomena, the genetic analysis of past populations has to deal with issues related to the nature of the sample. Published genetic analyses of archaeological populations are usually explicit about the fact that the sample rarely represents a Mendelian population, as the sampled individuals could have lived generations apart. However, few studies have dealt with the effects that kinship patterns, which often shape funerary customs and the spatial arrangement of burials, can produce on population genetic estimates. A set of simulations were carried out in order to study the effect of three kinship patterns (bilateral, matrilineal, and patrilineal) on diversity as measured through mitochondrial DNA, which remains an important marker in human population genetics and ancient DNA analysis. The simulated population was founded with a haplotype diversity of 1, and subdivided into six groups with identical kinship strategies, disposing of their dead in separate burial grounds. It was found that sampling a single burial site generated by a group with a matrilineal strategy will consistently underestimate the genetic diversity of the population, whereas patrilineal and bilateral strategies lead to estimates with confidence intervals that include the real population diversity. Care must however be taken with the sex of the sample as patrilineal strategies will tend to underestimate the diversity in the male fraction. These effects can also be of use for testing kinship hypotheses based on archaeological data.

Undernourished Amazon Brazilian children: still a problem?

LIGIA A. FILGUEIRAS^{1,2}, HILTON P. SILVA², EDSON M.L.S. RAMOS², EDILA AF. MOURA² and ARIANA KLS. SILVA^{1,2}

¹Natural Science, UEPA/SEDUC, ²IFCH, Federal University of Pará

Quilombolas and Riverine are traditional, vulnerable, peasant Amazonian populations with specific ways of lifestyle. Nonetheless, few studies show results on their health and bioanthropological conditions. We studied 861 0-9 year old children from two riverine areas (Caxiuanã National Forest -FLONA - Pará State; Mamirauá Sustainable Development Reserve - Amazonas State) and six Quilombola communities (Pará State) under WHO parameters and social determinants of health. Quilombola children were -3 and -2 HAZ score (0-4 = 5.8%; 5-9 years old = 1.7%, respectively); 5.2% were overweight

and 2.1% obese. Riverine children were -3 HAZ Z-score; 16.3% overweight and 3% obese, with Caxiuanã 0-4 male children in worse conditions ($p = 0.0038$) for its municipality is located in the lowest Brazilian Human Development Index. Generally, social determinants of health (SDH) continue to influence these populations' lives since there is lack of environmental sanitation, piped water, indoor bathrooms, difficult access to health due to distances between homes and health centers as most transportation is by small motor boats. Unhealthy food is easier reached since many of them have been receiving cash transfer programs as Bolsa Família, and they have quit fishing, farming, leading to food insecurity, higher BMI and health worsening such as chronic diseases in the future. It is noticeable overweight and obese conditions are spreading, as shown in recent studies worldwide, however, we still have great amount of malnourished children in the Brazilian Amazon region due to weak public policy implementation and government should interfere positively to change this trend.

Stressed to Death: Stable isotope evidence of pathophysiological stress from young people with leprosy buried at a Medieval English leprosarium

KORI LEA FILIPEK¹, CHARLOTTE ROBERTS¹, JANET MONTGOMERY¹, REBECCA GOWLAND¹ and JULIA BEAUMONT^{1,2}

¹Archaeology, Durham University, ²Archaeology, Bradford University

Our research aims to view patterns of pathophysiological stress in children, adolescents, and young adult people with bone changes of leprosy buried at a medieval leprosarium (9th-11th centuries AD), and explore indicators of nutritional stress, lifetime diet, and potential links to leprosy immunity. Incremental dentine has the potential to show the diet and pathophysiological processes of at the time of their death if the tooth is still forming. This study employs a novel isotopic approach to examine individual life histories of people displaying skeletal signs of lepromatous leprosy in Medieval Winchester. Whole-life dietary profiles (carbon and nitrogen stable isotopes) spanning birth to death from 10 young individuals (<25 years old) were obtained using collagen from high-resolution dentine sections of canines, and second or third molars. The data from the analysis of dietary carbon and nitrogen, used in conjunction with skeletal and clinical evidence, offers a unique view into the pathophysiological and nutritional stresses that may have compromised leprosy immunity. It also highlights the potential of dietary analyses to reveal early life-histories of pathophysiological stress of people with leprosy, as well as their care and treatment during their lives subsequent to admission into a leprosarium.

ABSTRACTS

Common Skeletal Fracture Patterns of Juvenile Remains

ALEXIS FLANNERY¹, CORTNEY N. HULSE¹ and KYRA STULL^{1,2}

¹Anthropology, University of Nevada Reno,

²Anatomy, University of Pretoria, South Africa

In instances of traumatic death of a juvenile, it can be particularly incumbent upon the researcher to identify and interpret trauma. The aim of this study is to examine skeletal injury patterns in a large, contemporary sample with known cause and manner of death to better inform bioarchaeologists and forensic anthropologists. A database of computed tomography images of subadults was established by a National Institute of Justice grant (2015-DN-BX-K409) and a subset of the database was used in the current research (n = 191). The subset included individuals between birth to 20 years, males and females, and a known cause of death (COD) and manner of death (MOD). Frequency distributions of fractures for each MOD and COD were created and compared to adult skeletal fractures with the same associated information. The most frequently injured anatomical area, overall and for all MODs, was the cranium, with a frequency of 68%, followed by the ribs and arms (both at 24%). The cranium was also the most frequently injured anatomical site for both ballistic and blunt trauma while the ribs were most frequently injured anatomical site for sharp force trauma. However, there were fewer instances of sharp trauma compared to any other trauma category. The subadult injury pattern is not entirely discordant from the adult sample, however the arms are fractured more often in the juvenile sample than in adults. The results suggest future research should be dedicated toward cranial trauma and upper limb traumatic injury.

This project was funded by the National Institute of Justice Grant (2015-DN-BX-K409).

Old World monkeys, apes, and others

JOHN G. FLEAGLE¹, BRENDA BENEFIT² and ELLEN MILLER³

¹Anatomical Sciences, Stony Brook University,

²Anthropology, New Mexico State University,

³Anthropology, Wake Forest University

Old World monkeys (Cercopithecoidea) are the most abundant and speciose group of extant catarrhines, and they have a fossil record extending back to the late Oligocene. Extant Old World monkeys are very distinctive in many aspects of their dental, cranial, and postcranial morphology, in particular the bilophodont configuration of their molar teeth. Nevertheless, there have been numerous instances in which fossil cercopithecoids have been mistaken for other taxa, and other instances in which fossils have been identified as cercopithecoids but are actually members of different taxonomic groups.

Prohylobates tandyi and *Dryopithecus mogharenensis*, from the early Miocene of Egypt were initially identified by Fourteau as fossil apes until Simons recognized their cercopithecoids affinities. *Zaltanpithecus simonsi* was originally identified as a artiodactyl, and a fossil gelada from the Pliocene of Northern India was initially identified as a fossil rhinoceros. In a reverse situation, the parapithecids from the Oligocene of Egypt were classified as early Old World monkeys by many authorities before they were correctly recognized to be a distinct radiation of early anthropoids not clearly related to any one group of later catarrhines. Likewise, the fossil ape *Oreopithecus* has from time to time been considered as a fossil Old World monkey.

Why would fossils from such a morphologically distinctive group of primates often be misidentified? There seem to be several common reasons, including dental wear and unexpected geographical locations, and because the bilophodont morphology that makes cercopithecoids distinctive among primates are widespread in other groups of mammals.

African mitogenome diversity in 18th century Charleston, South Carolina

RAQUEL E. FLESKES¹, ADE A. OFUNNIYIN^{2,3}, JOANNA GILMORE^{2,3}, GRACIELA S. CABANA⁴ and THEODORE G. SCHURR¹

¹Anthropology, University of Pennsylvania, ²The Gullah Society, Inc, ³Sociology and Anthropology, College of Charleston, ⁴Anthropology, University of Tennessee

In 2013, 36 human burials were discovered during construction near Anson Street in downtown Charleston, South Carolina. Public interest prompted the creation of a community-based participatory project to investigate the origins and identities of the Anson Street Ancestors. Bioarchaeological analysis suggested these individuals were of African origin and buried in the mid-to-late 18th century, while property records suggested they likely had enslaved status. Osteological analysis indicated the presence of men, women, and children of various ages, and strontium isotope data from enamel and bone samples indicated affiliations with the Charleston area and West Africa. To further elucidate the origins and relationships of these persons, ancient DNA was extracted from petrous, tooth or post-cranial samples, and libraries successfully prepared for 32 individuals. DNA libraries were subject to whole genome enrichment and read on an Illumina MiSeq. The resulting sequences were mapped against the rCRS sequences to define mitochondrial DNA (mtDNA) haplotypes. The Anson Street Ancestors had nearly exclusively African mtDNAs from haplogroups L0-L3 and U6, with one individual having a Native American A2 mtDNA and another a West Eurasian H mtDNA, suggesting complex ancestry for them. Despite

the number of juveniles buried at the site, none of the individuals exhibited direct maternal ancestry with each other. These data will help to illuminate the history and origins of enslaved Africans in 18th century Charleston, through which nearly 40% of enslaved persons passed through upon arrival in colonial America. This project further highlights the importance of engaging descendent communities in ancient DNA studies.

This research was funded by National Geographic Society grants #NGS-52378R-18 (A.A.O) and #EC-52936R-18 (A.O) and the University Research Foundation of the University of Pennsylvania (T.G.S.).

Experimental Approaches to Paleodiet – Investigating Effects of Wood Smoking on $\delta^{15}N$

KIMBERLY K. FOCKE¹, ALISON S. BROOKS¹ and CHRISTINE A. M. FRANCE²

¹Center for the Advanced Study of Human Paleobiology, George Washington University,

²Museum Conservation Institute, Smithsonian Institution

Stable isotope research on bone collagen and tooth enamel is widely applied in an attempt to understand the history and range of modern human and earlier hominin diets. The nitrogen isotope system has been extensively applied to the human bioarchaeological record to predict degree of carnivory, as nitrogen isotope ratios roughly track the trophic level of an organism. Though often utilized, this proxy is subject to potential complications stemming from a limited understanding of the behavior of nitrogen isotopes in food items during pre-consumption processing steps. This experimental study investigates the impact of wood smoking on the $\delta^{15}N$ values of animal food resources. Recent work suggests that volatilization of nitrogen-bearing biomolecules during wood-burning contributes to an altered $\delta^{15}N$ signature of the smoke relative to the wood. We predicted that this isotopic shift would affect animal tissue during traditional wood-smoking, and would therefore affect the $\delta^{15}N$ value of humans consuming that tissue. A matrix of three species of animal skeletal muscle and 5 species of tree wood were experimentally smoked and $\delta^{15}N$ values measured as offset from control samples. Results show a consistent positive shift in $\delta^{15}N$ of the tissue, along with subtle but present species differences amongst the experimental sample matrix. These results indicate that wood smoking is a food processing behavior that could potentially affect paleodietary reconstruction by the nitrogen isotopic system in certain archaeological populations. More work is underway to better understand the drivers of these shifts and investigate other important food processing behaviors.

Funding for this research was provided in part by the Leakey Foundation Research Grant 2019 cycle

ABSTRACTS

Mapping putative genetic barriers to gene flow in hybrid baboons

ARIELLE S. FOGEL^{1,2}, TAURAS P. VILGALYS², SANG YOON KIM², JEANNE ALTMANN^{3,4}, SUSAN C. ALBERTS^{2,3,5} and JENNY TUNG^{2,3,5,6}

¹University Program in Genetics and Genomics, Duke University, ²Department of Evolutionary Anthropology, Duke University, ³Institute of Primate Research, National Museums of Kenya, ⁴Department of Ecology and Evolutionary Biology, Princeton University, ⁵Department of Biology, Duke University, ⁶Duke University Population Research Institute, Duke University

Hybridization is an important evolutionary mechanism that can influence genetic variation, adaptation, and divergence. While hybridization has occurred in all major primate lineages, many hybridizing primates nevertheless remain taxonomically distinct. These observations present an intriguing puzzle: what forces maintain genetic integrity in the face of hybridization? To address this question, we investigated potential genetic incompatibilities that affect admixture dynamics in a naturally hybridizing yellow baboon (*Papio cynocephalus*) and anubis baboon (*P. anubis*) population in Kenya. We generated whole-genome resequencing data for 321 individuals in the population, estimated local genetic ancestry (i.e., homozygous anubis, homozygous yellow, or heterozygous ancestry, at each genomic locus), and identified pairs of loci that exhibit ancestry-associated linkage disequilibrium (AA-LD) between chromosomes. These AA-LD pairs are more likely to be both of yellow or both of anubis ancestry than in mixed ancestry states, suggesting that they may contribute to reproductive isolation between the parental taxa. We identified 1,472 locus pairs, including 1,573 unique variants that met stringent filters for putative AA-LD. Anubis ancestry (the minor parent in this population) was significantly reduced near these variants relative to the genetic background, controlling for local recombination rate. However, these variants were not enriched near genes that show divergent, species-specific expression patterns, or near putatively functional elements. Together, our results offer some of the first evidence that selection limits anubis introgression into yellow baboon genomes and that genetic interactions may structure barriers to hybridization between these taxa. Our findings motivate future studies to investigate the phenotypic mechanisms generating these patterns.

National Institutes of Health, National Science Foundation, the Leakey Foundation, the Alfred P. Sloan Foundation, and the North Carolina Biotechnology Center

Human biology among daasanach pastoralists in northern kenya: Water insecurity, water borrowing, and psychosocial stress

LESLIE B. FORD¹, HILARY BETHANCOURT¹, ZANE SWANSON², SERA YOUNG³, ROSEMARY NZUNZE⁴, HERMAN PONTZER^{2,5} and ASHER Y. ROSINGER^{1,6}

¹Biobehavioral Health, Pennsylvania State University, ²Evolutionary Anthropology, Duke University, ³Anthropology, Northwestern University, ⁴Kenya Medical Research Institute (KEMRI), ⁵Global Health Institute, Duke University, ⁶Anthropology, Pennsylvania State University

East African pastoralist populations have dealt with extreme aridity for millennia. Yet we know little about their water insecurity experiences or adaptive practices used at the household level to overcome water concerns. For some, water borrowing has developed as an adaptation to cope with water challenges; however, entanglement in water sharing networks may be associated with psychosocial stress and long-term health outcomes. In collaboration with the Koobi Fora Field School, the human biology project implemented the Water Insecurity, Stress, and Hydration (WISH) study in the summer of 2019 to assess the prevalence of water insecurity among Daasanach pastoralists in Northern Kenya. Interviews were conducted with 234 adults aged 18+ (55% female) from 135 households using the validated Household Water Insecurity Experiences Scale. Of individuals interviewed, 95% were water insecure; 25% indicated they borrowed water 0-2 times, 47% borrowed water 3-10 times, and 29% borrowed water 11+ times in the month prior. Predictors of water insecurity and perceived psychosocial stress (PSS) were assessed using Tobit regression models. Drinking water salinity (100 mg/L, $\beta=1.4$, $P=0.04$, 95% CI=0.06-2.7) and household size ($\beta=0.7$, $P=0.00$, 95% CI=0.3-1.1) were significantly associated with increased water insecurity scores. There was a significant interaction between water borrowing and water insecurity ($P=0.02$) on psychosocial stress. Low water insecurity with high levels of water borrowing and high water insecurity with low levels of water borrowing were both associated with higher PSS. This emphasizes that, as water problems increase, water borrowing networks are crucial for mitigating stress related to meeting water needs.

This work was funded by the PSU SSRI Human Health and Environment Seed Grant, NSF ARCH #1624398

Pelvic evidence for taxonomic heterogeneity within *Australopithecus* at Sterkfontein Member 4 (South Africa)

CINZIA FORNAI^{1,2}, VIKTORIA A. KRENN^{1,2}, NICOLE M. WEBB^{1,3} and MARTIN HAEUSLER¹

¹Institute of Evolutionary Medicine, University of Zurich, ²Department of Evolutionary Anthropology, University of Vienna, ³Department

of Paleoanthropology, Senckenberg Research Institute and Natural History Museum Frankfurt

Recent debate on the StW 573 skeleton from Sterkfontein Member 2, South Africa, has reignited discussion regarding taxonomic heterogeneity within the *Australopithecus africanus* hypodigm.

Here, we compare the alleged female Sts 14 pelvis and a new virtual reconstruction of the presumed male StW 431 pelvis from Sterkfontein Member 4 (2.6 to 2.1 Ma). After realignment of the fragments, the StW 431 ilium and ischio-pubic ramus were restored using the Sts 14 and A.L. 288-1 (*A. afarensis*) hipbones as templates, based on landmark-based morphing techniques. The well-preserved upper sacrum and sacroiliac joint allowed us to confidently align the pelvic elements.

A preliminary GM analysis using 24 landmarks suggested that the morphological distance between the StW 431 and Sts 14 hipbones did not exceed the intraspecific variation of the extant species within a comparative sample of 40 adult and subadult modern humans, 34 chimpanzees, 44 gorillas and 29 orangutans. Nevertheless, based on our pelvic reconstruction, StW 431 and Sts 14 showed remarkable differences mainly in the cranio-caudal position of the sacroiliac joint and ventro-dorsal orientation of the ilia. This cannot be fully explained by allometry, different developmental age or sexual dimorphism and thus might reflect distinct functional adaptations in the StW 431 and Sts 14 pelvises.

Combined with the profound morphological divergence between the StW 431 and Sts 14 sacra—which were larger only in 2% of all possible pairwise comparisons within a worldwide modern human sample of 76 sacra—our findings suggest that these individuals were likely members of different taxa.

This research was funded by the Swiss National Science Foundation grants No 31003A_176319.

Anti-predatory strategies produce distinct landscapes of fear mediated by social and environmental factors in red-tailed monkeys (*Cercopithecus ascanius*)

LILLIAN J. FORNOF^{1,2}, FIONA A. STEWART^{2,3} and ALEXANDER K. PIEL^{2,3}

¹Department of Biology, Swarthmore College, ²Issa Valley Research Station, Greater Mahale Ecosystem Research and Conservation, ³School of Biological & Environmental Sciences, Liverpool John Moores University

Recent evidence in a variety of prey species indicates that a group's spatial strategy to avoid predation and maximize resources can be modeled by a landscape of fear (LOF). Recently, LOF studies have begun to gain attention in primate species, whose social structure and anti-predatory strategies differ from the more studied ungulates. Additionally, LOF models are

ABSTRACTS

often generated from the measurement of a single anti-predatory strategy in primate species. This study takes a more complex approach to the study of LOF and habitat use by measuring multiple anti-predatory strategies as well as social and environmental factors in a group living primate. Here we tested a LOF hypothesis that anti-predatory strategies minimize predation risk and energetic cost while maximizing resources in red-tailed monkeys (*Cercocepithecus ascanius*). We modeled predation risk as a function of three behaviors, aggregation, alarm-calling, and anti-predatory vigilance, and explored how these strategies are deployed in relation to social (e.g., group size) and environmental factors (e.g., habitat type). We found that the anti-predatory behaviors are differentially predicted by the habitat, demographic factors, and the other anti-predatory behaviors used within the group. Additionally, the larger group performed relatively more anti-predatory behaviors. The LOFs that were generated map the variance of each strategy within the habitat and between the groups, recognizing the importance of multiple metrics for predation risk. This work reveals that the predation risk of a prey primate species is mediated by numerous and variable behavioral strategies that are further influenced by environmental and social factors.

This work was supported by the Giles K. '72 and Barbara Guss Kemp Student Fellowship from Swarthmore College.

Virtual Koobi Fora: Bringing the field into the classroom

FRANCES FORREST

Human Origins Educational Laboratory, American Museum of Natural History

The Koobi Fora virtual tour aims to invoke public engagement with archaeological and paleoanthropological fieldwork at one of the most important early hominin localities. The tour exists on an open access platform and can be downloaded for free and viewed on several devices including computers, smart phones, tablets, and virtual reality headsets including Google Cardboard^d. Viewers learn how fieldwork is conducted, challenges that arise, surface collection and excavation methods, all while experiencing the adventure of doing field work in a remote region of Africa. App users experience twelve scenes, each containing narrated content tailored to non-specialists. Points of interest encourage viewers to interact with the scenes at their own pace or via the guide mode. The virtual tour was presented to museum visitors during a regular weekend outreach event in the AMNH Hall of Human Origins. Visitors were given access to virtual reality headsets as well as laptops with still images from the field. The interactive nature of the app invoked noticeably more visitor participation and generated more meaningful conversation about the site than the

still images alone. One important finding was that the app more readily demonstrates science as an active, ongoing process. Although our results are preliminary, this initial investigation demonstrates the app's effectiveness in generating excitement and interest in ongoing scientific fieldwork. The app's success in encouraging scientific inquiry and the free platform make it a useful tool for presenting human evolutionary research in a way that is accessible to people of varied ages and science backgrounds.

NSF Archaeology Technological origins archaeology grant #1624398 and supplemental REU #1930719

Shorter heels result in more spring-like behavior of the Achilles tendon in running gaits

ADAM D. FOSTER¹, JESSE W. YOUNG², BRANDON BLOCK³, FLORIAN CAPOBIANCO III³, JOHN T. PEABODY³, NICHOLAS A. PULEO³ and AUSTIN VEGAS³

¹Anatomy, Campbell University School of Osteopathic Medicine, ²Anatomy and Neurobiology, NEOMED, ³OMS, Campbell University School of Osteopathic Medicine

Previous research suggests that the length of the Achilles tendon (AT) moment arm (MA) is positively correlated with energy costs of locomotion during endurance running behaviors (at speeds ~16 km/h). This finding is hypothesized to result from a shorter AT MA placing larger elastic loads on the AT, increasing energy storage and return. However, the correlation between the spring-like behavior of the AT and the AT MA has not been directly tested.

In this study, we test this hypothesis using inverse dynamics in human subjects (n=25) at speeds ranging from walking to a sprint and measure tendon cross-sectional area using ultrasound. The spring-like behavior of the AT was modeled using specific net work (SNW; net work/total work), a continuous variable that can range from zero (a perfect spring) to one (a perfect motor, lacking energy storage and return). Our results support previous work which shows that the AT MA is not significantly correlated with SNW in walking gaits, but is positively correlated with SNW in running (p=0.095) and sprinting gaits (p>0.001). When kinematic variables (out-lever length and GRF impulse) and tendon cross-sectional area were included as fixed effects, the AT MA remains significant and explains most of the variation ($\beta=0.434$, p=0.003). Our results suggest that when holding kinematic variables and tendon morphology constant, shorter heels result in more spring-like behavior of the AT, but only at sprint speeds. Our results support previous findings that shorter calcaneal tuber lengths in anatomically modern humans are linked with increased running economy.

Funding was provided by Campbell University and the Medical Student Summer Scholars Program.

A 3D Study on Form and Function in Tooth Enamel Microstructure

FREDERICK R. FOSTER

Anthropology, Rutgers, the State University of New Jersey

Tooth enamel is a strong indicator of diet because it is in direct contact with food at an early stage of digestion. Food mechanical properties influence the shape of tooth enamel and are expected to influence its structure as well. While considerable research has been devoted to assessing the shape of tooth enamel, its internal structure remains underexplored in dietary and evolutionary contexts. This is because the microstructure of tooth enamel is hierarchically organized and complex in three dimensions. Enamel microstructure is formed from nanometer-scale hydroxyapatite crystallites glued together to form micrometer-scale prisms, which are arranged in different patterns. The overwhelming majority of research on enamel microstructure uses 2D scans of sectioned teeth to extrapolate the orientation of enamel prisms. This relies on guess work as to the 3D orientation of microstructure that is difficult to support observationally. A high-fidelity understanding of prism orientation in 3D is central to ideas of enamel microstructure as a crack-stopping agent and strengthening mechanism. This study uses x-ray computed microtomography, and serial scanning electron microscope imaging with sample polishing to build a 3D picture of enamel microstructure and illustrate its complexity. Adaptation is explored by comparing microstructure in humans, chimpanzees and pygmy marmosets. Nanoindentation is used to assess functional consequences of variation in microstructural orientation and suggests the role of 3D complexity in dietary adaptation. The results of this study add an interpretive tool for evaluating dietary ecology from teeth and provide new opportunities for assessing dietary adaptation in the fossil record.

This project was funded by the National Science Foundation Doctoral Dissertation Research Improvement Grant (NSF BSC-1847941) and the Rutgers University, Center for Human Evolutionary Studies Albert Fellows Award.

Childhood and Change: An Evaluation of the Consequences of Climate and Culture Change on Diet and Health

NICHOLE A. FOURNIER¹, SHANNON TUSHINGHAM¹, ERIN THORNTON¹, CARA MONROE³, ALAN LEVENTHAL² and NORMA SANCHEZ⁴

¹Anthropology, Washington State University, ²Anthropology, San Jose State University, ³Anthropology, University of Oklahoma, ⁴Tribal Leadership, Muwekma Ohlone

ABSTRACTS

This study explores the impacts of climatic and socioeconomic change on the diet, life history patterns, and health of children from five Late Holocene San Francisco Bay Area Ohlone sites. The occupation of these sites corresponds with a transition from a largely marine-based, to a mainly terrestrially-based economy, as well as environmental fluctuations associated with the Medieval Climatic Anomaly (MCA). Previous research has focused mainly on the effects of these changes on adults. The present study addresses this question for children. The diet reconstruction is based on the carbon and nitrogen isotopic composition of bone and dental tissue from 45 juvenile individuals between the ages of 0-15 years. These data reveal patterns pertaining to diet throughout development, as well as life history milestones (e.g., age-at-weaning and the age at which children independently acquire the majority of their calories). Each individual in the sample was also assessed for skeletal indicators of poor nutrition/health. Collectively, the results suggest early ages of onset of both weaning and independent foraging. There also appears to be a correlation between skeletal indicators of poor nutrition/health and diets consisting of lower trophic level protein resources. Potential reasons for these findings, as well as their significant implications, will be discussed.

Funding for this research was provided by the Wenner Gren Foundation (Grant #9770), the Boeing Company, and the Society for California Archaeology.

Sulfur isotopes in modern deer bones of Virginia – establishing a $\delta^{34}\text{S}$ isoscape for archaeological studies of East Coast North Americans

CHRISTINE A.M. FRANCE¹ and JULIANNE J. SARANCHA²

¹Museum Conservation Institute, Smithsonian Institution, ²School of Earth and Space Exploration, Arizona State University

This project focuses on modern deer to map the bioavailable sulfur isotope distribution in Virginia as a proxy baseline for examining geographic origins. Stable oxygen isotopes are a well-established method to determine latitudinal region of origin in archaeological remains from North America. However, a longitudinal marker of movement between coastal and inland regions is currently lacking. Bone collagen sulfur isotopes have potential as a new longitudinal marker to examine the migration of early settlers from coastal colonies towards inland environments. This project focuses on a localized sulfur isoscape from modern deer in Virginia as the first such map of bone sulfur isotopes in North America. Results from over 200 deer across 25 counties (over 300 km distance) show more than 5 permil difference between the coast and mountains, making this the first viable method to track longitudinal origins in East Coast North America. The applicability to

other East Coast regions will be considered, as well as how this method may be used to examine archaeological geographic origins versus marine dietary input.

Anthropogenic effects on growth and development of captive and free-ranging *Macaca mulatta*.

GEORGE N. FRANCIS¹ and ANDREA R. ELLER²

¹Archaeology, UCL, ²Anthropology, Smithsonian Institution National Museum of Natural History

The phenotypic impact of anthropogenic pressures upon primates is increasingly prevalent, yet remains disproportionately understudied. Captive environments can pose unique pressures based on factors like physical activity levels and caloric availability; thus, maturation patterns should vary under differing captive conditions. The development and growth of two *Macaca mulatta* populations, under different levels of human management, were analyzed to assess the impact of anthropogenic environments on captive primates. To track development, we scored 13 epiphyseal fusion locales across long bones in a skeletal sample of lab-reared *M. mulatta* (n=154), including the right tibia, femur, humerus, ulna and radius. We employed a three-tier scoring system, consisting of "0" (unfused to diaphysis), "1" (fusing) and "2" (fused). To record growth and body size, we collected 29 linear measures of these long bones, taken via digital calipers to the nearest 0.1mm. Means and standard deviations were generated to compare samples; t-tests were used to determine significant differences between means. These values were compared to available data on the free-ranging, provisioned *M. mulatta* population of Cayo Santiago. The free-ranging monkeys (n=277) were found to exhibit larger postcranial lengths (p<0.05) and widths (p<0.05) than lab-reared specimens. Although larger limb bones are usually associated with delayed development, earlier epiphyseal fusion (up to 2.53 years) was also documented among free-range monkeys. These observations may reflect accelerated development resultant of a protein-rich diet provided to free-ranging monkeys, and may also reflect hindered growth caused by restricted movement experienced by lab-reared monkeys.

Proximal femoral shape: A new method for inferring past physical activity

SAMUEL FRANCIS^{1,2}, HADAS L. AVNI^{1,2} and HILA MAY^{1,2}

¹Department of Anatomy and Anthropology, Sackler Faculty of Medicine, Tel Aviv University, ²Shmunis Family Anthropology Institute, the Dan David Center for Human Evolution and Biohistory Research, The Steinhardt Museum of Natural History, Sackler Faculty of Medicine, Tel Aviv University

The femoral shaft is commonly used to gain insight on the physical burden and mobility of ancient populations. Historically, this information has been gained from analysis of femoral midshaft cross-sectional geometry. This methodology is based on the accepted notion that bones are developmentally plastic. Nevertheless, the femoral shaft is frequently broken in archeological material, thus locating the midshaft may be problematic. Geometric morphometrics approaches to osteological analysis have shown promise for advancing our understanding of biomechanics and adaptation. The aim of this study was to reveal the association between muscle strength and 3-dimensional shape of the proximal femur. The study included 42 individuals (24 males and 18 females) aged between 20 and 60 that underwent CT scans of the pelvis and/or lower limb for other medical purposes (ethical approval #0110-15-CMC). The cross-sectional area of the quadriceps and hamstrings muscle groups were measured using a planimetric method in the Philips Portal. The surface of the femur was segmented and reconstructed via Amira software (v.6.3). The 3D shape of the femur was obtained using a landmarks based geometric morphometrics method. The results of a two-block partial least square analysis showed very strong correlations (0.731≤r≤0.930) between muscle cross-sectional area and 3D femoral shape. The new method of 3D shape analysis of the femur allowed for reliable inference of muscle cross-sectional area, which is a surrogate for muscle force. To summarize, we suggest a new reliable and valid method for reconstructing physical burden and load from the femoral bone.

The authors wish to thank the Dan David Foundation for financial support.

Establishing a biological profile using your smartphone

ERIC FRAUENHOFER

Anthropology, State University of New York Buffalo State

The purpose of the research was to develop a mobile app for smart phones and tablets that could perform calculations based on the input of user measurements to establish the sex, ancestry, and stature of a biological profile for a skeleton using known and accepted methods. To test the usefulness of the app, 10 undergraduate students majoring in forensic science participated in a small experiment followed by a survey. Each student estimated the stature of a model skeleton of known height using the same method in three different trials: first, students calculated stature using a calculator; second, using a computer spreadsheet; and third, using the mobile app. Based on the results of the survey, students preferred using the mobile app for estimating stature. Additionally, students indicated they would prefer to use the mobile app if working in

ABSTRACTS

the field, but would prefer to use a spreadsheet or other computer program if working on a project with a large amount of data. Recommendations to improve the app included the option to save and export data, the option to test several methods at once, and the option to view a pictorial guide for measurements. These findings are important to the field of anthropology, particularly forensic anthropology, by demonstrating the need within the field for more mobile-friendly software for biological profile calculations using metric methods.

The research was funded by the Office of Undergraduate Research's Small Grant Program at the State University of New York Buffalo State.

Ontogenetic integration of the midline basicranium and cranial vault

JESSE FREDERICKS and JASON HEMINGWAY

Human Variation and Identification Research Unit, School of Anatomical Sciences, University of the Witwatersrand

The cranium is vital to bio-anthropological analyses as it is used for several applications in palaeoanthropological, bio-archeological and forensic contexts. Integration is necessary for organismal viability and the presence of genetic, developmental and functional associations have been explained by the long-established spatial packing, part-counterpart and functional matrix hypotheses. However, cranial features that form part of integrated complexes are often recorded as isolated characters, thereby skewing bio-anthropological studies involving nonmetric bio-distances and phylogenetics. Thus, this study aimed to assess the potential associations between growth of the midline basicranium and cranial vault shape using geometric morphometrics.

The study sample comprised 139 crania ranging from the time of birth to 30 years-of-age. Twenty one cranial landmarks were digitized, and midline basicranial synchondroses were assigned ordinal scores based on their state of fusion. The significance of the associations were tested, and illustrated via regression and partial least squares.

An overall increase in globularity was, in part, due to its developmental association with the increased length of the anterior cranial fossa and clivus, as well as a greater angulation of the anterior cranial fossa in relation to the clivus. The onset of fusion of the sphenoccipital synchondrosis appeared significant in relation to overall vault shape. The covariation between vault and basicranial shape was high. Thus, demonstrating the

importance of not assuming the independence of cranial features, but instead accounting for the effects of cranial integration by considering highly integrated traits as a single character complex.

This project was partly sponsored by the JJJ Smieszek Bursary, School of Anatomical Sciences, University of the Witwatersrand.

Toward an improved nutritional ecology of hunters: Macronutrient and mineral composition of wild animals consumed through the "bushmeat" trade in Nigeria

SAGAN FRIANT¹, CLEMENT B.I. ALAWA² and JESSICA M. ROTHMAN³

¹Anthropology & Huck Institutes of the Life Sciences, The Pennsylvania State University, ²Veterinary Medicine, University of Abuja, Nigeria, ³Anthropology, Hunter College of the City University of New York

Hunting increases access to nutrient rich animal-source food, contributing to improved human nutrition in many modern and ancient environments. However, our understanding of the nutritional contributions of wild animals to local diets is based on limited nutritional data. This research uses a mixed methods approach to examine the nutritional composition of "bushmeat" in Nigeria. We test the hypotheses that: 1) consumption of wild animals expands the range of macro- and micro-nutrients available to local diets; and 2) nutritional composition shapes local food preferences. We examined the macronutrient composition of different types of animals: wild meat (n=28), fish and seafood (n=16), and domestic meat (n=6) consumed in rural hunting communities in Nigeria. Our analysis shows that meat offered significantly higher energetic returns compared to fish and seafood (H=6.8, df=2, p < 0.05); however, contrary to the prevailing paradigm, wild meat was not characterized by a higher protein to fat ratio (H=2.25, df=2, p = 0.35). Mineral composition varied widely across species and animal parts, but they did not differ significantly between types of animals (p-values > 0.05). Lead (Pb) values from few hunted animals exceeded tolerable weekly intakes, suggesting possible toxicity risks. When combined with organoleptic and food preference data, our results suggest that local meat preferences are shaped, in part, by high fat to protein ratios and cultural salience of wild meat over domestic animals and fish. Results contribute to an improved understanding of human dietary strategies in response to availability of animal-derived nutrition in both ancient and modern environments.

This research was funded by the National Science Foundation (SBE #1604902), Primate Conservation Inc. (PCI# 1381), and Professional Staff Congress - City University of New York (PSC-CUNY).

Tough nut to crack: Durophagy and the tympanic plate in Cercopithecines

ELLEN E. I. FRICANO¹ and KAYA G. ZELAZNY²

¹Department of Medical Anatomical Sciences, Western University of Health Sciences, ²Department of Biology, College of Saint Scholastica

Given the tight spatial relationships between the temporomandibular joint and the auditory structures, it has been suggested that a bony tympanic tube may provide a buffer to dampen the noise of mastication. The present study tests the relationship between diet and tympanic traits in a sample of nine species of Cercopithecines (*Cercocebus ssp.*, *Erythrocebus sp.*, *Lophocebus ssp.*, *Macaca ssp.*, *Papio sp.*, and *Theropithecus sp.*). Two regions were considered in this study: the tympanic plate (TYMP) itself and the post glenoid tubercle (PGT), which lies at the division between the masticatory and auditory systems. The PGT has been suggested to protect the tympanic plate from potential posterior dislocation of the mandible and may help to further separate the forces of mastication and the tympanic plate. Linear measurements describing the shape of the TYMP and PGT were collected from CT scans using Amira software and were compared between durophagous and non-durophagous primates using two-way ANOVAs and partial correlations.

The authors found that among the Cercopithecines studied, the PGT was significantly shorter and closer to the TYMP in durophagous compared to non-durophagous species, but the scaled TYMP length did not differ significantly. Thus, the posterior boundaries of the temporomandibular joints of durophagous primates are closer to tympanic bone, potentially increasing rather than decreasing intracranial noise perceived in the ear. This morphology is, however, consistent with previous hypotheses that durophagous behaviors might correlate with antero-posterior elongate TMJs, allowing for greater range of motion.

Forced Migration and the Skeletal Record at Fort Amsterdam Depot, St Eustatius, Dutch Caribbean

FELICIA J. FRICKE¹ and JASON E. LAFFOON²

¹Classical and Archaeological Studies, University of Kent, ²Archaeological Sciences, Leiden University

St Eustatius is a small island in the north-eastern Caribbean. In the early 18th century, a fortification on its south coast (Fort Amsterdam) was converted into a depot holding enslaved people for transshipment to the nearby Spanish, English, and French islands. Documentary sources indicate that a burial ground adjacent to the fort was used for African ancestry individuals but does not indicate whether they were prisoners from the depot or enslaved people from nearby plantations. Excavated primarily in rescue situations as the sandy cliff collapses, the incomplete

ABSTRACTS

and fragmentary remains from Fort Amsterdam are nevertheless substantial enough for the isotopic analysis, palaeopathological analysis, and ancestry assessment of seven individuals which can help us to understand the embodied experiences of enslaved people. Results of the analysis showed that several of these individuals were of African ancestry and had probably spent their early childhood in sub-Saharan Africa. Metric analysis indicated that another individual may have had indigenous Caribbean ancestry, and palaeopathological information included evidence for trauma and metabolic disease. These results are important because of the paucity of information that we have concerning the enslaved people of the Dutch Caribbean, much less the enslaved people who came through the large depots of the region. Although this site represents challenges it has provided information which helps us to understand enslavement in the region from a bottom-up perspective.

Many thanks are due to the University of Kent Centre for Heritage and the UK Society for Latin American Studies.

A re-evaluation of the Atterton technique: A method for sex estimation using the clavicle

SADIE R. FRIEND and CASSADY URISTA
Anthropological Sciences, Radford University

In addition to pelvic and cranial methods for sex estimation, biological anthropologists commonly look to other postcranial elements to strengthen the probability of their estimates—the current study re-examines the applicability of the clavicle. Previous research conducted by Atterton and colleagues (2016) established a discriminant function using the variables of clavicular circumference and clavicular length for sex estimation in a medieval British sample with an accuracy rate of 89.6%. The current study determines the accuracy of the Atterton et al. discriminant function on two comparatively modern skeletal collections; the Bass Donated Skeletal Collection, which is predominantly composed of individuals from the early 20th century, and the Hamann-Todd Osteological Collection, primarily composed of individuals from the late 19th century. The success rate of the discriminant function was determined by comparing the results using general percent agreement. In this study, the function was successful in estimating the sex of 58% of females and 97% of males. When analyzed by ancestry it was successful for 89% of black individuals and 87% of white individuals. When comparing pooled individuals (of both sexes and ancestries), the function successfully estimated the sex in 98% of black males, 96% of white males, 62% of black females, and 55% of white females. The accuracy rate of this modern sample (87.5%) is consistent with that of the medieval population.

Another look at the funny bone: Humerus shape in extant Apes and fossil hominins

MARTIN FRIESS and MARGHERITA SBANCHI
Homme et Environnement, MNHN - Musee de l'Homme

One of the core challenges for paleoanthropologists is to assess early hominin locomotor behavior from often incomplete fossil remains. The increasing availability of 3D imaging, combined with current geometric morphometric (GM) approaches, offers the possibility to quantitatively compare morphological shapes not easily described with linear measurements. We illustrate this by conducting a 3D GM analysis of the humerus in extant hominoids and fossil hominins, in order to further document morphological differences related to locomotion in extant forms and to infer locomotor behavior in extinct forms. A sample of 100 humeri of extant apes (Gorilla, Pan, Pongo, Hylobates) and modern humans was surface-scanned. Fossil casts of early hominins, assigned to Paranthropus, Australopithecus and Homo, were also included. A total of 186 standard landmarks and semilandmarks were extracted and, after sliding the semilandmarks, Procrustes-aligned. Overall shape affinities of the complete humerus and the distal articular surface were assessed using Principal components analysis and within- and between-group Procrustes distances. The results confirm previously documented differences between major locomotor groups, with Hylobates having the most distinct shape. Human humeri are distinct as well, though show some overlap with Pan. Procrustes distances provide insight into how well fossil hominins fit into extant patterns. According to our findings, the humerus shape of australopithecids, including *Au. sediba* and *Au. anamensis*, is most similar to Orangutan, followed by chimpanzees and humans. However, the lack of clear difference between hominins and extant Apes is compatible with a wider range of locomotor behavior, rather than with a specialized one.

Movement ecology of Kinda baboons (*Papio kindae*) in Kasanka National Park, Zambia: A preliminary study

AMANDA J. FUCHS¹ and JASON M. KAMILAR^{1,2}
¹Department of Anthropology, University of Massachusetts, ²Organismic and Evolutionary Biology Graduate Program, University of Massachusetts

Primate movement strategies are known to be influenced by resource distributions, including seasonal changes in resource availability. Some of these movement strategies can be best modeled via Brownian motion, Lévy-walks and/or goal directed movements (i.e. mental maps). For example, primates may fit a Lévy-walk model when resources are patchily distributed. However, we are only beginning to understand

how primates navigate their environment. Here, we test whether the movement patterns of Kinda baboons (*P. kindae*) in Kasanka National Park (KNP) follow a Lévy-walk model. KNP is a heterogeneous field site with varied distributions of food and water resources. If Kinda baboons are exploiting a patchily distributed resource, then we expect their movement patterns to fit a Lévy-walk model. We collected movement and behavioral data every 30 minutes from a habituated troop in a June 2018 pilot study. We used the GPS data to quantify the troop's step-lengths. Also, we used the powerLaw package in R to test whether the distribution of step-lengths fit a Lévy-walk model (i.e. power law). We found that the baboons consume patchily distributed pods during 54% of their feeding time. In addition, we found that the distribution of Kinda baboon step-length fit a Lévy-walk model. In the future we will test Kinda baboon movement patterns throughout the year to account for seasonal variation in resource availability. This will shed light on movement strategies and the evolution of spatial memory in a heterogeneous habitat.

Funded by the Natural History Collections Summer Research Scholarship at the University of Massachusetts, Amherst, and the Department of Anthropology Summer Pre-dissertation Research Fellowship at the University of Massachusetts, Amherst.

Impaired, but cared for? Social implications of a case of Legg-Calvé-Perthes Disease and multiple trauma from the North Caucasian Bronze Age

KATHARINA FUCHS¹, BIASLAN C. ATABIEV² and JULIA GRESKY³

¹Institute of Clinical Molecular Biology, Kiel University, ²Institute for Caucasus Archaeology, Nalchik, ³Department of Natural Sciences, German Archaeological Institute, Berlin

This paper presents a case of a probable Legg-Calvé-Perthes Disease (LCPD) in an adult male individual from the central North Caucasian foothills 2250-1650 BCE. Besides contributing to the number of LCPD cases found in ancient skeletal material, the paper discusses how the osteobiography of this individual, which includes traumatic injury and idiopathic impairment of the lower limbs, gives evidence for the bioarchaeology of care in the North Caucasian Bronze Age.

Nowadays diagnosed in less than one of 10,000 patients, the Legg-Calvé-Perthes Disease fulfills the recent definition of a rare disease and is even rarer in the paleopathological record. While the primary etiology is discussed in clinical studies, its pathophysiology describes an idiopathic vascular necrosis of the femoral head during childhood that affects the development of the hip joint, including collapse, resorption, re-ossification, and eventual healing. It can result in an uneven growth

ABSTRACTS

and shape of both proximal femur and pelvis, including weakening and limited mobility, and favors a higher risk of osteoarthritis in the hip joint during adolescence and adulthood.

By following a multi-method approach, we discuss potential differential diagnosis of the osseous manifestations indicative for LCPD that have been identified in the skeletal remains from grave 067 of the cemetery 'Kudachurt 14'. In addition, fractures of the skull and right femur indicate a life history marked by severe trauma, recovery and physical restrictions. By integrating information on diet and socio-ritual status, we conclude on practiced social integration and medical care in this ancient North Caucasian population.

This research was funded by the Graduate School 'Human Development in Landscapes' at Kiel University (German Research Foundation DFG - GSC 208).

The role of long-term studies in education and conservation: The Lomas Barbudal Monkey Project as a case study

TLAOLI FUENTES-ANAYA^{1,2} and SUSAN PERRY^{1,2}

¹Dept. of Anthropology, University of California-Los Angeles, ²Behavior, Evolution and Culture Program, University of California-Los Angeles

The longer a field site runs, the deeper its connections with local communities and the better equipped it is to serve the habitat country with regard to conservation-related assistance and environmental education. In addition, long-term field sites provide excellent opportunities for young scientists to be trained in field methods and to have data collection opportunities. Here we present examples of ways that the Lomas Barbudal Monkey Project has contributed to conservation efforts in Costa Rica, helping with management plans, reforestation, and vigilance for the park service. We also describe some of the more effective ways in which we have provided environmental education to 11 K-12 schools near the reserve, and our efforts to provide educational materials to a more global audience. One of the Lomas Barbudal Monkey Project's most successful educational contributions is the training of so many early career field primatologists: 179 people from 18 countries have benefitted from some fieldwork opportunities at Lomas. Of the 98 interns who stayed a year or more, 66 applied to graduate school (65 being admitted), 15 former interns are now professors, 10 obtained postdoctoral fellowships, 21 work in environmental education, 19 are in conservation-related jobs, 6 work in the ecotourism industry, and 6 work in animal welfare jobs. Data from Lomas contributed to 4 master theses and 8 completed Ph.D. theses. Moreover, early exposure

to our informal environmental education efforts (in particular, to the communication of the life stories of individual monkeys) has resulted in many staunch local supporters of conservation.

Funding: Wild Capuchin Foundation, National Geographic Society grants to S. Perry (particularly grant NGS-45176R-18)

The Impact of Admixture on Neanderthal and Denisovan Ancestry in Modern Human Populations

ALYSSA FUNK¹, KELSEY WITT DILLON², LESLY LOPEZ³, JONATHAN RICE³ and EMILIA HUERTA-SANCHEZ²

¹Molecular and Cellular Biology, Brown University, ²Ecology and Evolutionary Biology, Brown University, ³Quantitative and Systems Biology, University of California, Merced

Admixture between previously isolated populations has occurred frequently throughout the course of human evolution, both between modern human populations and between humans and Neanderthals and Denisovans. Admixture is an important component in shaping patterns of genetic variation and disease risk. Despite the growing evidence of repeated and ongoing admixture events, most studies screen out admixed segments of the genome (or whole admixed populations) since admixed ancestry is a complicating factor for many analyses.

In this study, we examine the impact of admixture on the frequency of archaic alleles (both Neanderthal and Denisovan) in admixed populations in the Americas. We find the number of archaic alleles an individual possesses is positively correlated with European and Native American ancestry, and negatively correlated with African ancestry. Archaic alleles are found most often in regions of the genome with European and Native American ancestry; and Denisovan alleles are found most often in genome regions with Native American ancestry. We also examined archaic alleles present in regions previously identified as candidates for adaptive introgression. We propose several genes as candidates for local selection based on a high frequency of archaic alleles in admixed American populations, but low frequency in East Asian populations. We found it is possible to break down admixed populations by ancestry and find ancestry-specific trends in archaic allele frequency.

Individual Flexibility in the Construction of Social Niches by Wild Chimpanzees

JAKE A. FUNKHOUSER¹, DAVID MORGAN², STEPHANIE MUSGRAVE³ and CRICKETTE SANZ^{1,4}

¹Department of Anthropology, Washington University in St. Louis, ²Lester E. Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo, ³Department of Anthropology, University of

Miami, ⁴Congo Program, Wildlife Conservation Society

Individuals that live within fission-fusion social systems must successfully navigate dynamic social landscapes and varying ecological pressures to survive. However, the degree of individual flexibility within the construction of overlapping patterns of social relationships (i.e., social niches) is largely unknown. We investigated the construction of social niches by wild chimpanzees (*Pan troglodytes troglodytes*) in the Goulougo Triangle, Republic of Congo between two ecological contexts: fig-feeding and termite-gathering. We hypothesized that patterns of social relationships would differ between contexts and reflect behavioral responses to separate selective pressures. From a two-year period, we analyzed associations of 20 females and 14 males in both ecological settings across multiple timescales using multi-dimensional network analyses. As predicted, patterns of social associations differed between the two contexts: node strength and eigenvector centrality were greater in the fig-feeding niche, and network modularity was greater in the termite-gathering niche. Social niches at fig trees are constructed by many relationships, but during termite gathering they are constructed by stable associations with few individuals. Such flexible social niche construction may facilitate mating opportunities, serve to strengthen social bonds, and provide socialization opportunities for offspring during fig-feeding, as well as facilitate the transmission of technical information during termite-gathering. The flexible construction we observed is likely mediated by fission-fusion sociality where individuals have increased agency in where and with whom they spend their time, compared to stable systems. These results provide empirical insights into the pressures favoring individual flexibility and the evolution of dynamic primate social systems.

Arcus Foundation, Indianapolis Zoo, Cincinnati Zoo and Botanical Garden, Houston Zoo, Columbus Zoological Park, Nouabalé-Ndoki Foundation

Comparing the Accuracy of Close-Range Photogrammetry to microCT Scanning via Surface Deviation Analysis of 3D Digital Models of Hominin Molars

MARGARET J. FURTNER and JULIET K. BROPHY
Department of Geography & Anthropology,
Louisiana State University

The purpose of this study is to assess whether close-range photogrammetry is a viable alternative to microCT scanning for the construction of 3D models of isolated teeth. Photogrammetry is more cost-effective and less time-consuming than CT scanning, and in paleoanthropological contexts it eliminates the possibility of exposing fossils to doses of radiation that affect ESR dating. Samples of *Homo naledi*, archaeological, and contemporary human molars were scanned

ABSTRACTS

via microCT scanning and close-range photogrammetry. The photogrammetric scans included 96 digital images per tooth which were used to construct a 3D triangular mesh. The resulting models of the tooth crowns were compared to their corresponding CT models using point-to-point surface deviation analysis, which measures the distance between analogous points on each mesh. The surface deviation analysis produced surface differences with standard deviations as low as 0.031 mm, meaning that 95% of all points on the photogrammetric mesh fall within 0.062 mm of the corresponding point on the microCT mesh. Surface deviation analysis was also conducted to compare the difference between the raw CT meshes (~2,000,000 triangles) and their decimated counterparts (~20,000 triangles). The surface differences between the processed CT and photogrammetric meshes were comparable or had less differences than between the raw and unprocessed CT models, with the highest match rate of 80% in the archaeological sample. These results indicate that close-range photogrammetry can be used as an accessible alternative to microCT scanning for generating 3D surface models of isolated teeth.

This research was funded by the R.J. Russell Graduate Student Research Award and the G&A Graduate Research Materials Award through the Department of Geography & Anthropology at Louisiana State University.

Is depression an evolved costly signal of need?

MICHAEL GAFFNEY and EDWARD HAGEN
Anthropology, Washington State University

Major depression is considered to be a pathological response to stress that elicits aversive responses towards depressed individuals. Alternatively, depression might involve honest signals of need in response to stress and help to bargain for increased support from reluctant others. To test this hypothesis, we examined responses to a wide range of emotional signals in a vignette study in which we also manipulated information about the signaler's need and her levels of conflict with the social partner (participant) in a between-subjects factorial design. Specifically, a fictional sister asked the participant to help pay for medical treatment. The sister's true need for money was either clear or questionable, and her level of conflict with the participant was either high or low. The sister's signals were either verbal request, crying, depression, or, as a control, schizophrenic symptoms.

In our sample of 1,447 participants recruited from Amazon Mechanical Turk, depression increased belief in need and elicited more help than all the other proposed signals of need on our four outcome measures across all conditions. Simple crying and verbal requests were generally less effective. We also found evidence

for the predicted interaction between signal type and conflict on relationship outcomes. Because signals comprising symptoms of schizophrenia caused a dramatic reduction in support, we can discount the hypothesis that help was provided due to symptoms of mental illness. Our results suggest that depression, an apparent human universal, is a relatively successful way of signaling honest need and eliciting support, consistent with costly signaling explanations.

The First Decorative Dental Inlay Identified in a Pre-Hispanic Peruvian

CELESTE MARIE GAGNON¹, BRANDEN C. RIZZUTO², BETHANY C. TURNER³ and SCOTT E. BURNETT⁴

¹Anthropology, Wagner College, ²Anthropology, University of Toronto, ³Anthropology, Georgia State University, ⁴Anthropology, Eckerd College

This work documents the first unambiguous case of a pre-Hispanic Peruvian with dental inlays—an adult bearing two labially drilled maxillary canines, one of which retains a metallic inlay *in situ*. The individual's remains were recovered from a disturbed context in Huaca de la Luna, one of two monumental structures that anchor the north coast site of Huacas de Moche. This densely occupied site served as a primary ritual center of the Southern Moche State circa AD 400-800.

To characterize aspects of the individual's life history and the remaining inlay, we report the results of biochemical and pXRF analyses. Dentin was analyzed for collagen $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ characterization and AMS dates, and enamel for carbonate $\delta^{13}\text{C}$, $\delta^{18}\text{O}$, $^{87}\text{Sr}/^{86}\text{Sr}$, and $^{206,7,8}\text{Pb}/^{204}\text{Pb}$ characterization. Light isotopic data were compared to published data and 38 individuals recovered from the nearby site Cerro Oreja, the occupation of which predates that of the Huacas de Moche. The heavy isotopic data were compared to 14 individuals. Results indicate the affected individual lived during the Moche period, and consumed a ^{13}C -enriched diet including maize, meat from C_4 consumers such as camelids, and/or low-trophic-level marine foods. $^{87}\text{Sr}/^{86}\text{Sr}$ and $^{206,7,8}\text{Pb}/^{204}\text{Pb}$ values closely resemble those from Cerro Oreja, but $\delta^{18}\text{O}$ values are much higher, suggesting *chicha* consumption. pXRF results indicate that the inlay is composed of electrum but could also be silver or a silver-heavy alloy overlying a gold/tumbaga substrate. Together the data suggest that affected individual was likely a local resident whose social identity was connected to *chicha* consumption.

This research was funded by Wagner College's Anonymous Donor, Faculty Research, and Department of Anthropology grants.

Evidence of Selection in the *UCP1* Gene Region Suggests Local Adaptation to Irradiance Rather than Cold Temperatures in Savanna Monkeys (*Chlorocebus* spp.)

CHRISTIAN M. GAGNON¹, HANNES SVARDAL², ANNA J. JASINSKA^{3,4}, NELSON B. FREIMER³, PAUL J. GROBLER⁵, TRUDY R. TURNER^{5,6} and CHRISTOPHER A. SCHMITT¹

¹Department of Anthropology, Boston University, ²Department of Biology, University of Antwerp, ³Center for Neurobehavioral Genetics, University of California, ⁴Institute of Bioorganic Chemistry, Polish Academy of Sciences, ⁵Department of Genetics, University of the Free State, ⁶Department of Anthropology, University of Wisconsin

Members of the genus *Chlorocebus* are widely distributed throughout sub-Saharan Africa, and in the last 200 ky expanded from East Africa into the southern most regions of the continent. In these new environments, exposure to colder climates was likely a significant driver of selection. We investigated population-level genetic variation in the mitochondrial Uncoupling Protein 1 (*UCP1*) gene – implicated in non-shivering thermogenesis within brown/beige adipocytes – in 73 wild savanna monkeys from three taxa representing this southern expansion: *Chlorocebus pygerythrus* in South Africa and Botswana, *Chlorocebus cynosuroides* in Zambia, and *Chlorocebus hilgerti* in Kenya and Tanzania. Our analyses included 10 kb flanking regions upstream and downstream of coding regions to capture variation in potential cis-acting regulatory regions. Discriminant analysis of principal components and F_{ST} around *UCP1* shows overall differentiation consistent with phylogenetic distance. 21 SNPs show extended haplotype homozygosity consistent with positive selective sweeps ($p_{HS} > 1.3$), 7 of which are also out of Hardy Weinberg equilibrium. Phylogenetic generalized least squares models show significant negative relationships in selected derived allele frequencies with mean annual irradiance (7:87493023, intron 5-6, $p_{HS} = 1.8$, $b = -0.32$, $p = 0.0086$ and 7:87509248, upstream variant, $p_{HS} = 1.8$, $b = -0.10$, $p = 0.0003$), rather than with low temperatures, suggesting that sunbathing behaviors in combination with strength of irradiance may mediate adaptations in non-shivering thermogenesis to thermal stress in cold regions. Although compelling, these variants are all in non-coding regions with no previously known regulatory function, and require further validation and research.

Fertility and growth rate estimation based on age-at-death composition of skeletal sample: Stochastic approach accounting for sample size

PATRIK GALETA and ANNA PANKOWSKÁ
Department of Anthropology, University of West Bohemia

ABSTRACTS

Palaeodemographic reconstructions provide important insight into biocultural adaptation of past population to environmental and social change. A widely accepted tool for estimation of demographic rates is based on age-at-death indices, e.g. D5+/D20+, the number of deceased older than 5 years to those older than 20 years. The key advantage is that indices are not limited by the under-representation of infants and by the unreliable age-at-death assessment in adults. Little attention, however, has been paid to the fact that demographic composition of small skeletal samples might substantially differ from the general population due to random fluctuation. In this paper, we provide a methodology for estimation of the crude birth rate, total fertility, and population growth rate that acknowledge the stochastic variation due to small samples. Demographic rates were estimated using regression equations with D1+/D20+ or D5+/D20+ index as predictor. Contrary to others, demographic rates of each real skeletal sample are estimated using a unique set of 1000–5000 simulated skeletal samples with the same number of adults as in the corresponding real sample. To match prehistoric demographic settings, simulated samples are derived from model populations with life expectancy at birth between 20–30 years and subjected to annual growth rate between -2 and 4%. Simulation are done using scripts in R environment. Within skeletal samples with 100 adults, for example, correlation coefficients between demographic rates and indices varies around 0.9. Growth rate can be estimated within $\pm 0.5\%$ and fertility rate within ± 1.2 children.

This work was funded by the Czech Science Foundation, grant number 19-17810S.

The cost of gathering: Food choices and energy expenditure among the Baka, a forager-horticultural society from south-eastern Cameroon

SANDRINE GALLOIS and AMANDA G. HENRY
Faculty of Archaeology, Leiden University

Models about food choices and dietary behavior in the past often make simplistic assumptions about the relative costs of different foraging behaviors. With the Baka, a forager-horticultural group in Cameroon, we have been exploring the drivers of food behaviors, including food preferences and energetic costs of foods, especially wild edible plants.

We measured the energy spent by the Baka during their daily subsistence activities, using GPS trackers - heart rate monitors and time allocation recalls. A total of 246 records were gathered among 153 Baka adults (97 women and 56 men) from four different villages. We compare the metabolic equivalent of task -MET- of activities related to food acquisition and preparation.

While crop harvesting and agricultural work have the highest MET (mean \pm sd 8.3 \pm 1.8; 6.9 \pm 2.2 respectively), the MET of gathering activities (6.8 \pm 2.8) was higher than those of fishing and hunting activities (6.4 \pm 1.4; 6.3 \pm 2.4 respectively). More interestingly, the gathering of wild nuts in particular required more energy than all other activities (9.5 \pm 5.1).

While gathering of wild plants is frequently considered as low cost and high productivity, our results show that gathering, of certain plants in particular, might be more effort-demanding than other subsistence activities. We discuss these insights by putting them in the overall framework of drivers of food behaviors, merging them with the cultural and environmental factors that might explain Baka food choices and the place of wild edible plants in their diet.

This project was funded by the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation program [grant number STG-677576 ("HARVEST")].

Identity from the Ashes: Multidisciplinary approaches to identification of wildfire victims

ALISON GALLOWAY
Anthropology, UC Santa Cruz

On November 8, 2018, fire erupted on Camp Creek Road in Butte County. High winds drove flames through Concow, Magalia, and Paradise. Residents, if able, fled, many driving on crowded roads between walls of fire. Firefighters focused on evacuations and fire containment. Over 18,000 structures were destroyed and the number missing or dead was unknown at the start of recovery.

Location was critical in identification of the deceased but was complicated by the lack of normal navigational keys such as address numbers. Search and rescue teams and recovery teams resorted to Google Maps, matching driveway and entry characteristics. The large number of mobile home parks were an additional problem as unit numbers were no longer present and posted directories had burned.

CSU Chico led-teams staffed recovery efforts, maximizing the collection of small bones, implanted medical devices and dental remains essential for the post-recovery analysis. Many bodies consisted of calcined or badly charred bone. In the morgue, anthropologists focused on identification of incomplete, split or commingled remains by location. The actual identification depended on a teams of pathologists (who identified medical devices), odontologists (who worked on reconstructing and matching dentitions) and, most importantly, rapid DNA analysis once viable samples were found.

From a list peaking at over 1400 missing individuals, final death toll stands at 85. Most were elderly or disabled, unable to flee or whose escape was cut short. The majority have been positively identified and most of the remainder are identified by circumstances (location, biological profile and missing status).

This work was not funded.

The Pleistocene Peopling of the Tibetan Plateau: Environmental Background, Mechanisms and Processes

XING GAO¹, MINGJIE YI² and JOHN W. OLSEN³
¹Paleoanthropology, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences, ²Archaeology, School of History, Renmin University of China, ³Anthropology, School of Anthropology, University of Arizona

The timing and processes of the initial Pleistocene peopling of the Tibetan Plateau are challenging issues. Recent discoveries and research indicate the possibility that Denisovan groups may have occupied marginal areas of the plateau at least 160 kya, and the high-altitude Tibetan Plateau interior was explored at least 40 kya by early modern humans. Various models explaining the mechanisms and processes of the Paleolithic peopling of the plateau have been proposed, including a three-step migration and adaptation scheme, the suggestion that agriculture facilitated permanent human occupation of the plateau only after 3600 BP, and the possibility of admixture of different hominin groups before and after the Last Glacial Maximum (ca. 18-22 kya), among others. This paper reviews the history of archaeological investigations of these issues, reports new discoveries and research results, and explores the paleoenvironmental background of early human migration and adaptations to the roof of the world. We also evaluate various hypotheses of prehistoric human dispersals and survival in such a severe environment from the perspective of paleoecological and paleoenvironmental changes, possible pathways into and through this unique geographical setting, and the technological and behavioral patterns and capabilities of the prehistoric pioneers of the Earth's "third pole".

This research is supported by the Strategic Priority Research Programs of Chinese Academy of Sciences (grant no.: XDA2004010102 and XDB26000000)

The Pregnancy Pickle: Evolved immune compensation due to pregnancy underlies sex differences in human diseases

ANGELA R. GARCIA^{1,2}, HEINI NATRI^{1,2}, KENNETH BUETOW^{1,2}, BENJAMIN C. TRUMBULE^{1,3} and MELISSA A. WILSON^{1,2}

¹Center for Evolution and Medicine, Arizona State University, ²School of Life Sciences, Arizona State University, ³School of Human Evolution and Social Change, Arizona State University

ABSTRACTS

Sex differences exist across a range of human diseases, that to date have been understudied and largely unexplained. For example, females in industrialized populations exhibit a higher prevalence of most autoimmune diseases than do males. By contrast, females have a lower risk of developing cancer, with nearly all cancers showing a higher incidence in males. Here we present the Pregnancy Compensation Hypothesis (PCH), which explains both the proximate and ultimate (evolutionary) mechanisms responsible for sexual dimorphism observed in human disease, as mediated by selection on the immune system due to pregnancy and placentation. We suggest that because evolution has shaped the human immune system differently in females and males, dramatic shifts in our reproductive ecology and environment have led to sex differences in diseases to be more pronounced in urban, industrialized contexts. Under the PCH, we propose that the evolution of eutherian placentation exerted sex-specific selection on female immune function to tolerate fetal antigens while still defending the pregnant individual against pathogens. We theorize that this process is regulated proximately via hormones and mediated genetically by dosage on sex chromosomes, and that today, the mismatch between an ancestral environment and urban industrial environment interacts with this evolved compensatory immune regulation and results in the observed sex differences in disease risk. Finally, a sedentary lifestyle that affects reproductive hormone levels exacerbate these differences. We unpack the interrelated components of the PCH related to shifting reproductive states, parasite loads, and energetic availability, which are particularly relevant for sex differences in human disease.

This work was supported in part by a Wenner-Gren Foundation Dissertation Grant #9466.

Observing Similarities of Pre and Post-Contact Cranial and Dental Modification in Two Sites from Western Mexico (1350-1580 AD)

ARIEL GARCIA, MARIANA SANTOS and CHRISTINE LEE

Anthropology, California State University, Los Angeles

Barra de Navidad, Jalisco (1580±90 AD) and Amapa, Nayarit (1350±60 AD) are two sites located in modern day Western Mexico. These sites were settled by agricultural communities similar to those in central and southern Mesoamerica. This region widely practiced cranial and dental modification throughout both the Pre-Columbian and Post-Contact periods. A total of 7 individuals from Barra de Navidad (6) and Amapa (1) were analyzed for such cultural modifications. At Barra de Navidad (2) and Amapa (1), 43% of the sample population presented tabular oblique cranial deformation. Whereas 29% of the

sample population had dental modification in the form of filed teeth - 1 young adult male from Barra de Navidad and 1 young adult female from Amapa. The male from Barra de Navidad had filed central and lateral maxillary incisors. The female from Amapa also displays tooth filing, but unfortunately only the left central maxillary incisor was present for analysis. Patterns of tabular oblique cranial deformation fit a pattern observed through Western Mexico and Southern Mesoamerica that relate to social status and identity. In contrast, patterns of dental filing may be representative of different clan lineages, or performed as a rite of passage into adolescence. Considering the distance between both sites and the different time periods, it is interesting that the same patterns of dental modification are found in both sites. We suggest that although the pattern of dental filing is the same, it is not indicative of clan lineage but rather, may represent a rite of passage.

Dengue susceptibility and resistance in a Guatemalan cohort: incorporating an evolutionary perspective using signatures of natural selection

OBED A. GARCIA¹, LETICIA CASTILLO-SIGNOR², SONIA CAPETILLO³, EDGAR M. SANTOS⁴, NEVIS NUÑEZ⁵, VILMA VILLATORO⁶ and ABIGAIL W. BIGHAM⁷

¹Anthropology, University of Michigan, ²Dirección General Sistema Integrado Atención en Salud, Ministerio de Salud Pública y Asistencia Social de la República de Guatemala, ³Epidemiología, Dirección de Área de Salud Chiquimula, ⁴Epidemiología, Dirección de Área de Salud Guatemala Central, ⁵Epidemiología, Hospital Nacional de Coatepeque, ⁶Epidemiología, Dirección de Área de Salud Guatemala Nor Oriente, ⁷Anthropology, University of California Los Angeles

Evolutionary medicine seeks to incorporate perspectives from medicine, public health, and anthropology to understand how our evolutionary past affects our overall health in the present. We implement this approach to understand how past selection shapes modern genetic susceptibility to Dengue Virus. DENV is a mosquito-borne RNA virus belonging to the family Flaviviridae. It is widespread in subtropic and tropic environments, with up to 390 million infections each year. We leveraged indigenous American genomic signatures of selection to identify resistance and/or susceptibility loci to this modern pathogen in a Guatemalan cohort. We recruited dengue infected (60) and uninfected (120) participants from health centers throughout Guatemala. Infection was confirmed using the InBios DENV Detect IgG and IgM Capture ELISA method. Exome sequence data were generated using the IDT xGen Exome Research Panel. SNPs showing significant associations with DENV-infection were identified with logistic regression that used an additive model of inheritance. Covariates including control for population stratification were

included in the model. Functional impact of the significant SNPs was assessed using the Encode track of UCSC Genome Browser. This determined if significant SNPs lie in regions characterized by H3K27Ac marks, DNase I hypersensitivity, or ChIP-seq transcription factor binding and/or in regions characterized by miRNAs, snoRNAs, or lincRNAs. Furthermore, gene ontology analysis was conducted to reconstruct potential pathways affected by DENV-infection. Our results demonstrate the effect of past selection on modern infectious disease risk, bridging the gap between the medicine and anthropology—directions to which anthropology can steer the conversation towards an evolutionary framing.

Thank you to the National Science Foundation (Award #1824839), Wenner Gren Foundation, The Tinker Foundation, and the International Institute at the University of Michigan.

Did *Pierolapithecus* have an ape-like thorax? 3D shape analysis of the *Pierolapithecus catalaunicus* lower rib IPS21350.58 and its implications for understating its bauplan

DANIEL GARCÍA-À-MARTÀ-NEZ^{1,2}, NICOLE TORRES-TAMAYO², SHAHED NALLA³, DAVID ALBA⁴, SALVADOR MOYÉ-SOLÉ^{4,5}, SERGIO ALMÉCJA^{4,6,7} and MARKUS BASTIR²

¹Hominin paleobiology, Centro Nacional de Investigación sobre la Evolución Humana (CENIEH), Burgos, Spain, ²Paleoanthropology Group, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, Spain, ³Faculty of Health Sciences, University of Johannesburg, Johannesburg, South Africa, ⁴Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, Barcelona, Spain, ⁵Institució Catalana de Recerca i Estudis Avançats, Barcelona, Spain, ICREA, ⁶Human Biology, American Museum of Natural History (AMNH), NYC, US, ⁷Primateology, New York Consortium of Evolutionary Primateology (NYCEP), NYC, US

Pierolapithecus catalaunicus (12 Ma; Vallès-Penedès Basin, Spain) is a middle Miocene ape from NE Iberian Peninsula considered a stem hominid (i.e., early member of the great-ape-and-human clade). Even though there are signals of monkey-like features in its pelvis, other evidences point to a modern ape-like orthograde bauplan. This is partly based on the ribs morphology, indicating an ape-like wide and shallow ribcage, different from the narrow and deep monkey ribcage. However, the information about its ribs is based on qualitative comparisons, so an accurate 3D quantification is necessary to confirm this assessment. Here we use 3D geometric morphometrics of 8 landmarks and 44 semilandmarks per rib to explore if the best-preserved rib of *P. catalaunicus* (IPS21350.58) had an ape-like or monkey-like morphology. To explore that, we compared it with a sample of central-lower ribs (N=376) from extant monkeys (*Macaca*,

ABSTRACTS

Ateles, Alouatta), apes (*Pan, Pongo, Hylobates* and *Symphalangus*) and humans (*Homo*). PC1 clearly separates monkeys (negative scores) from apes and humans (positive scores), IPS21350.58 clearly plotting in the positive scores, close to the ribs 7-8 from *Pan* and *Pongo*. The negative values of PC1 are linked with elongated ribs dorsoventrally with no torsion, whereas the positive values are linked with curved ribs dorsoventrally with some torsion. Therefore, assuming individual rib/ribose covariation, it is highly likely that *P. catalanicus* ribcage was ape-like, confirming previous results. Finally, the fact that monkey-like features have been found in its pelvis, along with the modern ape-like ribcage morphology, suggests a mosaic evolution of the hominid torso.

Funded by AEI/FEDER EU (CGL2015-63648P, CGL2016-76431-P and CGL2017-82654-P), "Juan de la Cierva Formación" (FJCI-2017-32157) to DGM, and the Generalitat de Catalunya (2017 SGR 116, 2017 SGR 86, and CERCA Program).

Elemental signatures and growth defects in teeth show differential morbidity and mortality tied to variable weaning and dietary practices among missionized Guale on the Georgia coast (ca 17th century).

CAREY J. GARLAND and LAURIE J. REITSEMA
Anthropology, University of Georgia

The DOHaD hypothesis represents an important theoretical shift in bioarchaeology regarding how we interpret indicators of early life stress, adult health, and age-at-death. Considerations of cultural context, however, are necessary for more meaningful interpretations of links between childhood stress and subsequent mortality risk. This paper explores the implications of weaning age and diet for childhood stress and mortality risk among indigenous Guale interred at Mission SCDG (ca. 17th century) on St. Catherines Island, Georgia. One canine from 52 individuals were analyzed for internal enamel micro-defects (ASR) as indicators of childhood stress. Of these teeth, 28 were incrementally sampled for barium (Ba/Ca) values to estimate weaning age, and six were incrementally sampled for $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ values to reconstruct early life diet. Enamel defects are prevalent in the canines (96%), and individuals with the highest frequencies of ASR experienced increased risks for early death. Variations in childhood stress and subsequent mortality risk were in part related to weaning age and marine versus maize-based food consumption. A Cox hazard analysis indicates that weaning age is a significant predictor of age-at-death and ASR frequency. Moderate correlations also exist between ASR frequency and average post-weaning $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ values. These data suggest that individuals who weaned early and consumed less marine resources experienced heightened stress and mortality risks. Conversely, variations in these

experiences indicate that while Spain's political-economy was detrimental to indigenous health, some parents were faced with opportunities (e.g. weaning and dietary resources) to buffer their children from stress and long-term negative health outcomes.

This project was funded by a Sigma Xi and Society for Georgia Archaeology grant (Carey Garland), and a NSF Grant (#1628026) to the Elemental Analysis Facility at the Field Museum.

Growing during a catastrophe: ontogeny of body size and femoral bone strength in Late Medieval and Post-Medieval Europe

EVAN GAROFALO¹, COURTNEY ELEAZER², REBECCA SCOPA KELSO² and AUSTEN COX²

¹Basic Medical Sciences, University of Arizona College of Medicine, ²Biomedical Sciences, West Virginia School of Osteopathic Medicine

Patterns of endochondral and appositional skeletal growth may vary between populations with shifts in subsistence economy, nutritional status, living conditions, and labor practices. Studies have demonstrated delayed growth in stature and body mass in populations experiencing significant environmental stressors. However, few studies have demonstrated similar growth delays in bone mass and strength.

This study compares ontogenetic trajectories of subadult body size and bone growth in two cemetery assemblages: Barton-upon-Humber (14th-19th centuries AD, Lincolnshire, UK, n=112) and Alytus (14th-18th centuries AD, Lithuania, n=153). Barton-upon-Humber experienced relative environmental and economic stability, with little evidence of disease. Whereas, Alytus had a high prevalence of malnutrition and infectious disease alongside periodic catastrophic events (war, famine, plagues), impacting health and survivorship. Growth in body size (stature, body mass), appositional growth (percent femoral cortical area [%CA]), and overall bone strength (polar section modulus [Zp]) and rigidity (polar second moment of area [J]) were compared. Alytus is expected to exhibit delayed growth in body size, elevated endosteal resorption (decreased %CA), and reduced bone strength.

Results indicate that stature and body mass are similar between assemblages during early childhood but diverge in older childhood and adolescence, with significantly smaller body size in Alytus. Additionally, appositional growth and bone strength are significantly lower in early childhood at Alytus relative to Barton-upon-Humber but similar in older childhood and adolescence. Comparing contemporaneous samples with distinct health profiles, results

support assertions for the influence of environmental perturbations on appositional growth in early developmental periods and body size in later stages of development.

Research supported by the Wenner-Gren Foundation (EMG)

Faunal species identification from basic skeletal measurements: Differentiating 21 medium-to-large sized mammals

HEATHER M. GARVIN¹, RACHEL DUNN¹, SABRINA B. SHOLTS², M. SCHUYLER LITTEN², ANDREA CLENDANIEL³, ELIZABETH DOUGHER³ and NOAH SKANTZ¹

¹Department of Anatomy, Des Moines University, ²Department of Anthropology, National Museum of Natural History, Smithsonian Institution, ³Department of Applied Forensic Sciences, Mercyhurst University

Physical anthropologists commonly encounter faunal remains at field sites and in the laboratory, and the majority of remains presented to forensic anthropologists are actually non-human. Without an extensive zooarchaeological or comparative anatomical background, determining the non-human species from an isolated bone can be challenging. This study tests the ability of basic skeletal measurements to classify single bony elements into 21 North American faunal species. Fifty-eight length and breadth measurements were defined that could be collected reliably across 21 medium-to-large sized mammalian species (16 genera, 9 families). Data were collected from available humeri, radii, ulnae, femora, tibiae, fibulae, scapulae, ossa coxae, and fused metapodials from 652 individuals (~400 per element). Step-wise discriminant function analyses with a leave-one-out cross-validation were performed to evaluate accuracy in assigning each bone to its appropriate order, family, genus, and species. Species classification accuracies for long bones that were characterized by at least four measurements ranged from 75.8 to 92.0%, performing better than elements represented by fewer measurements. The humerus and femur were among the most reliable and higher performing elements, and when the two elements were combined species classification was 90.0%. As would be expected, taxa exhibiting greater size and morphological variation (e.g., Bovidae), and those with morphological similarities (e.g., dog vs wolf and coyote) displayed higher classification errors. The high classification rates, despite discriminating 21 species, suggest that a few basic measurements are highly useful for faunal species identification and may be used by physical anthropologists with limited faunal expertise to narrow down potential species.

Research supported by the National Institute of Justice (2018-DU-BX-0229).

ABSTRACTS

The Effects of Labor on the Biomechanical Properties of the Femora and the Humeri in the 19th and 20th Centuries

SHELBY GARZA and DANIEL WESCOTT
Anthropology, Texas State University

The cross-sectional geometry (CSG) of long bone shafts provides a generalized measure of the loading regime that occurred during life. The purpose of this study is to investigate differences in long bone strength and shape between manual and non-manual labor workers in both the 19th and 20th centuries. Additionally, this study will examine if secular change has occurred in long bone CSG between manual and non-manual individuals. Samples are drawn from the Robert Terry Anatomical Collection (n=27) and the Texas State University Donated Skeletal Collection (n=79). High-resolution x-ray computed tomography scans of the left femur and both humeri were obtained for each individual. The cross-sectional geometric properties were analyzed, and an ANOVA was run to test for significant differences between size, shape, and robusticity between the manual and non-manual labor workers. The results showed that the humeri of manual labor workers are significantly more robust than non-manual labor workers in the 20th century sample. However, the femora were significantly larger in the non-manual labor workers in the 20th century sample. In the 19th century sample, there were no significant differences in the size, shape, or robusticity of the humeri or femora between manual and non-manual labor workers. Secular change was also observed in the femur, with the 20th century sample having larger and more round femora in comparison to the 19th century individuals. These results suggest that the size and shape of the humeri is driven by labor more than the femora.

Analyzing levels of character conflict in hominin phylogenetic reconstruction

JOANNA R. GAUTNEY

Department of Sociology and Anthropology, Weber State University

Phylogenetic relationships among fossil hominin taxa remain a contentious topic in paleoanthropology, and recent discoveries of new taxa have only intensified the debate. Compounding this problem are the limitations of many of the analytical tools used to explore these relationships, along with ongoing disagreements over character choice. Previous studies have examined the relative reliability of different cranial regions with varying results and have indicated that certain regions of the cranium may contain higher degrees of character conflict than others. In this study, an exploratory data analysis of fossil hominin morphological data was conducted using the network-based analytical method NeighborNet. Graphs produced by this method

give a clear indication of degree of conflict present in a dataset. To evaluate the relative reliability of different cranial regions, a dataset of 198 craniodental characters was divided into six regions: masticatory characters, the vault, basicranium, face, temporal bone, and dentition. Each cranial region was then analyzed using the NeighborNet algorithm, and levels of conflict present in each region were compared. Results indicate that there are indeed higher levels of conflict present in some regions of the skull than others. Of the six regions, basicranial, dental, and temporal regions of the skull reflect the lowest degree of conflict, while the masticatory and facial characters contain the highest degree of conflict. These results are consistent with previous work showing that masticatory and facial characters are relatively unreliable indicators of phylogeny.

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Forelimb Anatomy of the Microsyopidae: implications for primate origins

DAN GEBO¹ and CHRIS BEARD²

¹Department of Anthropology, Northern Illinois University, ²Department of Ecology and Evolutionary Biology, University of Kansas

Although historical attempts to reconstruct the phylogenetic relationships of the extinct family Microsyopidae have yielded variable and often conflicting results, all recent analyses have interpreted these mammals as stem Primates or members of the crown clade Primatomorpha. Here we describe the forelimb anatomy of *Microsyops* and *Niptomomys*, two microsyopids from the Eocene of North America. In both cases the distal humeral anatomy of these two microsyopids mirrors that of crown clade primates from the early Eocene in having a spherical capitulum associated with a wide and distinct spatial gutter separating the capitulum from the trochlea. This euprimate-like distal humeral anatomy contrasts with that of other known plesiadapiforms, which have a subspherical capitulum and lack a distinct separation between the capitulum and trochlea. Microsyopid elbow morphology allows for an extensive range of forearm movements that are often utilized during arboreal locomotion on small diameter supports or during single-handed manual manipulation of food items.

Microsyopid elbow anatomy adds a new anatomical complex to the plesiadapiform-primate phyletic debate. Microsyopid elbow anatomy supports a closer evolutionary connection to "euprimates". Additional anatomical features that might also signal a phyletic link between Microsyopidae and "euprimates" are the arterial supply to the brain and the larger encephalization quotient of *Microsyops*. In contrast, the dental evidence for microsyopids has largely been

interpreted as "primitive" when compared to other plesiadapiforms. If microsyopids are the sister taxon of primates then the hypothesis of a Euprimates-Plesiadapoidea clade is incorrect. The phyletic position of the Microsyopidae continues to be controversial.

Epigenetic modulation of leptin's signaling by Uncoupling Protein Polymorphisms (UCP2 - UCP3) and serum lipids.

CHAD GERHOLD¹, M.J. MOSHER^{1,2} and MICHEAL H. CRAWFORD^{1,3}

¹Laboratory of Biological Anthropology, University of Kansas, ²Department of Anthropology, Western Washington University, ³Department of Anthropology, University of Kansas

Patterns in DNA methylation are attributed to individual genotypes at distinct loci speculated to underlie gene-environment interactions. Polymorphisms in mitochondrial uncoupling protein-2 and -3 (UCP2 & UCP3) and circulating leptin levels together influence energy homeostasis and lipid metabolism. Low leptin levels defend fat storage levels in adipose tissue while UCP2 and UCP3 influence tissue specific fuel selection, lipid oxidation and metabolic pathways. Here we hypothesize that UCPs SNPs and lipid levels are promoting variation in DNA methylation along leptin's core promoter region, thus modulating leptin's signaling. Data obtained from previous studies of 139 Kansas Mennonites (79 females/60 males) included whole exome sequences, methylation profiles for 7 CpG sites of leptin's core promoter region, anthropometric measurements, and fasting serum lipid and leptin levels. Least-squares regression was used to test for SNP/CpG/Environmental associations. Models were sex-stratified and corrected for age and waist-hip ratio. Statistical significance was assessed at $p < 0.005$ and $FDR < 0.10$. Results suggest sexual dimorphism in accumulation of methyl groups along leptin's promoter. Among males, LDL and HDL levels and multiple SNPs in UCP2 and UCP3 (rs660339, rs2075577, and rs2734828; $p < 0.005$) are associated with differential methylation patterns in CpG sites that may increase resting metabolic rate, not storage. In females methylation of the site modulating the last step in adipocyte maturation is associated with circulating blood leptin levels and UCP2 (rs660627; $p < 0.005$). These findings suggest epigenetic regulation consistent with dimorphic cold adaptation: females increase adipose stores; males increase metabolic response.

An Eco-Evolutionary Approach to Human Adaptability, Resilience, and Climate Change in the Arctic

DREW GERKEY

Anthropology, Oregon State University

ABSTRACTS

Although anthropogenic climate change poses existential challenges for Indigenous communities in the Arctic, these challenges are not entirely unprecedented. Over many generations, Arctic peoples have developed a wide range of behavioral strategies to navigate environmental change and uncertainty, and these strategies provide a foundation for contemporary adaptation. My presentation examines these contemporary strategies as “adaptations” in two senses: One used by inter-disciplinary scholars in sustainability science and another used by evolutionary anthropologists. Sustainability scientists have developed their concept of adaptation in close connection to challenges posted by anthropogenic climate change. Evolutionary anthropologists have developed their concept of adaptation in relation to the role of environmental change and uncertainty throughout the course of human evolution. I synthesize these two concepts of adaptation by drawing on recent theoretical research on eco-evolutionary dynamics and applying this approach to data from contemporary Arctic communities in Siberia and Alaska. My presentation focuses on analysis of cooperative behavior in two contexts—subsistence (production) and life history (reproduction)—using data from economic games (Siberia $n=136$, Alaska $n=283$), as well as data on social networks (Siberia $n=72$, Alaska $n=370$). Results from economic games demonstrate how cooperative behavior and cultural values facilitate risk-pooling as a strategy for overcoming environmental uncertainty. Results from social networks connect subsistence strategies to household demography and theories of human life history. Although these strategies have helped people in Siberia and Alaska navigate environmental change and uncertainty for generations, I discuss how they are responding to new challenges arising from anthropogenic climate change.

This research was supported by the National Science Foundation (#0729063, #1019303, #1743019) and a post-doctoral fellowship from the National Socio-Environmental Synthesis Center (SESYNC) under funding from NSF (DBI-1052875).

A molecular phylogenetic analysis of papionins using Maximum Parsimony, Maximum Likelihood and Bayesian methods

DAGMAWIT ABEBE GETAHUN^{1,2,3} and RYAN RAAUM^{1,2,3}

¹Department of Anthropology, The Graduate Center, CUNY, ²Department of Anthropology, Lehman College, CUNY, ³The New York Consortium in Evolutionary Primatology, (NYCEP)

The Old-World monkey tribe Papionini, is one of the most abundant and widely distributed primate groups with very diverse ecological coverage. These primates also have a good fossil record. As a result, they have been thought to be an ideal

model for studying and modeling primate diversity and evolutionary patterns. Although papionins are one of the best studied groups of primates in terms of their behavior and morphology, there have been several contrasting views on their phylogeny based on molecular versus morphological evidence.

In this study we gathered one of the most robust molecular datasets of papionins consisting of ~47 kbp of DNA sequence data that incorporates 63 partitions. This data was collected from 44 cercopithecoid species, 34 of which are papionins. We used three different phylogenetic analyses methods to investigate the phylogeny of papionins. All our results showed high levels of support for the division of the 3 major clades within the papionins: the *Mandrillus-Cercocebus* clade, the *Theropithecus-Lophocebus-Papio* clade and the *Macaca* clade. The Maximum Likelihood and Bayesian analyses were able to better identify relationships at the specific level both within the Papionina and Macacina.

Furthermore, a divergence analysis was also conducted and shows divergence times within papionins that are congruent with new fossil discoveries. This analysis shows the split between the *Theropithecus+Lophocebus+Papio* clade and the *Mandrillus+Cercocebus* clade at around 8 Ma. The *Cercocebus-Mandrillus* split around 6 Ma and the *Lophocebus-Papio* split shortly after the *Theropithecus* split at about 4.5 Ma.

Craniofacial Traits and Body Composition in Two Genetically Varied Populations: Heritability and Associations

SUDIPTA GHOSH¹, TASBULAT DOSAEV² and GREGORY LIVSHITS³

¹Anthropology, North-Eastern Hill University, ²Department of Anatomy, Asfendiyarov Kazakh National Medical University, Kazakhstan, ³Department of Anatomy and Anthropology, Tel-Aviv University

The central theme of the present paper is to examine if craniofacial features can influence body composition variations in human and whether such influence can be considered universal for the entire human species. Further, the paper emphasizes on the contribution of common genetic (additive) and shared familial environmental factors on craniofacial characters in humans. Two pedigree-based samples were collected from two ethnically, genetically and geographically distinct populations from India (Santhal) and Russia (Chuvash). Canonical correlation analysis (CCA) was used to compare the association between craniofacial and body composition characters in two studied populations. Contribution of genetic and familial environmental factors on craniofacial features in terms of both shape and form was analysed through variance decomposition analysis by implementing the Mendelian Analysis

package (MAN). Our results suggest that craniofacial characters significantly ($p<0.001$) influence body composition of a person. For example, craniofacial character like total facial height has found to be considerably correlating with lean mass or fat free mass of the human body composition. Interestingly, such pattern is common across ethnically and genetically diverse populations, irrespective of their significant body size and shape differences. Similarly, despite the great geographic and ethnic variations between the studied populations, heritability estimates were impressively equivalent for traits like head circumference (54.0%^{Santhal} vs. 52.7%^{Chuvash}), head breadth (55.3%^{Santhal} vs. 50.9%^{Chuvash}) and bi-zygomatic breadth (59.1%^{Santhal} vs. 50.4%^{Chuvash}). These results perhaps indicate that association of craniofacial traits with body composition pattern is not only universal in human but also follows similar trend across the species.

Ministry of tribal affairs, Government of India & Israel Science Foundation.

Sexual Orientation Disparities in Adult Male Stature Are Not Due to Prenatal Androgen Exposure: Evidence from the Cebu Longitudinal Health and Nutrition Survey

JAMES K. GIBB¹, THOMAS W. MCDADE^{2,3} and MICHAEL A. SCHILLACI¹

¹Anthropology, University of Toronto, ²Anthropology, Northwestern University, ³Institute for Policy Research, Northwestern University

A growing body of research suggests that sexual minority men (SMM) are shorter than heterosexual men (HSM) due to differences in prenatal androgen exposure. However, studies examining sexual orientation disparities in adult stature have not used longitudinal data to examine the growth process underlying these differences. Using anthropometric data from the Cebu Longitudinal Health and Nutrition Survey, we assess the physical growth of 608 Filipino males of diverse sexual orientations in order to understand the pathways influencing sexual orientation disparities in adult stature. Mean stature for SMM was 60 mm less than the HSM mean in this sample and exhibited elevated measures of relative body mass index and perceived stress. SMM and HSM did not exhibit any significant differences in digit ratio, a putative marker of prenatal androgen exposure. The difference in stature between each group did not exist during infancy, and only emerged when the men were about 11 years of age, correlating with decreased triceps skinfold measures—an indicator of adiposity and available energetic resources. This study is the first to investigate sexual orientation differences in growth among males. Our findings suggest that shorter stature for SMM emerges during late childhood and early adolescence, rather than being present from birth. The lack of significant differences between the

ABSTRACTS

two groups is informative as it contradicts the prevailing scientific evidence. Our findings suggest that postnatal conditions such as socioeconomic status, nutrition, and psychosocial stress may have a greater influence on the adult stature for SMM than exposure to prenatal androgens.

New skeletons of *Cercopithecus dryas* and their implications for locomotor evolution and taxonomy within the guenon radiation

CHRISTOPHER C. GILBERT^{1,2,3}, JULIA L. ARENSON^{2,3}, JOHN A. HART^{4,5}, TERESE B. HART^{4,5}, KATE M. DETWILER⁶ and ERIC J. SARGIS^{5,7,8}

¹Department of Anthropology, Hunter College, CUNY, ²PhD Program in Anthropology, The Graduate Center, CUNY, ³New York Consortium in Evolutionary Primatology, (NYCEP), ⁴Lukuru Wildlife Research Foundation, Quartier de Kingabois, Commune de la Gombe, Kinshasa, Democratic Republic of Congo, ⁵Division of Vertebrate Zoology, Yale Peabody Museum of Natural History, ⁶Department of Anthropology, Florida Atlantic University, ⁷Department of Anthropology, Yale University, ⁸Division of Vertebrate Paleontology, Yale Peabody Museum of Natural History

Two skeletons of the rare monkey *Cercopithecus dryas* were recently obtained from central Congo Basin's TL2 region. Little is known of *C. dryas* behavior, but molecular data suggest it represents the sister taxon to *Chlorocebus* (vervet monkeys), which is usually recovered as part of a "terrestrial" guenon clade (i.e., *Chlorocebus*, *Erythrocebus*, and *Allochocebus*) in nuclear gene analyses. Nearly all modern studies of cercopithecoid morphology and evolution trace their origins to Eric Delson's landmark contributions (e.g., his PhD thesis, *Evolutionary History of the Primates*), and here we build on his foundational work by analyzing these skeletons in an evolutionary and functional context, treating them like fossil taxa to infer likely behavioral adaptations. Twenty-two variables across 149 guenon skeletons representing twenty-two species were determined to be highly correlated with published data on guenon substrate preference. A principal components analysis of all specimens largely separated locomotor groups (arboreal vs. semi-terrestrial vs. terrestrial). A regression between PC1 and % terrestriality is robust ($r^2=0.827$) and estimates *C. dryas* spends less than 20% of its time on the ground. A discriminant analysis of all specimens results in a correct substrate classification rate of 83.78%, with most misclassifications between semi-terrestrial and terrestrial specimens; *C. dryas* individuals are classified as semi-terrestrial (male) to arboreal (female) with high posterior probabilities, suggesting *C. dryas* is more arboreal than *Chlorocebus* and other terrestrial clade taxa. Thus, *C. dryas* morphology indicates more arboreal

adaptations in this forest-dwelling species and perhaps suggests unappreciated locomotor (and taxonomic) diversity within the terrestrial guenon clade.

This study was generously funded by the AAPA Professional Development Grant Program, the PSC-CUNY Faculty Award Program, and Hunter College.

Foot angles during bipedal gradient walking with burdens

CRISTINA GILDEE¹, MIGUEL OCHOA¹, HANNAH ZAEHRINGER¹ and PATRICIA A. KRAMER^{1,2}

¹Department of Anthropology, University of Washington, ²Department of Orthopaedics and Sports Medicine, University of Washington

The ability to carry a burden long distances and over a variety of terrains has been an important factor in population mobility throughout human evolution. Gradient walking has been shown to alter gait kinematics, including walking cadence and stride lengths; however, it is unclear what effect carrying a burden has on gait variables such as ankle dorsi-/plantar flexion while gradient walking. We hypothesized that the angle of the foot to the substrate will differ during uphill walking in the burdened condition compared with downhill walking and the unburdened conditions.

Foot angle during incline walking was examined in 8 able-bodied subjects in two burden conditions: wearing a 10 kg backpack and unburdened. Kinematic analysis (Qualisys, Gothenburg, Sweden) was used to quantify lower limb motion in each subject while walking up and down a 20° incline at a self-selected comfortable walking pace. Linear regression was used to explore relationships between maximum and minimum foot angles and burdened condition, while controlling for mass, stature, and leg length.

Maximum foot angles in downhill walking are significantly different from uphill walking ($p < 0.001$) with burden condition as a significant predictor ($p = 0.05$). Minimum foot angle in downhill walking are also significantly different from uphill walking ($p < 0.001$); however, burden condition is not a significant predictor ($p > 0.36$). A more detailed exploration of burden carrying in gradient walking is warranted given the strong predictive relationship between burdened walking, gradient, and foot angle.

This work was supported in part by the University of Washington's Graduate Opportunities and Minority Achievement Program.

Cross-cultural associations between gendered perceptions of happiness and leisure time parity among older adults

THERESA E. GILDNER

Department of Anthropology, Dartmouth College

Increased leisure time has been linked with greater perceived happiness, suggesting that reduced workloads may substantially improve well-being. Yet, sex differences are apparent in perceived leisure time among high-income populations. Women are generally expected to spend more time completing household work compared to men, which may decrease leisure time and associated happiness ratings. Still, gendered differences in the relationship between perceived leisure time and happiness have not been tested in lower income countries, particularly among older adults. This study uses data from the World Health Organization's Study on global AGEing and adult health (SAGE) to test whether perceived free time parity is associated with reported happiness equality among adults >50 years old in five middle-income nations (China, Ghana, India, Mexico, and the Russian Federation). Logistic regressions were conducted (by country) testing whether perceived leisure time parity between the sexes was associated with perceptions of equal happiness between men and women, while controlling for several lifestyle factors ($n = 41,248$). As hypothesized, in all countries individuals who thought women had equal or greater leisure time compared to men were significantly more likely to also report that women were as happy or happier than their male counterparts (OR = 3.82-11.29, all $p < 0.001$). These results may indicate that perceptions of who has more free time are important in shaping individual impressions of gendered happiness patterns. Further, these findings suggest that ensuring men and women have equal leisure time might help achieve parity in happiness, even at older ages.

Support: NIH NIA Interagency Agreement YA1323-08-CN-0020; NIH R01-AG034479.

An investigation of social interactions among rhesus macaques (*Macaca mulatta*) as a predictor of human-monkey interactions at the Jakhoo temple in Shimla, Himachal Pradesh, India

TANIYA GILL

Anthropology, University of Delhi

Humans have become a part of commensal macaque's social environment. Previous studies have examined the individual differences in the feeding strategies of macaques during HM (human-monkey) interactions with inconclusive results. Through this paper, we have tried to examine whether the direction of conspecific social interactions can predict HM interactions.

The study was conducted among adult rhesus macaques (*Macaca mulatta*) at the Jakhoo temple in Shimla located in Himachal Pradesh, India where people regularly engage in interactions with them. Behavioral data was recorded using focal animal sampling and human-monkey event sampling methods.

ABSTRACTS

The hypothesis was based on the 'priority of access to resources' model which states that access to resources depends on the social position of the individual. Our first prediction was based on the assumption that the low ranking monkeys were pushed away by high ranking ones when the group is provisioned, therefore, they resort to interacting with humans directly to procure food. The second prediction was based on the assumption that the individual monkeys who received more conspecific aggression, irrespective of their rank, tended to interact more with humans. The results confirmed a previously known information that male monkeys have higher frequency of interactions with humans. Interestingly, it was found that the social rank of the individuals did not influence the number of HM interactions initiated by monkeys, whereas, this frequency was correlated with the direction of in-group aggression. Hence, the individuals who received more conspecific aggression initiated higher frequency of interactions with humans.

Does the naturalistic fallacy impede students' understanding of the evolution of human behavior?

LIAM GLEASON and SARAH MATHEW

School of Human Evolution and Social Change,
Arizona State University

The naturalistic fallacy is a common logical error whereby people infer that a behavior is "good" or "correct" because it has been favored by natural selection. While science education research has emphasized how an individual's religious beliefs may influence the extent to which they learn and attain competence in evolutionary theory, there is little known about how general human moral reasoning, including the tendency to commit the naturalistic fallacy, hinders an individual's understanding of human behavior from an evolutionary standpoint. Using surveys conducted among students enrolled in anthropology courses at Arizona State University, we examine whether competency in understanding and avoiding the naturalistic fallacy facilitates competency in applying evolutionary principles to examine human behavior. Subjects are presented with either a module that trains students to avoid the naturalistic fallacy (experimental condition), or an unrelated reasoning fallacy (control condition), before they are all presented with a module illustrating how human behavior evolves through natural selection. Preliminary results indicate that students were able to separate conceptualization from moralization. We will present data regarding students' understanding of the process of evolution, their understanding of the naturalistic fallacy, and whether subjects who were trained to recognize the naturalistic fallacy had improved learning of evolutionary concepts of human behavior. By understanding if students commit logical fallacies

when attempting to conceptualize or moralize evolution, we can better design best practices for teaching about the evolutionary foundations of our behavior.

Understanding hominid facial diversity using 3D geometric morphometrics and population genomics

ALFIE GLEESON^{1,2}, AIDA ANDRÉS² and AIDA GOMEZ-ROBLES^{1,2}

¹Department of Anthropology, University College London, ²Department of Genetics, Evolution and Environment, University College London

The hominid face incorporates a range of extremely diverse phenotypes across and within species. A balance between selective pressures and neutral processes drives the evolution of phenotypic diversity, but the extent to which each contribute to the evolution of the face of hominids is unclear. A powerful interdisciplinary way to understand the origin of facial morphological diversity, is to compare morphological and genetic diversity in extant hominid groups using geometric morphometrics and population genomics. Previous studies based on limited configurations of cranial landmarks have shown a correlation between cranial diversity and neutral genetic variation across extant hominids. Some species, however, deviate from this general pattern, perhaps as the result of species-specific selective pressures. If that were the case, the evolution genes involved in the genetic basis of face morphology should explain the species-specific deviation from the general patterns. Using previously published genome-wide association studies (GWAS), we identified 844 genes associated with facial phenotypic variation in humans. We investigated signatures of selection in those genes in twelve extant hominid species or subspecies, and explored their association with anatomical variation in corresponding facial regions using an extensive set of 1116 landmarks and surface semilandmarks. Results show increased levels of intraspecific anatomical variation in gorillas and orangutans, although the extent of variation differs across facial regions. Similarly, some genes associated with facial variation appeared to show signatures of balancing selection. Our results highlight the importance of bringing together genomic and phenotypic approaches to advance our understanding of facial variation and evolution.

AG supported by the Biotechnology and Biological Sciences Research Council [grant number BB/M009513/1], AGR supported by UCL-Excellence programme.

Ancestry and Admixture Estimates for Filipino Crania Using Morphoscopic Traits Under a Multivariate Probit Regression Model

MATTHEW C. GO^{1,2} and JOSEPH T. HEFNER³

¹Department of Anthropology, University of Illinois at Urbana-Champaign, ²Central Identification Laboratory, SNA International, supporting the Defense POW/MIA Accounting Agency, ³Department of Anthropology, Michigan State University

Probit regression has yet to be applied as a classification tool for ancestry estimation in forensic anthropology. The goals of this study were to: (1) evaluate the performance of probit analysis in ancestry estimation using ordinal data, and (2) explore human cranial variation for an understudied population. Morphoscopic data from Filipino crania (n = 140) were subjected to multivariate probit models using ancestral reference populations representing Africa, Asia, and Europe in a three-group model, with the addition of Hispanics in a four-group model. Posterior probabilities were calculated for each classification group and interpreted as admixture proportions of an individual. Model performance was also evaluated for individuals with missing data. The overall correct classification rates for the three-group and four-group models were 72.1% and 68.6%, respectively. Filipinos classified as Asian 52.9% of the time using three groups and 48.6% using four groups. A large portion of Filipinos also classified as African. Classification trends or accuracy rates between complete crania and crania with at least one missing variable showed no significant differences. Morphoscopic traits under multivariate probit models perform well when populations are represented in both training and test sets. Classifying Filipinos, which were excluded from the training set, showed only moderate success. Probit can also accommodate individuals with missing data. Filipinos are more phenotypically similar to Africans than the other Asian samples used here, but still affiliate most closely as Asian. Incorporating Filipino reference groups in ancestry estimation methods would provide significant additional variation to the broad continental category of Asian.

Funding was provided by the U.S. National Institute of Justice (Award Numbers 2017-IJ-CX-0008 and 2015-DN-BX-K012) and the Social Sciences and Humanities Research Council of Canada (Award Number 752-2016-0221).

A modern methodological approach to the analysis of cribra orbitalia as an indicator of health status and mortality

KANYA GODDE¹ and SAMANTHA M. HENS²

¹Anthropology Program, University of La Verne, ²Department of Anthropology, California State University, Sacramento

ABSTRACTS

Cribra orbitalia is commonly used as an indicator of health status in bioarchaeological contexts. While underlying causal conditions vary, the presence of cribrous lesions in skeletal populations suggests individuals may have suffered higher frailty with a concomitant increase in risk of death.

This research investigates the relationship between cribrous lesions and mortality across Medieval and Post-medieval populations from London using a modern statistical approach. We examined seven cemeteries from the Wellcome Osteological Research Database representing Medieval (N = 922: Guildhall Yard, Bermondsey Abbey, Merton Priory, St. Mary Graces) and Post-medieval (N = 510: Chelsea Old Church, St. Bride's lower churchyard, Cross Bones) sites that had recorded lesion scores, sex, status, and age indicator data. Transition analysis and Bayesian informative priors generated highest posterior density ages for each individual. A binomial logistic regression generated odds ratios for the risk of dying with cribra orbitalia and age at death, sex, status, and time period. Accounting for age-at-death, a survival analysis, Cox proportional hazard model, estimated hazard ratios of dying with cribra orbitalia across covariates including: sex, status, and time period.

Results of the logit model indicated that age-at-death was significant ($p=0.0415$); individuals showed ~1% decrease in risk of dying with cribra per year. Those with cribrous lesions were dying younger than those without lesions, indicating the presence of selective mortality in our samples. The Cox model showed significant hazards, with the rate of cribra decreasing over time ($p<0.0001$). Post-medieval individuals were ~73% less likely to die with cribra than their Medieval counterparts.

Natural and human impacts on vertebrate megafauna in southwest Madagascar

LAURIE R. GODFREY¹, KATHLEEN M. MULDOON², STEPHEN J. BURNS³, BROOKE E. CROWLEY⁴, ZACHARY S. KLUKERT⁵, NICK SCROXTON⁶ and LOVASOA RANIVO HARIMANANA⁷

¹Anthropology, University of Massachusetts Amherst, ²Anatomy, Midwestern University, ³Geosciences, University of Massachusetts Amherst, ⁴Anthropology and Geology, University of Cincinnati, ⁵Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, ⁶School of Earth Sciences, University College Dublin, Ireland, ⁷Bassins sédimentaires Evolution Conservation, Université d'Antananarivo, Madagascar

Madagascar is rapidly losing forest and numerous endemic species are currently threatened with extinction. The story of Madagascar's biodiversity loss is complex. We summarize results of our paleontological and paleoclimatological expeditions to Tsimanampesotse National Park and the surrounding region (Itampolo and Antsirafaly, southwest Madagascar). In reconstructing

the decline and disappearance of the regional megafauna, we draw from stalagmite records of fluctuation in climate that extend well past the Last Glacial Maximum, and an associated fossil record that extends back >8,000 years. From caves at Tsimanampesotse and Itampolo, we recovered 41 stalagmites; from Tsimanampesotse we recovered subfossils belonging to thirteen extinct vertebrate species (including large-bodied lemurs and a previously-undescribed carnivore larger than *Cryptoprocta spelea*), two Critically Endangered species, five Vulnerable or Endangered species, and many vertebrate species still common in the region. At Antsirafaly, we recovered eight extinct vertebrate species (including additional large lemurs and the gigantic elephant bird, *Vorombe titan*). Stable oxygen isotope ($\delta^{18}O$) records in stalagmites coupled with subfossil remains of freshwater birds provide strong evidence of periodic wet intervals in the southwest, and support climate shifts as a factor influencing local extirpation of some species. However, human impacts are also clear, and likely triggered the extinction of the megafauna. Indeed, a spike in the regional frequency of megafaunal butchery (~800–900 CE) roughly coincides with an island-wide peak (~750–850 CE) in the pace of megafaunal decline. This occurred during a relatively wet period; there is no evidence that aridification triggered this crash.

This project was supported by the National Science Foundation [BCS-1750598 to LRG, BCS-1749211 to KMM, BCS-1749676 to BEC, AGS-1702891 to SJB and AGS-1702691 to David McGee].

The value of long-term research for assessing social and genetic influences on sociality

IRENE GODOY¹, PETER KORSTEN¹ and SUSAN E. PERRY²

¹Animal Behaviour, Universität Bielefeld, ²Anthropology, University of California, Los Angeles

Sociality has been linked with measures of biological fitness in several primate species. Determining how within and between individual variation in relevant social traits arises is crucial for understanding constraints on the evolution of sociality. Here, we use advanced statistical methods, known as animal models (that incorporate pedigree information), to disentangle social and genetic influences on sociality across the lifespan (range: 0–26 years of age) in a long-lived wild primate. We leverage a longitudinal database spanning 18 years of observation on individually recognized white-faced capuchin monkeys (*Cebus capucinus*), and pedigrees going back several generations for many individuals. Using social proximity data from 371 individuals with known mothers (n=110 mothers) representing 2438 monkey-years (range: 1–18 years per monkey), we find that sociality decreases with age for both sexes, and that male alpha status, number

of maternal kin, and group size may also influence sociality. In our statistical models, we are able to partition social and additive genetic (i.e., heritable) sources of variation in a course-grained measure of sociality, demonstrating a moderate heritability of our sociality measure (h^2 : 0.171, 95% HPD interval: 0.098–0.262). These results indicate that it is possible to use animal models to disentangle social and genetic influences on variation in a behavioural trait in wild primates, though further work is still necessary to rule out other possible socially transmitted influences on sociality.

Funding Citation: NSF (1638428, 0613226, 848360, 1232371, 9633991, 9870429), NGS (6 grants), Leakey (9 grants), Templeton World Charity Foundation, Wenner-Gren (2 grants), ISHE, Wild Capuchin Foundation, MPI-EVAN, UCLA, Univ.Michigan

Predicting local bioavailable ⁸⁷Sr/⁸⁶Sr isotopes and similarity search in multi-dimensional isotope data sets

ANDREA GOEHRING, GISELA GRUPE and FABIOLA LENGFELDER

Faculty of Biology, Department Biology I, Anthropology and Human Genomics, Ludwig Maximilian University Munich

The definition of local bioavailable ⁸⁷Sr/⁸⁶Sr isotopic signatures is crucial for the detection of non-local skeletal finds and provenance analysis. A multi-isotope approach by use of additional isotopic ratios permits the establishment of an isotopic fingerprint that can be used for similarity search.

A mixing model was developed for the prediction of local ⁸⁷Sr/⁸⁶Sr signatures for selected sites along an archaeological important passage across the European Alps (Inn-Eisack-Adige passage across the Brenner Pass). This model was based on strontium concentrations and isotopic ratios of environmental samples (wood, water, soil) and correctly predicted the isotopic signatures of local vertebrates.

A multi-isotope fingerprint consisting of stable strontium, lead, and oxygen isotopes in the bioapatite of archaeological animals and human cremations (omitting the thermally unstable $\delta^{18}O_{\text{phosphate}}$ in the latter) along the Alpine passage was forwarded to a Gaussian Mixture Model (GMM) clustering for the scope of similarity search. GMM clustering was capable of identifying groups of animals and humans that were spatially separated with a high probability (average $p > 0.9$). This way, local, non-local and also mixed isotopic signatures in the multi-isotope fingerprint were firmly detected.

GMM clustering was also successfully applied to a palaeoecological study in an ecological complex region at the Baltic coast (Viking Age Haithabu and medieval successor Schleswig). A multi-isotope fingerprint in vertebrate skeletal finds including humans that consisted of $\delta^{13}C_{\text{collagen}}$, $\delta^{15}N_{\text{collagen}}$,

ABSTRACTS

$\delta^{13}\text{C}_{\text{carbonate}}$, $\delta^{18}\text{O}_{\text{carbonate}}$, $\delta^{18}\text{O}_{\text{phosphate}}$, $\delta^{34}\text{S}_{\text{collagen}}$, and $^{87}\text{Sr}/^{86}\text{Sr}_{\text{apatite}}$ permitted the definition of e.g. fishing grounds, quantification of the “sea spray” effect, and provenance analysis.

German Science Foundation, grants no. GR 959/16-1,2 and GR 959/20-1,2

Sex-specific phenotypic effects and evolutionary history of an ancient deletion polymorphism of the human growth hormone receptor

OMER GOKCUMEN¹, SKYLER RESENDEZ¹, MARIE SAITOU¹ and XIQUAN MU²

¹Biological Sciences, University at Buffalo,

²Ophthalmology, University at Buffalo

The deletion of the third exon of the growth hormone receptor (GHRd3) is one of the most common genomic structural variants in the human genome. This deletion has been linked to response to growth hormone, placenta size, birth weight, growth after birth, time of menarche, adult height, and longevity. However, its evolutionary history and the exact mechanisms through which it affects phenotypes remain unresolved. While the analysis of thousands of genomes suggests that this deletion was nearly fixed in the ancestral population of anatomically modern humans and Neanderthals, it underwent a paradoxical adaptive reduction in frequency approximately 30 thousand years ago, a demographic signature that roughly corresponds with the emergence of multiple modern human behaviors and a concurrent population expansion. Using a mouse line engineered to contain the deletion, pleiotropic and sex-specific effects on organismal growth, the expression levels of hundreds of genes, and serum lipid composition were documented, potentially involving the nutrient-dependent mTORC1 pathway. These growth and metabolic effects are consistent with a model in which the allele frequency of GHRd3 varies throughout human evolution as a response to fluctuations in resource availability. The last distinctive prehistoric shift in allele frequency might be related to newly developed technological buffers against the effects of oscillating resource levels.

National Science Foundation (no. 1714867).

Investigating age-related variation in the methyloyme of rhesus macaques

ELISABETH A. GOLDMAN¹, KENNETH L. CHIOU^{2,3}, MICHAEL J. MONTAGUE⁴, ARIANNE MERCER², SIERRA SAMS², MELWEEN I. MARTINEZ⁵, JULIE E. HORVATH^{6,7,8}, LAUREN J.N. BRENT⁹, MICHAEL L. PLATT^{10,11,4}, KIRSTIN N. STERNER¹ and NOAH SNYDER-MACKLER^{12,3}

¹Department of Anthropology, University of Oregon, ²Department of Psychology, University of Washington, ³Nathan Shock Center of Excellence in the Basic Biology of Aging, University of Washington, ⁴Department of Neuroscience,

University of Pennsylvania, ⁵Caribbean Primate Research Center, University of Puerto Rico, ⁶Department of Biological and Biomedical Sciences, North Carolina Central University, ⁷Genomics & Microbiology Research Lab, North Carolina Museum of Natural Sciences, ⁸Comparative Medicine Institute, North Carolina State University, ⁹Centre for Research in Animal Behaviour, University of Exeter, ¹⁰Department of Psychology, University of Pennsylvania, ¹¹Department of Marketing, University of Pennsylvania, ¹²Center for Studies in Demography & Ecology, University of Washington

A key characteristic of the epigenome is its capacity to dynamically respond to external stimuli, acting as an interface that allows signals from the environment to “get under the skin” and drive individual variation in the aging trajectory. DNA methylation, a type of epigenetic modification, can influence gene expression and grows more susceptible to perturbation with increasing age. In many cases, the biological significance and consequences of these age-related changes are not clear. To better understand patterns of age-dependent methylation change, we generated genome-wide methylation data from blood collected from 546 rhesus macaques (308 female, 238 male) from Cayo Santiago. RRBS libraries were prepared using standard protocols and run on an Illumina NovaSeq. We used PQLseq to fit a binomial mixed model to a subset of our methylation data containing 63,971 CpG sites. We identified 75 sites that are differentially methylated with age (q -value < 0.05) from this preliminary analysis and are expanding the analysis to include the complete dataset. In addition, we are using this greatly expanded dataset to further optimize an age predictor model (“epigenetic clock”) we have developed for rhesus macaques. Our current model predicts age with a median error of 2.88 years ($r=0.64$, $p < 2.997e-13$). Rhesus macaques are closely related to humans with similar life history and disease risk, making them an ideal model of human aging. This research will make an important contribution to the field by examining how genetics, environment, and behavior intersect to influence aging and age-related diseases in rhesus macaques.

Funding for this study was provided by NIH R00-AG051764.

Reconstructing the A.L. 288-1 distal femur using virtual geometric methods

DEANNA M. GOLDSTEIN and ADAM D. SYLVESTER
Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine

Reconstructing damaged fossils is essential for a complete understanding their functional morphology. The distal femur is especially important because of its weight-bearing role in walking. Here we use the thin plate spline (TPS) interpolation function to reconstruct the distal articular surface of A.L. 288-1ap.

Damaged portions were trimmed from an A.L. 288-1ap surface model, removing the entire patellar surface. Sliding semilandmarks were distributed across the articular surface of modern human ($n=35$), chimpanzee ($n=35$), and australopithecine (A.L. 129-1a, A.L. 333-4, and TM1513) distal femoral surface models, and slid to minimize bending energy of the TPS function relative to an updated Procrustes average. Landmarks representing missing portions of A.L. 288-1ap were not constrained to tangent planes or vectors during sliding. Separate reconstructions were generated using the average chimpanzee, human, and australopith as references. Similar reconstructions were simulated on virtually damaged A.L. 129-1a, A.L. 333-4, and TM1513 surface models. Root mean square (RMS) values between each reconstruction and the original fossil were used to evaluate reconstruction accuracy in virtually damaged fossils.

Results suggest that australopith-based reconstructions of virtually damaged femora are most similar to original fossil morphology (mean RMS for australopith, chimpanzee, and human-based reconstructions are 0.48, 0.68, and 0.64 respectively). The australopith-based reconstruction of A.L. 288-1ap was therefore considered to approximate original morphology best. When A.L. 288-1ap is reconstructed using other australopiths, patellar surface morphology is more similar to the chimpanzee-based than human-based reconstruction, suggesting that the patellar surfaces of australopiths used to reconstruct A.L. 288-1ap are most similar to chimpanzees.

A new approach to the paleopathological study of anemia(s): Comparative elemental profile by x-ray fluorescence (pXRF) in the Coimbra Identified Osteological Collections

RICARDO A.M.P. GOMES¹, LIDIA CATARINO² and ANA LUISA SANTOS¹

¹Departament of Life Sciences, CIAS, University of Coimbra, ²Departament of Earth Sciences, Geosciences Center, University of Coimbra

Clinically, there are many forms of anemia, however its identification in paleopathology is not so simple. This investigation tests the hypothesis that bone trace elements’ concentration may vary in consequence of anemia, as well as in individuals with *cribra orbitalia* (CO) and porotic hyperostosis (PH).

Forty-six individuals from the Coimbra Identified Collections were studied: 19 with cause of death recorded as anemia(s) (13 females, 6 males; 21 to 90 yrs; $\bar{x}\pm\text{SD}=47,11$; $\text{SD}=17,42$) and 27 (13 females, 14 males; 7 to 70 yrs; $\bar{x}\pm\text{SD}=36,85$; $\text{SD}=7,26$) as control (e.g. trauma). According to the literature, 15 trace elements (Al, Si, P, S, Cl, K, Ca, Sc, Mn, Fe, Cu, Zn, Sr, Ba, Pb) were measured by pXRF, on bregma, frontal,

ABSTRACTS

parietal and occipital bones, and eight elemental ratios (Ca/P;Sr/Ca, Pb/Ca;Sr/Pb, Zn/Fe;K/Fe, K/PMn/P) were calculated. Phosphorous concentration (U=162,0;W=352,0;p=0,035), Ca/P (U=166,0;W=544,0;p=0,043) and Pb/Ca ratios (U=162,0;W=540,0;p=0,035) presented significant differences between groups. Nevertheless, PCA shown an overlapping distribution among the two. Strictly speaking, individuals from the control group could have manifested the anemic condition, because only the cause of death was recorded, with no previous clinical information. CO was observed in one individual (control) and PH in 15 (32.6%; 6 anemic, 8 control). There were not significant elemental differences amongst individuals with cranial porosity (n=16) and without (n=31).

The anemic group had lower phosphorus concentration, which might be related to the association between hypophosphatemia and anemia (e.g. individuals with alcoholism, malnutrition and others). Although not conclusive, the results suggest that phosphorus concentration, Ca/P and Pb/Ca ratios can be of use to discriminate anemic individuals in paleopathological investigations.

FCT Grant SFRH/BD/145343/2019, CIAS FCT-Pest-E/SADG/UI0283/2019

Using facial variation to discriminate among ape subspecies. Implications for hominin classification

AIDA GOMEZ-ROBLES^{1,2} and ALFIE GLEESON^{1,2}

¹Department of Anthropology, University College London, ²Department of Genetics, Evolution and Environment, University College London

Recent fossil findings show that multiple hominin species have inhabited the world during the last million of years. Some of these species are closely related, having diverged at some point during the late Lower or Middle Pleistocene, and show minor anatomical differences. Chimpanzee and gorilla subspecies have also diverged from each other during the last million of years, and provide a valuable analogue to ascertain the extent to which closely related groups can be discriminated on the basis of the anatomy of particular craniofacial regions. We studied three chimpanzee subspecies (*Pan troglodytes troglodytes*, *Pan troglodytes verus* and *Pan troglodytes schweinfurthii*) and two gorilla subspecies (*Gorilla gorilla gorilla* and *Gorilla gorilla diehli*). We used a set on more than 1000 landmarks and surface semilandmarks describing craniofacial anatomy in particular anatomical regions: parietal, frontal, supraorbital, nasal, maxillary and zygomatic. Results show incomplete separation but discernible subspecies-specific trends in most facial regions, indicating that even small cranial fragments can be useful to discriminate among closely related groups. In general, subspecies with deeper divergence

times show clearer anatomical differences and higher classification accuracy, indicating a clear association between anatomical divergence and time since common ancestry. Results also allow for a comparison of the amount of variation that is observed intraspecifically among subspecies versus the amount of variation that is observed among different species, thus providing a useful comparative context for the analysis of hominin intra- and interspecific variation.

AGR is supported by the UCL-Excellence programme. AG is supported by the Biotechnology and Biological Sciences Research Council [grant number BB/M009513/1].

Predicting if menarche has occurred based on osteological and dental development

ELLIE GOODERHAM, SHERA FISK, LAURE SPAKE, LUÁSA MARINHO and HUGO F.V. CARDOSO
Archaeology, Simon Fraser University

Estimating menarche in archaeological populations can provide information about temporal and geographic variation in sexual maturation of populations and the environmental factors that impact its timing. This study develops predictive models to aid bioarchaeologists in their investigation of whether menarche had occurred based on osteological and dental development. For this analysis, cross-sectional data (n=33) of girls aged between 6 and 19 years from the Montreal Human Growth Research Centre was used. In addition to menarchal age, hand-wrist and dental maturation data was available from radiographs and orthopantomograms. Maturation of hand and wrist bones were scored based on TW2 methods (Tanner et al. 1975) and dentition was scored using the Demirjian et al. (1973) method. Girls were dichotomized into menarche attained and not attained and then logistic regression was used to create models for the prediction of menarchal status, based on hand-wrist and dental development. Sensitivity, specificity and classification rates (>90%) were used to assess the quality of the models. Hand-wrist maturation stages were better predictors of menarchal status than dental maturation stages. This study confirms the general importance of osteological indicators as predictors, relative to dental indicators, and introduces a novel approach which can be used to estimate the age of menarche in archaeological populations.

No reported external funding.

Structural changes with increasing age and athletic history in the human forearm

ALICE F. GOODING and LAWRENCE H. CATES
Geography and Anthropology, Kennesaw State University

Although bone geometry in the adult arm has been correlated with habitual activities, it remains unclear how it may shift with the changes in physiological and mechanical demands that accompany aging. Because of their function in swinging and gripping motions, skeletal elements of the forearm are expected to be mechanically sensitive to activity and age-related bone loss. Here we examine changes in the radial and ulnar diaphyses as a function of age, athletic history, and current activity level.

Cross-sectional geometric properties at five diaphyseal sites (20, 35, 50 and 80% of bone length) were extracted from pQCT scans of the right and left forearms of 47 competitive tennis players (22 females, 27 males, aged 40-99 years). Training activities, playing style, grip strength, and life-style habits were recorded using participant surveys.

In both bones, measures of bone mass were positively correlated with years played, while strength and rigidity increased with hours currently spent playing. Within each limb, loss of cortical mass with age was consistent between sites, but strength and rigidity were age and site-specific. When comparing the limbs, proximal sites did not differ. However, all geometric measures in the dominant arm were increased in the distal sites of the radius and decreased in the ulna. The forearm therefore exhibits a complicated sensitivity to factors that influence its mechanics, with an inverse relationship in load-sharing toward the wrist. Furthermore, after the age of 40, activity history plays a significant role in the structure of the two bones.

DNA methylation-based forensic age estimation in human bone

SHYAMALIKA GOPALAN^{1,2}, JONATHAN GAIGE² and BRENNAN M. HENN^{2,3,4}

¹Center for Genetic Epidemiology, University of Southern California, ²Department of Ecology and Evolution, Stony Brook University, ³UC Davis Genome Center, University of California, Davis, ⁴Department of Anthropology, University of California, Davis

DNA methylation is an epigenetic modification of cytosine nucleotides that represents a promising suite of aging markers with broad potential applications. In particular, determining an individual's age from their skeletal remains is an enduring problem in the field of forensic anthropology. All DNA methylation-based age prediction methods published so far focus on tissues other than bone. While high accuracy has been achieved for saliva, blood and sperm, which are easily accessible in living individuals, the highly tissue-specific nature of DNA methylation patterns means that age prediction models trained on these particular tissues may not be directly applicable to other tissues. Bone is a prime target for the

ABSTRACTS

development of DNA methylation-based forensic identification tools as skeletal remains are often recoverable for years post-mortem, and well after soft tissues have decomposed. In this study, we generate genome-wide DNA methylation data from 32 individual bone samples. We analyze this new dataset alongside published data from 133 additional bone donors, both living and deceased. We perform an epigenome-wide association study on this combined dataset to identify 108 sites of DNA methylation that show a significant relationship with age (FDR < 0.05). We also develop an age-prediction model using lasso regression that produces highly accurate estimates of age from bone spanning an age range of 49-112 years. Our study demonstrates that DNA methylation levels at specific CpG sites can serve as powerful markers of aging, and can yield more accurate predictions of chronological age in human adults than morphometric markers.

Funding was provided by the National Institute of Justice GRFP (2016-DN-BX-0011). JG was supported by a grant from the URECA summer program at Stony Brook University.

Postcranial size dimorphism in *Australopithecus afarensis* and *A. africanus*

ADAM D. GORDON

Department of Anthropology, University at Albany (SUNY)

Hominin evolutionary scenarios invoke sexual size dimorphism (SSD) because it is linked to various selection pressures in extant primates. Previous work has generally (although not universally) found postcranial dimorphism in *A. afarensis* to be significantly greater than in humans and chimpanzees and equally or more dimorphic than gorillas and orangutans, while *A. africanus* femoral dimorphism does not differ significantly from any of these taxa. However, there have not yet been published analyses of direct comparisons of postcranial SSD in these two fossil hominins.

This study performs such a comparison using multivariate postcranial data sets for *A. afarensis* (n=15), *A. africanus* (n=24), and four extant hominoid taxa spanning a wide range of SSD (*Pan troglodytes* [n=48], *Homo sapiens* [n=48], *Pongo* [n=27], and *Gorilla gorilla* [n=48]). To address differences between the two fossil samples in sample size and missing data patterns, a resampling procedure was developed that allows for direct comparisons among all taxa.

Results show *A. afarensis* is significantly more dimorphic than *A. africanus* ($p = 0.018$). Additionally, both fossil taxa are significantly more dimorphic than *Pan* and *Homo*, the difference being between a *Gorilla*- or *Pongo*-like level in *A. africanus* and a *Papio*-like level in *A. afarensis*. Such high SSD is only observed in extant primates with high levels of sexual selection, but it remains to be

determined whether variation in the high levels of dimorphism observed among *Australopithecus* species is due to variation in sexual selection alone or in other selective forces that can affect dimorphism (e.g., ecological stressors).

Data collection was funded in part by the National Science Foundation (BCS-0137344) and a Wenner-Gren Foundation Hunt Postdoctoral Fellowship.

An investigation of the inter and intra post mortem microstructural change seen in a experimental series of pigs exposed to a marine environment

HALEY P. GOREN and LYNNE S. BELL

School of Criminology, Simon Fraser University

The identification of post-mortem microstructural change to human bone can provide information on decompositional history and body deposition. The objective of this study was to assess the total distribution of post-mortem microstructural change within and between individual marine-submerged pig skeletons. An experimental series consisting of 14 juvenile pig carcasses were submerged within the Strait of Georgia B.C., between four to eight months. Seven pigs were individually submerged within caged platforms and the remaining seven were tied to open platforms. For this study, six elements were selected from each carcass: first rib, radius, ulna, middle-rib, tibia, and femur. Two transverse thin sections were sampled at each bone mid-shaft (n=148) and examined using circularly polarized transmitted light. The distribution of tunneling was assessed by measuring maximum ingress and tunnel diameter at 40 locations of the peripheral cortex. Results of analysis indicated peripheral tunneling from the periosteum to the central cortex. Tunnels were observed as radiating, bifurcating, and also observed as isolated tunnels and in clusters. All element types were impacted by tunneling. Tunnel diameters ranged between 2.00mm to 11.96mm, with a 3.1mm mean. Ingress measurements ranged between 7.54mm to 253.43mm with a 91.82mm mean. Distribution of post-mortem microstructural change across skeletal elements showed the averaged maximum penetration ingress was deeper in the uncaged (98.52mm), when compared to caged material (72.57mm). The averaged tunnel diameters showed a non-significant difference between uncaged and caged elements. Knowledge of marine post-mortem microstructural change assists the interpretation of events produced by different environments.

This work was supported by DDRC and CFI/BCKDF funds to LSB

Sexual selection, signaling and facial hair: US and India ratings of variable male facial hair

PETER B. GRAY¹, LYNDESEY K. CRAIG¹, JORGE PAIZ-SAY¹, LAVIKA P², SANJITHA KUMAR² and MADHAVI RANGASWAMY²

¹Anthropology, University of Nevada, Las Vegas,

²Psychology, CHRIST (Deemed to be University)

The ability to grow facial hair might have served as an honest ancestral signal of male age, social dominance, strength and health. Male facial hair may also have had signaling value for attractiveness, though subject to potential conflicts between status-related benefits, sexual coercion and intimate care for a mate and offspring. Male facial hair can also be modified, giving rise to cultural variation in the potential signaling function of facial hair. To address the putative ancestral social signaling value of male facial hair, in concert with variable cultural meaning, we surveyed N=250 US men and women and N=281 Indian men and women, ages 18-25, about sociodemographics and attitudes toward male facial hair. Participants rated a randomized series of nine images of a composite male model with facial hair with respect to: preferred style, estimated age, attractive to potential partners, assertive, physically strong, friendly, and healthy. Types of facial hair were grouped into four categories: *clean shaven*, *partial* (e.g., Van Dyke and soul patch), *stubble* and *beard*. Supporting hypothesized differences, results show that more male facial hair was positively associated with age estimates and assertiveness and negatively with friendliness, though unrelated to physical strength. Supporting hypotheses, women preferred less facial hair and rated less facial hair as more attractive. Some sample differences arose such as Indian participants perceiving greater age estimate ranges than US respondents. These data indicate patterned variation in evaluations of male facial hair that can be situated within an evolutionary- and cultural-ly-evolved signaling framework.

Nonapeptide receptor neuroanatomy in monogamous and promiscuous *Eulemur*

NICHOLAS GREBE¹, ANNIKA SHARMA¹, SARA FREEMAN², KAREN BALES³ and CHRISTINE DREA¹

¹Evolutionary Anthropology, Duke University,

²Biology, Utah State University, ³Psychology, University of California Davis

Oxytocin (OT) and arginine vasopressin (AVP) are two mammalian neuropeptides with important roles in mating and social bond formation. Many functional models for OT/AVP directly stem from work examining differences in these hormonal systems between closely related rodent species, but translating these findings to human biology is not straightforward. Non-human primates offer an opportunity to bridge this gap. This project makes use of natural variation in mating systems within *Eulemur*, a genus of strepsirrhine

ABSTRACTS

primate, to characterize interspecific variation in the OT/AVP system. Species within *Eulemur* exhibit both monogamous and promiscuous mating systems—the only primate genus known to possess such variation. We thus performed oxytocin receptor (OXTR) and vasopressin receptor (AVPR1a) autoradiography on banked *Eulemur* brain tissue from 12 individuals, representing seven species, to measure and compare receptor densities across the brain. We find conserved binding in several regions, such as those involved in visual attention, consistent with previous work in non-human primates. However, in partial support of the prediction that brain organization of OT/AVP underlies monogamous pair-bonding, we also find some evidence of differential OXTR/AVPR1a expression in target brain regions including olfactory pathways, the nucleus basalis, and nucleus accumbens. Mapping differences in OXTR/AVPR1a distribution across *Eulemur* and other primate species better positions the field to understand evolutionary mechanisms driving diversity and maintenance of mating systems in primates, while also shedding light on neurobiological bases.

This material is based upon work supported by the National Science Foundation under Grant #SBE-1808803.

Seasonal Isotope Ecology in the East African Miocene Ape *Afropithecus*

DANIEL R. GREEN¹, SUSANNE COTE², WENDY DIRKS³, DONALD J. REID⁴, IAN S. WILLIAMS⁵ and TANYA M. SMITH⁶

¹Department of Human Evolutionary Biology, Harvard University, ²Department of Anthropology and Archaeology, University of Calgary, ³Department of Anthropology, Durham University, ⁴Center for the Advanced Study of Human Paleobiology, George Washington University, ⁵Research School of Earth Sciences, Australian National University, ⁶Australian Research Centre for Human Evolution, Griffith University

Environmental seasonality is commonly invoked as a driver of novel adaptation and evolution in great apes and hominins, but is difficult to reconstruct in association with fossil remains. Here we measure seasonally variable oxygen isotope compositions ($\delta^{18}\text{O}$) in two early Miocene *Afropithecus turkanensis* molars from Kalodirr, Kenya, using a Sensitive High Resolution Ion Microprobe (SHRIMP SI). Standardized $\delta^{18}\text{O}$ values sampled along the enamel-dentine junction are related to temporal records of enamel formation. To situate *Afropithecus* specimens ecologically, we collected comparative SHRIMP $\delta^{18}\text{O}$ data from molars of two recent Liberian chimpanzees (*Pan troglodytes verus*) and five Ethiopian baboons (*Papio hamadryas*) from the Awash National Park. Sequential *Afropithecus* measurements reveal annual seasonal fluctuations in $\delta^{18}\text{O}$ values that span 7.6 ‰ across both molars (range = 19.3–26.9 ‰). The range in *Afropithecus* is slightly less than that observed in

chimpanzees (range = 13.1–21.8 ‰), but exceeds baboons (range = 23.0–28.8 ‰). $\delta^{18}\text{O}$ values in *Afropithecus* are intermediate between those of forest-dwelling chimpanzees and grassland baboons, and are consistent with inferences from other sources that Kalodirr may have included mosaic environments. Our results also provide environmental context in support of characterizations of *Afropithecus* as a thick-enamelled hard-object feeder. Spatially precise and developmentally informed microsampling strategies have the potential to recover seasonal climatic and behavior patterns as long ago as the early Miocene, and will contribute to elucidating the complex relationship between seasonality, primate behavior, and evolution.

Funded by the Australian Academy of Science Regional Collaborations Programme, Australian National University, Griffith University Environmental Futures Research Institute, and Harvard University.

Applicability of tooth measurements in estimating ancestry between modern Japanese and Florida Seminole samples

MADELYN K. GREEN¹, MARK HUBBE^{1,2} and SEAN D. TALLMAN^{3,4}

¹Department of Anthropology, The Ohio State University, ²Instituto de Arqueología y Antropología, Universidad Católica del Norte, ³Department of Anatomy and Neurobiology, Boston University School of Medicine, ⁴Department of Anthropology, Boston University

Many Asian and Asian-derived (i.e., Native American) populations are often grouped in a single, broad ancestry category despite distinct population histories. As such, few attempts have been made to study the morphological affinities between these populations. Here, we explore their differences through the analysis of dental metric variation, which show high heritability values, and as such are efficient in identifying biological differences between populations. This study tests the null hypothesis that Asian and Native American groups show no differences in dental dimensions. Dental casts were measured from a modern Native American (Florida Seminole; n=45) and a modern Japanese (Jikei University, Tokyo; n=111) samples, representing a relatively sexually unbiased sample (f=67; m=89), with ages ranging from juveniles to adults. Mesiodistal and buccolingual tooth dimensions were compared between Seminole and Japanese groups for males, females, and pooled sexes using canonical discriminant function analyses (DFA) to assess classification rates based on ancestry. The results show very high correct classification rates, ranging from 89.8% (males), to 100% (females), to 96.2% for pooled sexes. The high rates of correct classification indicate that Seminole and Japanese tooth dimensions exhibit significant, population-specific patterns that are able to accurately discriminate between them. These results demonstrate that

the significant differences in tooth dimensions between Seminole and Japanese populations support the applicability of using population-specific DFA classification functions to test ancestry between Asian and Native American populations, and could be used to improve the rate of positive identification of isolated skeletons of forensic relevance.

This research was supported by the National Science Foundation/Japanese Society for the Promotion of Science (1713808).

Set apart from within: Articulated women in commingled tombs from Early Bronze Age Arabia

LESLEY A. GREGORICKA¹, JAIME M. ULLINGER² and ALECIA SCHRENK³

¹Department of Sociology, Anthropology, & Social Work, University of South Alabama, ²Department of Sociology, Criminal Justice, and Anthropology, Quinnipiac University, ³Department of Anthropology, University of Nevada, Las Vegas

During the Umm an-Nar (2700-2000 BCE) period in southeastern Arabia, monumental tombs contained the commingled remains of hundreds of people of all ages and sexes. However, two fully articulated individuals were recovered from predominantly commingled mortuary contexts at Shimal (Unar 2) and Tell Abraq. Both were young adult females who had been intentionally protected from commingling. This research examined the social identities that facilitated their special treatment in death through mortuary and bioarchaeological analyses.

The poorly preserved skeleton of the local ($^{87}\text{Sr}/^{86}\text{Sr} = 0.70882$) Unar 2 female revealed a lytic lesion on the left talus, suggestive of a tumor which may have impacted her mobility. She was interred with a fully articulated dog, the only burial of its kind in the region. The Tell Abraq individual exhibited non-local strontium ($^{87}\text{Sr}/^{86}\text{Sr} = 0.70862$) isotope ratios in her first and third molars, indicating that she migrated to the site in her mid-teens, where she contracted paralytic poliomyelitis before her death at 18-20 years of age.

Both women suffered from conditions which impaired their mobility. While they were permitted access to these collective tombs, they were also segregated within these structures and received differential mortuary treatment. This may suggest that they were honored in death for some special social role (e.g., hunting with a companion animal). Conversely, they may have been purposefully excluded from normal interment practices due to disease stigma related to mobility, resulting in these women being denied access to joining the ancestor collective created via commingling.

This research was funded by the National Science Foundation (Award #1852426).

ABSTRACTS

The influence of speed on craniovertebral kinematics in *Sapajus apella*

NEYSA GRIDER-POTTER^{1,2}, MYRA F. LAIRD³, CALLUM F. ROSS⁴, MARTIN D. HERMAN⁵ and MICHAEL C. GRANATOSKY⁶

¹Graduate School of Human Sciences, Osaka University, ²Postdoctoral Fellow, Japan Society for the Promotion of Science, ³Department of Integrative Anatomical Sciences, University of Southern California, ⁴Department of Organismal Biology & Anatomy, The University of Chicago, ⁵Section of Neurosurgery, The University of Chicago, ⁶Department of Anatomy, College of Osteopathic Medicine, New York Institute of Technology

Head stability facilitates gaze and balance, important components of navigating complex environments. However, the importance of head stability during locomotion and the role of the neck in facilitating that stability are not well understood. Increasing speed presumably demands head stability because the substrate changes quickly relative to the animal, which in turn requires gaze stability. Thus, we expected head stability to increase with locomotor speed. We also hypothesized that cervical vertebral kinematics buffer the head from trunk movements, thereby maintaining head stability across increasing speeds. We predicted that the angular kinematics of more cranial vertebral levels should correlate more strongly with cranial motion than more distal vertebral levels.

These predictions were tested using X-ray Reconstruction of Moving Morphology (XROMM) analysis of craniovertebral kinematics in two adult capuchin monkeys. Angular kinematic data were collected from subjects walking on a flat-belt, simulated terrestrial treadmill at various speeds. Linear mixed models demonstrate that locomotor speed does not significantly influence craniovertebral movement on the flat, predictable treadmill. The lack of variability in head movement could indicate the importance of head stability at any speed or possibly reflect the stability of the terrestrial substrate. There is also no clear pattern of correlation in pitch, roll, and yaw among vertebral levels, which is unexpected given the coupling patterns of motion described in the human literature. It may be that neuronal mechanisms cause cervical muscular contraction to stiffen the neck during locomotion and the majority of motion happens at the craniocervical and cervicothoracic junctions.

This research was supported through National Science Foundation's Doctoral Dissertation Research Improvement Grant (BCS-1731142), National Science Foundation (NSF-BCS-1440516, NSF-BCS-1440541, NSF-BCS-1440542, NSF-BCS-1440545, NSF-BCS-1627206), and the AAPA Cobb Award.

Alzheimer's disease symptoms: A comparison of the United States and Mexico

ERIC E. GRIFFITH

Anthropology, UMass Amherst

This project draws on interviews conducted in Puebla, Mexico and Springfield, Massachusetts to identify cross-cultural differences in how Alzheimer's disease (AD) symptoms are recognized. In Mexico little is known about which symptoms motivate a caregiver to seek an AD diagnosis and which symptoms are most troublesome to families.

Methods: Fifty-seven caregivers of people diagnosed with AD were interviewed across two field sites over 24 months. The caregivers lived with a family member who had an AD diagnosis. The diagnosed person was also interviewed.

Interviews were open-ended, lasting 2-4 hours, and prompted caregivers to self-identify symptoms. Follow-up interviews used neuropsychology questionnaires (e.g. Neuropsychiatric Inventory) to identify other symptoms.

Results: Latency from first symptom appearance to AD was longer in Mexico (4.1 years \pm 3.1) than the US (2.2 years \pm 1.2). Caregivers in Mexico reported psychiatric symptoms (e.g. irritability, depression) as most bothersome, whereas US caregivers reported disorientation and verbal repetitions. Apart from verbal repetition, caregivers rarely reported memory changes as a primary problem in either country.

Conclusion: Mexican caregivers sought diagnosis at a later stage of AD and for different reasons than caregivers in the US. Those differences can be traced to divergent definitions of normal/abnormal aging. Similarly, caregivers in Mexico were more troubled by behavioral disturbances than their US counterparts, possibly explained by cultural differences in coping strategies for age-related cognitive decline. The impact of an AD diagnosis varies between the US and Mexico, suggesting that education initiatives and post-diagnosis counseling/advising ought to reflect local realities.

Thank you to the Wenner Gren Foundation for a Dissertation Fieldwork Grant (Grant Number: 2016-2995)

What age-related changes in response to vocalizations can tell us about the development of social cognition in *C. capucinus* at Lomas Barbudal

JULIE GROS-LOUIS¹ and SUSAN PERRY^{2,3}

¹Psychological and Brain Sciences, University of Iowa, ²Anthropology, University of California-Los Angeles, ³Behavior, Evolution and Culture Program, University of California-Los Angeles

Capuchins change in responsiveness to vocalizations over development, presumably reflecting an increasing awareness of the call meanings. Using

longitudinal data from Lomas Barbudal, we documented focal animals' responses (ignore, look at, run towards or away) to their groupmates' calls. We examined changes in responsiveness to three vocalizations—alarms, screams, and gargles—at four ages: 0-2 months, 6-7 months, 12-13 months and 24-25 months. These calls differ in their functions: alert, recruitment, and (putatively) dyad-specific bond-testing, respectively.

A three-way repeated measures ANOVA comparing responsiveness to alarms, screams and gargles found a significant main effect of age, $F(3,21) = 6.159, p = .004, h^2 = 0.468$, and a significant interaction between age and call type, $F(6,42) = 8.693, p < 0.001, h^2 = 0.554$. There were fewer responses at 0-2 months than 6-7 months ($p = 0.004$). Furthermore, there were significant differences in responsiveness to these calls at 12-13 months, $F(2,14) = , p < 0.001, h^2 = 0.753$. Individuals responded significantly more to alarms and screams than gargles ($p = 0.002$ and $p = 0.021$, respectively) and slightly more to alarms than to screams ($p = 0.057$).

At 24-25 months, individuals also responded differentially to the three calls, $F(2,14) = 8.491, p = 0.004, h^2 = 0.548$. Individuals responded more to alarms and screams than to gargles ($p = .010$ and $p = 0.011$, respectively) The findings of this interaction suggest that there is differential responding to vocalizations and changes in responsiveness are not just a function of age.

MPI-EVAN, UCLA and grants to S. Perry: NSF (1638428, 0613226, 848360), National Geographic Society (7968-06, 8671-09, 20113909, 9795-15, 45176R-18), Templeton World Charity Foundation (0208), WCF, and 5 Leakey Foundation grants.

How many tooth hops does it take to accurately measure saw blade teeth-per-inch in bone?

ALICIA R. GROSSO, ANNE BEGLEY and SHARON A. TOTH

Anthropology Department, University of Pittsburgh

Forensic anthropological research has demonstrated that tooth hop (TH) is a valuable measurement from saw-cut bones as it can be used to indicate the number of teeth-per-inch (TPI) of a saw. But how many hops in a chain do you need? It is hypothesized that more hops in a chain would increase accuracy when estimating blade TPI; however, the amount of bone impacts the presence of long chains. This study used one unused hand saw to cut seven pig humeri. Individual hops were measured and sorted into groups based on number of hops in their respective chains, single ($n = 196$), double ($n = 141$), or three-plus ($n = 57$). Random measurements were also collected between adjacent saw teeth for comparison ($n = 49$). ANOVA, comparing the effect of chain size on TH mean, shows no significant differences among groups measured from

ABSTRACTS

bone ($p > 0.05$). However, when blade measurements were included, means were significantly different ($p < 0.05$). Pairwise ANOVA results show that blade mean is significantly different from single and double groups but is not significantly different from the three-plus group. Thus, three or more hops in a chain did more accurately reflect blade TPI. However, when comparing standard deviations between blade and bone measurements, the analyst would have to report a confidence interval much wider than that of the actual blade to account for all variation introduced when cutting bone tissue. Ultimately, one-hop or two-hop chains should not be discarded as chains with three or more are rarer to find.

Morphometric analyses support a separate evolutionary lineage for *Tarsius pumilus*

NANDA B. GROW

Department of Sociology, Social Work, and Anthropology, Utah State University

Recent genetic analyses reveal a complicated history of tarsier dispersals to Southeast Asian islands, and suggest a monophyletic origin of Sulawesi tarsiers. A revised taxonomy that divides tarsiers into three genera based on insular geography may not account for these complex dispersal events. One unresolved issue is the relationship of *Tarsius pumilus* (pygmy tarsier) to other species. The purpose of this study is to clarify relationships between extant tarsiers using multivariate morphometric analyses. I compared tarsiers from Sulawesi (*T. pumilus*, *T. spectrum*, *T. wallacei*), Borneo (*Cephalopachus bancanus*), and the Philippines (*Carlito syrichta*) (N=67) using external linear measurements (forelimb, hindlimb, thigh, hindfoot, upper arm, forearm, tail, body). I transformed size-standardized data using principal components analysis, where the first three components explained 87.37% of the variation. To test the hypothesis that *T. pumilus* classifies with Sulawesi tarsiers, I performed a canonical discriminant function analysis to predict group membership by species and geographic location. Although 94.83% of subjects accurately classified by species and 100% correctly classified as pygmy compared to non-pygmy, geographic classification was not as straightforward. A discriminant function analysis on the first three principal components was significant (Wilk's $\lambda = 0.209$, $F = 32.06$, $p < 0.001$), but a *post hoc* analysis misclassified 27.59% of *T. pumilus* and *C. syrichta* individuals. In the canonical plot, *T. pumilus* was morphologically distinctive from Sulawesi tarsiers and overlaps with Philippine tarsiers. Considered with forthcoming DNA evidence, these results suggest that "pygmy" tarsiers are not dwarfed lowland Sulawesi tarsiers and represent a distinct dispersal.

Sexual dimorphism in the chimpanzee pelvis: Implications for understanding human pelvic evolution

NICOLE D.S. GRUNSTRA^{1,2,3}, EVA ZAFFARINI⁴, BARBARA FISCHER¹ and PHILIPP MITTEROECKER²

¹Evolutionary Anthropology, Konrad Lorenz Institute, ²Department of Theoretical Biology, University of Vienna, ³Mammal Collection, Natural History Museum Vienna, ⁴Department of Cell Biology and Anatomy, University of Calgary

The strong pattern of pelvic sexual dimorphism present in humans is widely held to be an obstetric adaptation to birthing large neonates. In chimpanzees, where the neonate is much smaller relative to the birth canal, pelvic sexual dimorphism is not nearly as evident and the role of body size dimorphism has been variously argued to drive or obscure pelvic dimorphism. However, few studies have investigated sexual dimorphism in the chimpanzee pelvis in the same level of detail as in humans. We conducted a geometric morphometric analysis of the chimpanzee (*Pan troglodytes*) pelvis using 279 3D landmarks on 20 adult females and 14 adult males. Overall pelvic shape was significantly sexually dimorphic, with females showing larger sub-pubic angles and other more birth-amenable shape features than males. When considering the birth canal separately, females were found to have a medio-laterally wider and thus rounder canal than males. Pelvic shape variation had an allometric component but the sexual dimorphism was largely unrelated to this allometric trend. The observed pattern of dimorphism in the chimpanzee pelvis closely matches the pattern known in humans. Given that the chimpanzee pelvis likely poses no obstetric constraints, our findings suggest that pelvic sexual dimorphism can exist in the absence of obstetric selection and may be a shared pattern among hominids or even mammals, which has important implications for our understanding of the evolution of pelvic sexual dimorphism and cephalopelvic disproportion in the human lineage.

N.D.S.G. and P.M. were supported by the Austrian Science Fund (FWF) grant P29397, E.Z. by the European Community Action Scheme for the Mobility of University Students (ERASMUS).

Differences in enamel extension rates in modern southern Africans and Europeans correspond with differences in their crown formation times

DEBBIE GUATELLI-STEINBERG¹, GINA MCFARLANE², CAROLINA LOCH³, SOPHIE WHITE³, ROSIE PITFIELD², PRISCILLA BAYLE⁴, BRUCE FLOYD⁵ and PATRICK MAHONEY²

¹Anthropology, The Ohio State University, ²Skeletal Biology Research Center, University of Kent, ³Oral Science, University of Otago, ⁴Environment and Anthropology, University of Bordeaux, ⁵School of Social Sciences, University of Auckland

Understanding proximate causes of variation in modern human crown formation times provides a context for understanding them in fossil hominins. In a previous study, anterior tooth crowns of modern northern Europeans were shown to take longer to form than those of southern Africans, but the proximate causes of this difference were not investigated. Differences in rates of enamel extension, the rates at which crowns grow in height, can cause differences in overall crown formation time, but so can differences in the heights of crowns. The present study asks whether differences in the crown formation times of southern African and northern European anterior teeth are better explained by differences in their enamel extension rates or crown heights. Accordingly, enamel extension rates were measured at regular intervals along the enamel-dentine junction in the maxillary canine teeth of 13 southern African and 10 northern European females. Southern African teeth had statistically significantly faster rates of enamel extension in the cusp than did northern Europeans (averaging 24.7 vs. 19.5 micrometers per day, respectively), with crown heights that were not significantly different. Thus, relative to northern Europeans, southern Africans have higher initial rates of enamel extension that appear to influence their shorter crown formation times, since the crown heights of females from the two population samples are similar. These results suggest that analyses of crown formation time in fossil hominins should include both rates of enamel extension and crown height to assess the proximate causes of species differences and similarities in crown formation time.

Study undertaken as part of The Biorhythm of Childhood Growth project funded by The Leverhulme Trust (grant number RPG-2018-226). The Royal Society provided an equipment grant (grant number RG110435).

Trabecular bone in the ankle of a rapid-growing avian bipedal model in response to locomotor inactivity

AMERICA M. GUERRA¹, NICHOLAS B. STEPHENS¹, SUZANNE M. COX², MATTHEW Q. SALZANO^{2,3}, STEPHEN J. PIAZZA², JONAS RUBENSON² and TIMOTHY M. RYAN¹

¹Anthropology, Pennsylvania State University, ²Biomechanics Laboratory, Department of Kinesiology, Pennsylvania State University, ³Integrative & Biomedical Physiology, Pennsylvania State University

Under the framework of bone functional adaptation, bone structure is predicted to reflect the loads experienced during an animal's lifetime. From this premise, paleoanthropologists often use variation in bone structure to infer an individual's behavior. However, the precise relationship between skeletal loading and bone structure remains unclear. To determine if differences in trabecular bone arise in relation to variation in load stimulus, we conducted a controlled experimental study where

ABSTRACTS

three groups of juvenile guinea fowl (*Numidia meleagris*) were exercised over a period of 20 weeks. An exercise group (n=8) was permitted to run and perform high-power perch jumps, while the sedentary group (n=8) and a sedentary group with additional induced paralysis of the gastrocnemius via botulinum injection (n=8) were housed in pens that only allowed for standing or walking. Following sacrifice, microCT scans (25 µm) of the complete ankle joint trabecular bone was quantified using Medtool. Trabecular bone volume fraction, degree of anisotropy, average spacing, average thickness, and number were not significantly different between groups. However, groups differed in local distribution of trabecular structure within the joint. The exercise group exhibited the widest range of variability in all variables. These results only incorporate information about trabecular bone. Future analyses will quantify cortical thickness and midshaft variables to explore if more diagnostic differences exist when the complete bone structure is considered. The results of this analyses increases our understanding of the complexities underpinning bone functional adaptation, which may be informative in relation to interpretations based on extant and extinct hominoids.

Pervasive genomic evidence for adaptation to a leaf-based diet in sifakas (genus *Propithecus*)

ELAINE E. GUEVARA^{1,2}, TIMOTHY H. WEBSTER³, RICHARD R. LAWLER⁴, BRENDA J. BRADLEY¹, JEANNIN RANAIVONASY⁵, JOELISOA RATSIRARSON⁵, R. ALAN HARRIS^{6,7}, YUE LIU⁶, S.C. MURALI⁶, M. RAVEENDRAN⁶, DANIEL S.T. HUGHES⁶, DONNA M. MUZNY⁶, ANNE D. YODER⁸, KIM C. WORLEY⁹ and JEFFREY ROGERS⁶

¹Center for the Advanced Study of Human Paleobiology, The George Washington University, ²Department of Evolutionary Anthropology, Duke University, ³Department of Anthropology, University of Utah, ⁴Department of Sociology and Anthropology, James Madison University, ⁵Département des Eaux et Forêts, University of Antananarivo, ⁶Human Genome Sequencing Center, Baylor College of Medicine, ⁷Department of Molecular and Human Genetics, Baylor College of Medicine, ⁸Department of Biology, Duke University

Sifakas (genus *Propithecus*) are large diurnal lemurs that exhibit a folivorous dietary repertoire and possess a suite of anatomical traits that are associated with obtaining nutrients from leaves. We generated whole genome sequence data for Coquerel's sifaka (*P. coquereli*) and Verreaux's sifaka (*P. verreauxi*) and performed comparative analyses of protein coding regions. We found evidence of accelerated evolution of genes in several complementary pathways related to folivory. For example, the GO terms *intestinal absorption*, *xenobiotic transport*, and *sensory perception of taste* were enriched among genes showing relatively high rates of amino

acid substitution in sifakas. These categories included genes that influence intestinal microvilli morphology, which could modify nutrient absorption. They also included genes that play roles in metabolizing xenobiotic compounds, which could contribute to the ability to cope with ingested plant secondary compounds, as well as several bitter taste receptor proteins that exhibited amino acid substitutions at sites predicted to alter signal transduction. We also found that sifakas show molecular evolution that is convergent with other folivores, including snub-nosed monkeys, which are characterized by a highly specialized ruminant-like digestive system. Together, our findings indicate that a reliance on a folivorous diet has been a strong selective pressure in sifaka evolutionary history. Although sifakas exhibit a less strictly folivorous diet than colobines and facultatively include a relatively high proportion of fruit and other plant parts in their diet, the ability to efficiently digest leaves has been critical to their ecology.

Funding for this project was provided by the Baylor College of Medicine, the Duke Lemur Center, The George Washington University, and Yale University.

The Interchange of Cultures: Egyptian-Nubian Entanglements in Mortuary Practices in Ancient Nubia

KARI A. GUILBAULT and MICHELE R. BUZON
Anthropology, Purdue University

Cultures do not exist in a stagnated state. Rather, influences such as colonialism, change cultures over time. Archaeological context and evidence from skeletal material can provide a frame of reference for inferences to cultural changes in ancient populations. The ancient site of Tombos is situated on the bank of the Nile River, at the Third Cataract in modern-day Sudan. Egyptian sovereignty led to co-inhabitation with Nubian locals at Tombos during the New Kingdom, (~1400 B.C.E.) through the Napatan period, ~650 B.C.E. In this study, we present the examination of three distinct interment locations at Tombos in order to investigate variable usage by different community subgroups in the different burial areas (Chi-squared, Fisher's exact tests, $p \leq 0.05$). The findings of this study show that 59.0% (121/205) of the interred were buried in the elite pyramid area, 26.3% (54/205) in the middle-class chamber tombs area, and 14.6% (30/205) in the Nubian-style tumulus cemetery. Immigrants, identified by non-local strontium isotope values, were found in significantly higher numbers in the chamber tombs (34.7%, 17/49) in comparison with the pyramid (14.3%, 8/56) and tumulus (0.0%, 0/15) graves. No significant differences were found in burial position (extended Egyptian vs. flexed Nubian) between the pyramid (95.3%, 58/68), chamber (90.2%, 37/41) and tumulus (95.5%, 21/22) groups. The results highlight the confluence of social groups contributing to the

interchange of cultures. In addition, these findings suggest that interactions between Egyptians and Nubians at Tombos may have differed by social group.

Australopithecus afarensis endocasts suggest ape-like brain organization

PHILIPP GUNZ¹, SIMON NEUBAUER¹, DEAN FALK^{2,3}, PAUL TAFFOREAU⁴, ADELINE LE CABEC^{1,4}, TANYA M. SMITH⁵, WILLIAM H. KIMBEL⁶, FRED SPOOR^{1,7,8} and ZERESENAY ALEMSEGED⁹

¹Human Evolution, Max Planck EVA Leipzig, ²Department of Anthropology, Florida State University, ³School for Advanced Research, Santa Fe, ⁴European Synchrotron Radiation Facility, ⁵Australian Research Centre for Human Evolution, Griffith University, ⁶Institute of Human Origins, Arizona State University, ⁷Centre for Human Evolution Research, Natural History Museum London, ⁸Department of Anthropology, University College London, ⁹Department of Organismal Biology and Anatomy, University of Chicago

Debates about evidence for brain reorganization in *Australopithecus* have often focused on the position of the lunate sulcus, ever since Raymond Dart's seminal description of the Taung child's natural endocranial imprint in 1925. In non-human apes a well-defined lunate sulcus approximates the anterior boundary of the primary visual cortex of the occipital lobes. Some have argued that an evolutionary reorganization of the parietotemporo-occipital association cortices displaced the lunate sulcus posteriorly on endocasts of australopithecids, and eventually led to the disappearance of a clear endocranial impression in humans. Hypothetically, such brain reorganization in early hominins could have been linked to behaviors that were more complex than those of their great ape relatives (e.g. tool manufacture, mentalizing, vocal communication.)

Conventional and synchrotron computed tomographic (CT) scans of original fossils from Dikika and Hadar (Ethiopia) yielded (i) an exceptionally preserved endocranium of the Dikika infant DIK-1-1, (ii) a precise age at-death based on virtual dental histology for DIK-1-1, (iii) new endocranial volume estimates of the best-preserved *Australopithecus afarensis* fossil crania, and (iv) previously undetected endocranial features on well-known *Australopithecus* fossils. An endocranial segmentation of DIK-1-1 reveals detailed sulcal impressions, including an unambiguous lunate sulcus in an anterior (ape-like) position. Moreover, the micro-CT data reveal a clear, previously undetected impression of an ape-like lunate sulcus on the partial cranium A.L. 162-28 from Hadar.

ABSTRACTS

Contrary to previous claims, *A. afarensis* endocasts reveal an ape-like brain organization, and no sulcal features derived towards humans.

Max Planck Society (Evolution of Brain Connectomics), European Synchrotron Radiation Facility (ec597), US National Science Foundation (BCS 1126470), M. and W. Hearst, Institute of Human Origins at Arizona State University.

Analysis of the Effects of Maize Reliance on Populations Across Virginia During the Late Woodland Period

KAITA N. GURIAN

Anthropology, The Ohio State University

In prehistory, an increasing reliance on maize has been linked to a decrease in population health. Previous studies have used stable isotopes, developmental defects of enamel, and caries to assess maize reliance and its effects on the health of archaeological populations. The aim of this research is to better understand the effect of maize agriculture on populations in different physiographic regions in Virginia during the Late Woodland period (C.E.1000) through an analysis of caries, enamel defects, and stable isotopes ($\delta^{13}\text{C}/\delta^{15}\text{N}$).

A meta-analysis of research collected on six burial mound sites (Edgehill Site, Potomac Creek Site, Hatch Site, Rapidan Mound, Lewis Creek Mound, Hayes Creek Mound) across three physiographic regions (Coastal Plain, Piedmont, Ridge and Valley) in Virginia was used to test if a differing reliance on maize agriculture in each region resulted in different health outcomes. Reliance on agriculture was defined as a population with a caries percentage over 8.6%.

Stable isotope data indicated a larger dependence on maize in more inland regions of Virginia. Analysis of health impacts showed that while all sites had a percentage of caries over 8.6% and a high percentage of linear enamel hypoplasias, inland sites were found to have a higher percentage of carious lesions located on the occlusal surface. This research indicates that although all populations in Virginia had agriculture, not only is there a progressive increase in maize reliance moving inland, it is associated with an increase in occlusal surface lesions.

Diet modification following the alteration of traditional adaptive strategies and community development in Maya maize agriculturalists from Yucatan, Mexico

FRANCISCO D. GURRI

Sustainability Science, El Colegio de la Frontera Sur

Two seasonal food frequency questionnaires were conducted during the 2017-18 agricultural cycle from Maya maize agriculturalists in two types of rural towns in central Yucatan, Mexico: those that offer nontraditional employment, rapid access

to large cities, and have many grocery stores; and smaller communities which lack any local nontraditional labor opportunities, depend on poor transportation networks and infrastructure, and have few if any food stores. In this study we seek to understand the specific effect of community growth and degree of abandonment of traditional adaptive strategies on diet. We expected that alteration of traditional adaptive strategies would reduce seasonality and have a greater effect on foods consumed than town development. We ran a repeated measures analysis of variance between seasons holding Household Adaptive Strategy and Community Type as Inter-Subjects factors on the sum of all foods consumed per type as classified by the WHO. A significant interaction effect between seasonality, local development, and transformation of traditional adaptive strategies was encountered. Seasonal variation affected all households. In transformed households, this variation reduced micronutrient consumption and increased sugar intake relative to traditional ones; a process that was exacerbated in developed communities. If adaptive strategy alteration was not accompanied by community development, it brought a significant reduction in micro and macro nutrient consumption. Curiously, the diet of traditional households changed little with community development, although they did reduce fat and sugar intake in the larger towns.

The data for this presentation was obtained from CONACYT-240697 research grant.

Life after degradation: *Microcebus jollyae* inhabit degraded forest and non-forest habitats in Kianjavato, Madagascar

NICOLA K. GUTHRIE¹, NANCIA N. RAOELINJANAKOLONA², VERONARINDRA RAMANANJATO², EDWARD E. LOUIS JR³ and STEIG E. JOHNSON¹

¹Anthropology and Archaeology, University of Calgary, ²Mention Zoologie et Biodiversité Animale, University of Antananarivo, ³Conservation Genetics Department, Omaha's Henry Doorly Zoo and Aquarium

Many species of lemurs inhabit highly fragmented landscapes in Madagascar. Species survival may be improved if species are able to adapt to novel habitats outside of forest patches. In this study, we investigate whether the Endangered Jolly's mouse lemur, *Microcebus jollyae*, has similar abundances in non-forest and forest patches. Our study was conducted in Kianjavato, Madagascar from April 2018 – July 2019. We set Sherman traps along 24 transects (300m in length) in two forest fragments: degraded Sangasanga (98.8ha, n = 6 transects) and relatively intact Vatovavy (353.3ha, n = 7 transects) and in non-forest within 600m of these fragments (n = 7, n = 4, respectively). We captured a total of 41 individual mouse lemurs over 3289 trap-nights (number of traps x number

of nights). Capture rates per 100 trap-nights (relative abundance) were 1.49 inside and 1.58 outside Sangasanga, and 0 inside and 1.83 outside Vatovavy. There was no significant difference when comparing capture rates inside and outside of each forest fragment or when comparing inside both fragments. Our results show that *M. jollyae* are able to inhabit non-forest and more degraded forest which may be due to increased insect abundance in more open habitat structures. These results suggest that protecting only intact forest may not be adequate for sustaining populations of this Endangered species.

This study was funded by the Natural Sciences and Engineering Research Council of Canada and the University of Calgary

Behavioral adaptations to life in the interior high Andes, 9–7ka

RANDALL HAAS¹, TAMMY BUONASERA^{1,4}, JENNIFER CHEN², JELMER EERKENS¹, SARAH NOE³, GLENDON PARKER⁴, KEVIN SMITH¹, CARLOS VIVIANO⁵ and JAMES WATSON⁶

¹anthropology, UC Davis, ²anthropology, Penn State, ³anthropology, UC Santa Barbara, ⁴graduate program in Forensic Science, UC Davis, ⁵archaeology, independent, ⁶Arizona State Museum, University of Arizona

Human populations began using the Andean highlands of South America sometime before 11 ka. How humans adapted to the cold, hypoxic, fuel-starved landscape is an active area of research. Current models suggest that initial occupation was logistical or seasonal, that permanent occupation began around 9 ka, and that subsistence economies emphasized vicuña and deer hunting. Archaeological excavations and artifact analyses at the newly discovered site of Wilamaya Patjxa provide tests of expectations derived from this hypothesis. Oxygen and carbon isotope values in human bone dating between 9–7 ka reveal a high-elevation signature. Demographic data show that all age groups and both sexes were present. Burial assemblages indicate both female and male participation in big-game hunting and processing. The faunal assemblage is dominated by vicuña and taruca bone. These results are consistent with a model of permanent occupation of the highlands by 9 ka and extend current empirical support in the interior highlands by 2000 years. The results further reveal that big-game hunting was not gendered in ways that are observed among later hunter-gatherer societies, suggesting a potentially key behavioral feature of early highland adaptation.

ABSTRACTS

KSD-VP-1/1 from Woranso Mille, Ethiopia, does not conform to known *Australopithecus afarensis* pelvic morphology

MARTIN HAEUSLER¹, CINZIA FORNAI^{1,2}, VIKTORIA A. KRENN^{1,2} and NICOLE M. WEBB^{1,3}

¹Institut of Evolutionary Medicine, Universitaet Zuerich, ²Department of Evolutionary Anthropology, University of Vienna, ³Senckenberg Research Institute and Natural History Museum Frankfurt, Frankfurt

Despite accumulating craniodental evidence for the co-existence of multiple hominin species broadly contemporaneous with *Australopithecus afarensis* in East Africa, interpretation of morphological variation and sexual dimorphism is more challenging in postcranial fossils commonly attributed to *A. afarensis*. The 3.6-million-year-old KSD-VP-1/1 skeleton from Woranso-Mille, Ethiopia, is pivotal in this context given its completeness, large body size and purported male sex. The hipbone and sacrum are expanded by numerous matrix-filled cracks, though plastic deformation is absent. Based on high-resolution CT-scans provided by the Woranso-Mille project we isolated and virtually realigned all bone fragments, using 3D prints as validation. Missing regions of the hipbone were estimated using landmark-based warping methods and A.L. 288-1 (*A. afarensis*) as a template. Our reconstruction suggests a remarkably long iliac blade and an unusually narrow sacroiliac joint. Both possibly primitive characteristics clearly distinguish KSD-VP-1/1 from other australopithecines. A corresponding Procrustes distance-based pairwise permutation showed that the difference in sacroiliac joint morphology between KSD-VP-1/1 and A.L. 288-1 exceeds 98.5% of pairwise comparisons within our modern human and orangutan sample. In a 3D geometric morphometric analysis of the hipbone based on 24 homologous landmarks and 60 extant humans, 40 chimpanzees, 40 gorillas and 29 orangutans, as well as A.L. 288-1, Sts 14 and STW 431 (both *A. africanus*), and MH2 (*A. sediba*), KSD-VP-1/1 plotted at the border of the australopithecine distribution. This discrepancy increased when size-adjusted residuals were used to control for allometric influences on shape. These findings might suggest functional and taxonomic diversity within the *A. afarensis* hypodigm.

This research was funded by the Swiss National Science Foundation Grant No. 31003A_176319.

Impact of Sample Collection Preparation on Metabolomic and Microbiome Profiles

JACOB J. HAFFNER^{1,2}, DAVID JACOBSON^{1,2}, TANVI P. HONAP^{1,2}, EKRAM HOSSAIN^{2,3}, KRITHIVASAN SANKARANARAYANAN^{2,4}, LAURA-ISOBEL MCCALL^{2,3} and CECIL M. LEWIS, JR^{1,2}

¹Department of Anthropology, University of Oklahoma, ²Laboratories of Molecular Anthropology and Microbiome Research, University

of Oklahoma, ³Department of Chemistry and Biochemistry, University of Oklahoma, ⁴Department of Microbiology and Plant Biology, University of Oklahoma

Molecular anthropology has overwhelmingly focused on DNA, but much of molecular biology happens above the genome. One emerging field, metabolomics, the "omic" scale study of metabolites, is closely tied to the biological phenotype. Metabolomic studies share technical challenges of genetic studies, with in-field sample preservation being a crucial concern. Few molecular anthropology studies have explored how molecules, especially metabolites, are preserved within samples and how molecular preservation impacts results and interpretations. The common storage practice for metabolomics involves freezing samples upon collection, but this is likely infeasible for much of molecular anthropology, such as studies conducted in remote field sites. Storage solutions designed to preserve DNA and RNA, such as Ambion Invitrogen RNA^{later}, are offered as alternative storage processes. However, with respect to metabolomics, these storage solutions have had limited analysis. Presented here is a study of time, temperature, and storage method on the preservation of the metabolome and microbiome. Ten human fecal samples representing diverse gut ecologies were aliquoted, homogenized, kept at varying storage temperatures (22-25°C, 4°C, and -80°C), and underwent a customized RNA^{later} treatment protocol. The effects of these preservation methods on metabolomic and bacterial taxonomic inventories were characterized through untargeted liquid chromatography-tandem mass spectrometry and 16S rRNA gene amplicon sequencing, respectively. Our results demonstrate metabolomic and microbiome characterization can be robust to varying refrigeration strategies, even over two weeks, yet we find no effective protocol to use RNA^{later} in metabolomic sample conservation. These findings inform best storage methods and indicate how sample treatment impacts sample integrity.

Does variation in female reproductive status explain variation in female smoking? Evidence from cross national and longitudinal studies in low- and middle-income countries

EDWARD H. HAGEN¹, TIFFANY ALVAREZ¹ and DAN T. A. EISENBERG²

¹Department of Anthropology, Washington State University, ²Department of Anthropology, University of Washington

Variation in female smoking is usually ascribed to variation in women's social and economic power and attendant norms regulating women's substance use. Nicotine and other constituents of tobacco, however, are potent teratogens. Moreover, nicotine activates virtually all neurophysiological toxin defense mechanisms, such

as bitter taste receptors, nuclear receptors, xenobiotic transporter proteins, metabolizing proteins, and conditioned aversions. This raises the possibility that, to protect their fetuses and nursing infants, reproductive-aged women who have an earlier age of first marriage and first birth, shorter interbirth intervals, and extended periods of breastfeeding, avoid regular consumption of teratogenic substances like tobacco. This avoidance should abate post-menopause. Previously, in data aggregated at the nation level, total fertility rate was found to be negatively associated with the prevalence of female tobacco use, controlling for gender inequality, with an increase in the prevalence of female smoking seen post-menopause.

To test the gender inequality vs. fetal protection hypotheses of female smoking using individual-level data, we conducted a cross-sectional study using Demographic and Health Survey data from 34 countries (N=572,958) and a longitudinal study of data from Cebu, Philippines (N=3,327). We found that pregnancy, breastfeeding, and having young children were negatively associated with female smoking, and postmenopausal status positively associated, even after controlling for indices of women's social, economic, and educational status. Furthermore, the indices of women's status were negatively associated with smoking, contrary to the gender inequality hypothesis. These results suggest that fetal protection helps explain female smoking decisions.

This investigation was supported in part by funds provided to EHH for medical and biological research by the State of Washington Initiative Measure No. 171

Quantifying intraspecific variation in a Caribbean fossil primate

LAUREN B. HALENAR-PRICE^{1,2}, SIOBHÁN B. COOKE^{2,3}, ZACHARY S. KLUNKERT^{2,3,4}, ZANA SIMS³, JUAN ALMONTE⁵, PHILLIP LEHMAN⁴ and MELISSA TALLMAN^{2,6}

¹Department of Biology, Farmingdale State College (SUNY), ²NYCEP Morphometrics Group, ³Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, ⁴Dominican Republic Speleological Society, ⁵Museo Nacional de Historia Natural "Prof. Eugenio de Jesús Marcano", Santo Domingo, Dominican Republic, ⁶Department of Biomedical Sciences, Grand Valley State University

Skeletal variation is a critical consideration for research on extant primates, but due to an incomplete fossil record, a thorough understanding of this variation is often impossible for extinct species. Here, we assess variation in the Hispaniolan taxon, *Antillothrix bernensis*. This species is now represented by six crania, five mandibles, and dozens of postcranial elements from three paleontologically rich caves. These remains allow us to perform a detailed study of species-level variation, a rare opportunity for any fossil taxon, and a first for platyrrhines.

ABSTRACTS

We assessed skeletal variation in *Antillothrix* using a 3DGM approach; average Procrustes distances among species and genera were calculated from landmark data to assess the range of variation present in extant samples. The level of variation observed among the four adult fossil crania corresponded with that of an average extant platyrrhine genus, or a relatively sexually dimorphic species. They share a depression at glabella, but orbit and neurocranial shape vary conspicuously. There is also a relatively substantial size difference among the four specimens. Humerus and femur results are consistent with those from the cranium, exhibiting variation comparable to that within a single extant genus. Variation in tooth shape is comparable with extant species. Several *Antillothrix* individuals exhibit congenitally absent third molars - a rarity among extant taxa.

Based on geographic and potential temporal distance among the specimens, one might expect a high level of variation. Their isolated island habitat might suggest the opposite. But *Antillothrix* fits the pattern of variation seen in extant platyrrhine genera.

The early Miocene mammals from Mfangano Island: Implications for early hominoid evolution and faunal turnover

ABIGAIL S. HALL and KIERAN P. MCNULTY
Anthropology, University of Minnesota

Early Miocene deposits on Mfangano Island, Kenya, have produced nearly 750 mammalian specimens, including fossils attributed to two apes, *Ekembo hesloni* and *E. nyanzae*, critical for understanding the early Miocene hominoid radiation. Fossil mammals from Mfangano come from two formations; the older Wayando Formation (~20 Ma) and the younger Kiahera Formation (between 18 and 19 Ma). However, exact provenance data for many specimens are lacking, making it difficult to place fossils in relative stratigraphic position. Nevertheless, this collection is important in that it represents a period during which a major faunal turnover event is hypothesized to have happened. Here, historic and recent fossil assemblages from Mfangano were re-analyzed and compared to contemporaneous assemblages to better understand mammalian community structure of Mfangano relative to other early Miocene sites. Our results show the faunal assemblage is most similar to the younger Hiwegi Formation in terms of basic species-level presence/absence data. Contrarily, Mfangano differs from the Hiwegi assemblages but is strikingly similar to older Tinderet assemblages in the proportions of rodent specimens assigned to specific genera (specifically the *Diamantomys/Paraphiomys* ratio). Further resolving relationships between Mfangano's mammal community and those from other localities is difficult without better provenance data. Nevertheless, this study

demonstrates the importance of continued fossil collection, accompanied by detailed provenance data, to inform our understanding of the major faunal turnover event in the early Miocene, and the ecological context for the first appearances of the early ape *Ekembo*.

"Risky" behaviors and zoonotic emerging infectious disease in Central Africa: Examining the distribution of behavioral risks of exposure to potentially zoonotic pathogens across a diverse population in Central African Republic

ELIZABETH S. HALL and MELISSA J. REMIS
Anthropology, Purdue University

Dzanga Sangha Protected Areas Complex (DSPAC), Central African Republic (CAR) lies in a geographic hotspot for zoonotic emerging infectious disease (ZEID) events; however, the likelihood of exposure to potential zoonotic pathogens varies across populations. This study examines specific behavioral risks of zoonotic pathogen exposure from nonhuman primates (NHPs) across gender and subsistence pattern among a diverse mix of indigenous BaAka hunter-gatherers, local fishermen and farmers, and migrant groups dependent upon forest resources in DSPAC. From April 2017-July 2018, we conducted 1,600 ethnographic behavioral surveys from 1,098 individuals residing in Bayanga, the largest town in DSPAC and in two villages located near Bayanga. Of individuals surveyed, 98 (8%) reported direct contact with wild NHPs, including keeping NHPs as pets ($n = 88$), or being scratched or bitten by NHPs ($n = 16$). Keeping a primate as a pet was not correlated with gender or subsistence pattern, nor was it correlated with injury from a primate. Of these injuries ($n = 12$), 9 (75%) were reported by male BaAka who had been injured by wild gorillas while hunting other species ($n = 7$) or while participating in conservation activities in the region ($n=2$). Further understanding of ways behavioral risks of infection are distributed across a population can inform public health measures to reduce risk of local ZEID events.

This material is based upon work supported by the National Science Foundation under Grant No. 1732307.

Modern human molar morphology does not reveal geographical origin

VANDA HALÁSZ¹, CINZIA FORNAI^{1,2} and GERHARD W. WEBER^{1,3}

¹Department of Evolutionary Anthropology, University of Vienna, Austria, ²Institute of Evolutionary Medicine, University of Zurich, Switzerland, ³Core Facility for Micro-Computed Tomography, University of Vienna, Austria

Comprehensive studies elucidating the 3D shape and size variation of upper and lower permanent first molar crowns in geographically diverse populations are lacking. In this contribution we

combined 3D geometric morphometric (GM) analyses based on micro-CT scans from 80 molar crowns (45 uM1s and 35 IM1s) with a qualitative analysis of 10 discrete traits (ASUDAS classification). We included populations with different geographical origin and subsistence background: Sub-Saharan Africans, Southeast Asians, Bedouins, Avars, South Americans, and Central Europeans. For the quantitative approach, four sets of landmarks were considered: the occlusal aspect of the enamel-dentin-junction (EDJ), cervical and crown outlines, and a dataset including the EDJ and the cervical outline, thereby combining the occlusal topography with the crown base. The GM results show that shape and form variation were high within each population, but different populations overlapped widely. For both upper and lower M1s, crown gross morphology varied between either narrow and high or broad and low, with the distal region varying the most. Size analysis confirmed that Europeans possessed smaller teeth than any of the other populations considered. The upper and lower molar EDJ ($r1=0.85$) and whole dentinal crown ($r1=0.61$) showed high pairwise correlation. Significant population-specific trait frequencies were found for the anterior transverse ridge and the anterior accessory tubercles. Additionally, we could show a positive correlation between the intercuspal distances and Carabelli's trait expression. In conclusion, upper and lower molar morphology is highly integrated, but first molar crown form does not allow attributing individual teeth to their own populations.

C. Fornai was financially supported by the Swiss National Science Foundation grant no. 31003A 176319.

Sex Differentials in Mortality in the Bedlam Burial Ground

ALLISON HAM and SHARON N. DEWITTE
Anthropology, University of South Carolina

Previous bioarchaeological studies of the post-Black Death (CE 1350-1540) period in London, England, have revealed that males had lower mortality risks than females under both normal and crisis (i.e., famine) mortality conditions. The creation of London's Bedlam Burial Ground (CE 1569-1738) occurred in response to a growing population and a high mortality rate, and use of the cemetery coincided with multiple disease epidemics in the city. By analyzing the Bedlam burials, this study aims to infer whether the sex patterns of mortality risks seen in the post-Black Death period continued into the post-medieval period in London. This study applies hazards analysis to examine sex differences in risks of mortality in the remains of individuals ($n=395$) from the Bedlam Burial Ground. A Gompertz-Makeham model was employed to assess risk differences in mortality, using sex as a covariate affecting the baseline hazard. To avoid the limitations of traditional age estimation methods,

ABSTRACTS

transition analysis age estimates were used. The results of the analysis reveal lower risks of mortality for males compared to females, which is consistent with previous studies demonstrating lower risks of mortality for males during normal and crisis mortality conditions. These findings improve our understanding of sex differences in mortality risks during the post-medieval period in London. Furthermore, the observed male survival advantage may suggest differences in exposure to biological stressors and access to resources between the sexes during the post-medieval period in London.

Funding for this project was provided by the University of South Carolina Office of the Vice President for Research.

KNM-ER 2598: site context and new fossils

ASHLEY S. HAMMOND^{1,2}, SHARON KUO³, DAVID R. BRAUN^{4,5}, DAN PALCU^{6,7} and SILINDOKUHLE S. MAVUSO⁸

¹Division of Anthropology, American Museum of Natural History, ²New York Consortium of Evolutionary Primatology (NYCEP), ³Department of Anthropology, Penn State University, ⁴Department of Anthropology and Center for Advanced Study of Human Paleobiology, The George Washington University, ⁵Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ⁶Paleomagnetic Laboratory 'Fort Hoofddijk', Utrecht University, ⁷Instituto Oceanográfico, Universidade de São Paulo, ⁸School of Geosciences, University of the Witwatersrand

The KNM-ER 2598 occipital was reportedly found below the KBS Tuff, potentially making it the oldest evidence for *Homo erectus*. Questions have been raised about whether the fossil may have deflated from a younger horizon. We relocated the KNM-ER 2598 find location using aerial imagery from the 1970s. During 2017-2019 field seasons, we performed intensive surface survey and fossil collection within 50 meters of the reconstructed location. We further investigated whether the location was in situ and determined its stratigraphic position relative to the nearby tuffs. The sandstone clasts associated with the find locality were described to provide a geochemical provenance to the lithologies of the surrounding KBS and Upper Burgi Members.

New hominin elements include multiple cranial vault fragments, a partial left ilium, and a proximal metatarsal. None of the elements can definitively be associated with KNM-ER 2598 at this time. However, the cranial vault fragments are consistent with KNM-ER 2598 in suture morphology and thickness. The ilium differs from other ilia from the Upper Burgi Member (KNM-ER 5881, KNM-ER 3228) but is consistent with early *Homo* morphology. Georeferenced aerial imagery shows that the KNM-ER 2598 site is within collection Area 13, rather than Area 15 as originally described. The location is associated with distinct

grey, trough cross and planar laminated sandstones that correlate throughout the region. The site is stratigraphically positioned approximately 3m below the KBS Tuff. Our findings favor an age of nearly 1.9 myr and provide additional evidence that the location has yielded early *Homo* fossils.

The research was supported by the National Science Foundation (BCS-1930719) and the National Museums of Kenya.

Sex-Based Differences in the Aging of the Spine (Vertebral Body) from Bronze Age Human Remains at the Dahekou Site in Yicheng County, Shanxi Province, China

TAO HAN^{1,2}, TING GAO¹, YE FEI¹, QUANCHAO ZHANG¹ and QIAN WANG³

¹Department of Archaeology, Jilin University, ²Science and Technology Archaeology Centre, Chengdu Institute of Cultural Relics and Archaeology, ³Department of Biomedical Sciences, Texas A&M University College of Dentistry

Health disparities between sex-age groups in bioarchaeological settings are an important indicator of the differentiation of sex-based socioeconomic status in ancient human societies. In this study, sex-based differences in the aging of the vertebral column were investigated in human skeletons excavated from a Bronze Age cemetery of the Western Zhou Dynasty at Dahekou site, Yicheng County, Shanxi Province, China. Signs of aging-related lesions and adaptations in the vertebral column were visually screened in forty-seven adult males and seventy-nine females (age at death was estimated ≥ 20 years). Results demonstrated that females overall had a higher incidence of the vertebral compressive fractures than males, while males expressed overall more severe vertebral osteophytosis than females. The vertebrae most severely affected by osteophytosis were Cervical 5-6, lower thoracic and all lumbar vertebrae. Males also had a higher incidence of vertebral facet joint osteoarthritis in cervical and thoracic divisions than females. These findings demonstrate different factors in different patterns of the aging of the spine between two sexes, while the aging of female vertebral column might be more subjected to hormone deficiency related pathophysiology such as osteoporosis, the aging of the male vertebral column might be more subjected to labor-induced heavy physical stresses. This knowledge of sex-based differences in physiological and physical stresses in the etiology and pathophysiology of skeletal degenerative diseases will help differentiate them from other sociocultural factors contributed to health disparities in bioarchaeological studies.

Subcortical systems in human evolution

KARI L. HANSON¹ and MARY ANN RAGHANTI²

¹Department of Anthropology, Institute for Neural Computation, and Kavli Institute for Brain and

Mind, UC San Diego, ²Department of Anthropology, School of Biomedical Sciences and Brain Health Research Institute, Kent State University

The evolution of the human brain has been characterized by a threefold expansion in size in contrast to our closest living relatives, the great apes. Much of this expansion has involved the cerebral cortex, but significant reorganization of the brain's subcortical structures has also occurred. In particular, the striatum, comprised of structures critically involved in social and reward-based learning, behavioral control, and language production, represents a site of modification in mammalian evolution in both macro- and microstructure. Importantly, the human striatum is smaller than would be expected for a primate brain of its size. This gross reorganization is further supported by key specializations of cell types and neurotransmitter distributions. This presentation outlines the specializations of the human and hominoid striatum that support increased complexity in social, emotional, and cognitive systems. Specifically, a unique neurochemical profile in key striatal territories characterized by increased innervation of dopaminergic, serotonergic, and neuropeptide Y positive fibers, alongside a decrease in cholinergic innervation as compared to apes, likely contributes to enhanced sensitivity to social stimuli and behavioral styles. Differences in the distribution and morphology of interneuronal subtypes may further contribute to these unique specializations. We contrast these findings to neuroanatomical variation in human neurodevelopmental disorders, where functional implications of perturbations of neural circuitry can be discerned.

The postcranial morphology and inferred locomotor behavior of the early Pleistocene Eurasian cercopithecine *Paradolichopithecus arevenensis*

WILLIAM E.H. HARCOURT-SMITH^{1,2,3,4}, MONYA ANDERSON⁵, AILEEN FERNANDEZ⁶, NELSON TING⁶, STEPHEN FROST⁶ and ERIC DELSON^{1,2,3,4}

¹Anthropology, Lehman College CUNY, ²Vertebrate Paleontology, American Museum of Natural History, ³Anthropology, Graduate Center CUNY, ⁴NYCEP, ⁵Anthropology, Texas A&M University, ⁶Anthropology, University of Oregon

Paradolichopithecus is a genus of extinct cercopithecine monkey found at early Pleistocene sites across Europe and Asia. Its phylogenetic position within the Cercopithecinae has been the subject of some debate, centering on whether the taxon is more closely related to macaques or baboons. Much of this debate has focused on craniodental remains, including a number of well-preserved crania and mandibles from sites in France, Romania, Greece, and Tajikistan. Previous studies on the postcranium of *Paradolichopithecus* indicate a large-bodied (~30kg) relatively terrestrial species, though these studies have largely centered on visual comparisons.

ABSTRACTS

Here we analyze the morphology of the humerus, ulna, femur, tibia, astragalus, 3rd metatarsal and several assorted pedal phalanges allocated to *Paradolichopithecus avernensis* from the sites of Graunceanu (Romania), and Vatera (Greece). We use a combination of qualitative assessment and quantitative comparative analyses using linear metrics and 3D geometric morphometrics. For all quantitative analyses we include a large sample of extant cercopithecoid taxa representing both colobines and cercopithecines from Eurasia and Africa, and a wide range of locomotor modes and substrate preferences.

Despite suggestions that *Paradolichopithecus avernensis* may be most closely related to extant *Macaca*, we find that the postcranial morphology of this taxon is closest to that of *Theropithecus*, *Mandrillus*, and *Papio*. This may to some degree be due to the allometric consequences of its large size. We infer that the locomotor behavior of this taxon is most-likely, therefore, to be similar to that of extant large-bodied terrestrial papionins.

Canine size is genetically correlated with body size in the Cayo Santiago rhesus macaques

ANNA M. HARDIN

Department of Pathology and Anatomical Sciences, University of Missouri-Columbia

Positive phenotypic relationships between post-canine tooth size and body size are observed among primate species, yet are less apparent within populations. Quantitative genetic analyses of covariance between these traits may shed light on the mechanisms through which tooth size and body size evolve together in primates.

In this study, genetic correlations between body size and dental dimensions were estimated in the Cayo Santiago rhesus macaques (*Macaca mulatta*). Linear measurements were collected from 364 individuals. Body size was estimated using the geometric mean of ten appendicular skeletal dimensions. Heritabilities and genetic correlations were estimated using bivariate animal models and a pedigree representing 527 individuals, including 152 dummy sires, in MCMCgIimm (v. 2.29, R v. 3.6.1). Sex and age were included as fixed and random effects respectively in the models.

Heritability estimates for skeletal size ranged from 0.33 to 0.39 and from 0.28 to 0.39 for dental measurements. Genetic correlations between skeletal size and canine dimensions were positive, whereas genetic correlations between skeletal size and molar dimensions are weakly negative. Skeletal size was positively correlated with honing premolar length and negatively correlated with honing premolar breadth.

These results indicate a genetic relationship between body size and canine-premolar honing complex size that is distinct from the relationship between body size and molar size. Dimensions of the canine-premolar honing complex may therefore better reflect within-population variation in body size than molar dimensions in some primate populations. If shared among populations, these genetic correlations could also impact evolution through sexual selection in cercopithecine primates.

NSF GRF 00039202; NSF DDRIG 1650802; NIH NIDCR F32DE024732

Developmental exposure to high altitude enhances aerobic capacity in hypoxia

TAYLOR S. HARMAN¹, ABIGAIL W. BIGHAM², MELISA KIYAMU³, GIANPIETRO E. REVOLLEDO¹ and TOM D. BRUTSAERT¹

¹Department of Exercise Science, Syracuse University, ²Department of Anthropology, University of California, Los Angeles, ³Ciencias y Filosofía, Universidad Peruana Cayetano Heredia

High altitude native populations exhibit physiological adaptations to their environments. Though development and genetics both play a part in these adaptations, there is evidence of a stronger developmental role. In the largest study of its kind, we investigated the role of developmental exposure to high altitude in maximal oxygen uptake ($\dot{V}O_{2max}$) in hypoxic conditions. We recruited two groups of healthy adults (ages 18-35) of Quechua ancestry in Lima, Peru. The groups were: (1) Quechua Born and raised at Sea-Level (BSL, n = 129); and (2) Quechua Migrants (M, n = 107) born and raised at an altitude 3000m or higher, who migrated permanently to sea-level at some point during their lives. All participants were tested at UPCH in Lima, Peru. $\dot{V}O_{2max}$ was assessed via graded exercise test on a cycle ergometer in simulated high altitude conditions ($F_{O_2} \approx 0.126$). We found that the M group had significantly higher $\dot{V}O_{2max}$ measurements (31.3 ± 0.6 mL/kg/min) than the BSL group (27.8 ± 0.5 mL/kg/min, $p < 0.001$). Additionally, we examined the relationship between duration of childhood exposure to high altitude and $\dot{V}O_{2max}$. Interestingly, no significant relationship was found, which suggests the critical developmental window may be in utero; contrary to previous hypotheses which emphasized childhood exposure. Ultimately, our results demonstrate that developmental exposure to high altitude improves $\dot{V}O_{2max}$ in hypoxic conditions.

This work was supported by the National Science Foundation (BCS 1132310).

Calcaneal external shape of *Australopithecus sediba*

CHRISTINE M. HARPER, CHRISTOPHER B. RUFF and ADAM D. SYLVESTER

Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine

Due to its role in weight-bearing, the calcaneus has the potential to reveal important form-function locomotor signals. The *Australopithecus sediba* calcaneus has been particularly scrutinized because of its unique morphology; however, the entire shape of U.W. 88-99 has not yet been analyzed. Here we analyzed the entire calcaneal shape of gorillas (n=86), chimpanzees (n=112), orangutans (n=31), baboons (n=29), hylobatids (n=32) and modern humans (n=130) to put U.W. 88-99 into a phylogenetic/locomotor context.

Calcanei were either surface or micro-CT scanned and external shape analyzed using a three-dimensional geometric morphometric sliding semilandmark analysis. Semilandmarks were slid relative to an updated Procrustes average to minimize the bending energy of the thin plate spline interpolation function. Landmark configurations were aligned using a Generalized Procrustes Analysis and shape variation summarized using principal components (PC) analysis. Procrustes distances between U.W. 88-99 and all (sub) species/populations were calculated.

Humans and non-human primates separate across PC1. U.W. 88-99 demonstrates an intermediate morphology, falling between humans and gorillas, but closer to humans. This separation is driven by a great ape-like posterior talar facet and a human-like anterior/middle talar facet, suggesting unique load transfer through the subtalar joint, but maintenance of the ability to invert/evert the foot for arboreality. Additionally, the calcaneal tuberosity is more supero-inferiorly oriented than in gorillas. Of the gorilla populations, U.W. 88-99 is closest to mountain gorillas, demonstrating an adaptation for terrestriality. The U.W. 88-99 cuboid facet, despite its damage, is unique relative to other groups, likely adapted for both arboreal and terrestrial behaviors.

This project was supported by NSF grant # BCS - 1824630.

Ontogenetic change in carotid foramen and transverse foramen size reflects change in brain metabolic rate and blood flow rate during growth in humans

ARIANNA R. HARRINGTON¹, CHRISTOPHER W. KUZAWA² and DOUG M. BOYER¹

¹Evolutionary Anthropology, Duke University, ²Anthropology, Northwestern University

The human brain's energy requirements reach a peak during childhood, resulting trade-offs with body growth rate and an unusually slow and protracted period of childhood growth. However,

ABSTRACTS

because the metabolic rate of the brain reflects developmental changes in energetically costly neuronal processes, which are decoupled from changes in brain size, estimation of ontogenetic changes in the energetic costs of the brain are difficult to measure in fossil and other osteological samples. Because brain metabolic rate is correlated to blood flow rate (Q) to the brain, here we test a method which predicts Q from bony foramina that pass arteries supplying the brain. Radii of the carotid and transverse foramina were measured from n=238 human individuals aged 0-20 years from cadaveric medical CT scans, and Q was predicted for the internal carotid (ICA) and vertebral (VA) arteries. Predicted total brain Q (Q of ICA + VA) was compared to literature-derived empirically measured Q and brain metabolic rates. Although predicted total brain Q is lower than measured total brain Q at a given age, the pattern of ontogenetic change is similar. The age of maximal predicted total brain Q and perfusion (Q/ brain mass) occurs around 5-7 years, which roughly matches the age of maximum measured total brain Q and mass-specific rate of brain metabolism, respectively. This suggests that during human ontogeny, the sizes of the carotid and transverse foramina reflect change in blood flow and metabolic requirements of the brain, opening opportunities to reconstruct developmental brain energetics from skeletal samples.

This research was funded by NSF BCS-1825129 (to DMB and ARH), NSF BCS-1552848 and (to DMB), and NSF DBI-1701714 (to DMB).

The Intertwined Recent Population Histories of Korea and Japan as Detected by Cranial Geometric Morphometrics.

KATHERINE I. HARRINGTON¹, CHRISTOPHER J. BAE¹ and JOHN H. RELETHFORD²

¹Anthropology, University of Hawaii at Manoa, ²Anthropology, State University of New York College at Oneonta

Korea and Japan are known to have a closely intertwined history and are considered to be closely related populations. Using 3D geometric morphometric (GM) methods, landmark data (p~44) were collected on adult crania from four temporal subpopulations: Korean Joseon Dynasty (1392-1910, n~76), Modern Koreans (post-1910, n~94), Japanese Edo Period (1603-1868, n~199), and Modern Japanese (post-1868, n~189). These data were used to test several hypotheses about the admixture between the populations in more recent time periods, including whether there was more admixture during the early modern or modern periods and the continuity of the geographic populations through time. General Procrustes, principal component (PC), canonical variance (CV), and discriminate function (DF) analyses were performed on the data. Three sets of analyses were completed: entire cranium, facial region, and cranial vault (n and

p varied with each analysis due to the varying condition of individual remains). The results of the PC analysis show that there is considerable overlap in the variation between the four populations, confirming that more recent Korean and Japanese populations are closely related. However, the CV analysis shows clear groupings in that there is more continuity from the Joseon Dynasty to Modern Koreans than there is for the Edo Period and Modern Japanese samples and shows distinct separation between the Modern Korean and Modern Japanese samples. The DF cross-validation results support this. In all of the analyses, the entire cranium and cranial vault performed better than the facial region at distinguishing the four sub-populations.

Funding was generously provided by: Center for Korean Studies (UHM), Center for Japanese Studies (UHM), Department of Anthropology (UHM)

Discerning independent natural selection

NATHAN S. HARRIS and ALAN R. ROGERS

Anthropology, University of Utah

We develop two complementary methods to classify signals of selection as either ancestral, occurring in the common ancestor of two populations, or independent, occurring following their common ancestor. These methods were then used to scan the genomes of the 1000 Genomes Project phase 3 populations for regions in which the evidence for ancestral or independent selection is strongest. We identify several regions of the genome that likely experienced selection independently in different populations. We show that the glycoporphin cluster, associated with malarial resistance, has experienced selection independently several times not only within Africa but in Europe and East Asia as well. In addition, a region on chromosome 10 centered around the ECD gene shows strong evidence for selection in the ancestor of East and South Asians.

This work was supported by NSF BCS~1638840 (ARR), NSF GRF~1747505 (AAA), and the Center for High Performance Computing at the University of Utah (ARR).

Heritability and preliminary genetic association with social behavior and competence among juvenile rhesus macaques

R. ALAN HARRIS¹, ZSOFIA KOVACS BALINT², MUTHUSWAMY RAVEENDRAN¹, VASILIKI MICHOPoulos^{2,3}, JOCELYNE BACHEVALIER^{2,4}, JESSICA RAPER^{2,5}, MAR SANCHEZ^{2,3}, CHRIS GUNTER^{5,6,7} and JEFFREY ROGERS¹

¹Human Genome Sequencing Ctr, Baylor College of Medicine, ²Yerkes National Primate Res. Ctr., Emory University, ³Dept. of Psychiatry and Behav. Sciences, Emory University School of Medicine, ⁴Dept. of Psychology, Emory University, ⁵Dept. of Pediatrics, Emory University School of Medicine, ⁶Dept. of Human Genetics, Emory University School of Medicine, ⁷Marcus Autism Center, Children's Healthcare of Atlanta

Individual differences in social behavior and social competence is a fundamental aspect of primate biology. Variation in social interactions contribute to differences in survival and reproductive success and thus have significant implications for the evolution of behavioral diversity within and between species. Past studies of primates have investigated the relative contributions of genetic and non-genetic factors to individual behavioral variation, but most used one or another artificial experimental manipulation to elicit the behaviors of interest. Here we report analyses of undisturbed social behavior and interactions among 206 juvenile rhesus macaques in large social groups at Yerkes National Primate Research Center. Individuals were observed (mean 2 hours) and specific behaviors recorded (e.g. groom, play, solitary play, threats, etc.). We reduced data dimensionality using exploratory factor analysis and developed a validated version of the human Social Responsiveness Scale for juvenile rhesus macaques (jmSRS). Quantitative genetic analyses identified multiple social behaviors, four multivariate behavioral factors and two jmSRS scores that exhibit significant genetic heritability. Examples: Factor 2 (play, leave behind, proximity duration) $h^2 = 0.652$ ($p=2 \times 10^{-5}$); Factor 4 (groom solicit, solitary play duration, etc) $h^2 = 0.842$ ($p=4.0 \times 10^{-7}$); Solitary play duration $h^2 = 0.861$ ($p=9.3 \times 10^{-5}$); Sit alone $h^2 = 0.738$ ($p=0.0033$). We also performed preliminary genotype association analyses against a panel of 87 potentially relevant genes. Several loci including *KDM6B* and *ABCA13*, two genes previously associated with autism spectrum disorders in humans, generate preliminary association results. Implications for our understanding of behavioral diversity and evolution in primates will be discussed.

This work was supported by Yerkes NPRC base grant (P51-OD011132), NIH-R24-OD011173 to J.Rogers and Emory Univ. Research Comm. 2019-2020 grant.

Female fertility rates between subspecies of captive rhesus macaques

EMILEE N. HART¹, HANS-MICHAEL KUBISCH¹, KATHRINE P. FALKENSTEIN¹ and RICHARD S. MEINDL²

¹Tulane National Primate Research Center, Tulane University, ²Department of Anthropology, Kent State University

Rhesus macaques (*Macaca mulatta*) have been denoted as "weed species" implying that this species, naturally found in secondary riverine forests, can survive in a multitude of ecological niches with very high fertility rates. Previous research comparing the female fertility rates among macaque species has shown that the *sinica* group was the most prolific. The current study focuses on two of the subspecies of captive *M. mulatta*: Indian-derived and Chinese-derived at the Tulane National Primate Research Center

ABSTRACTS

(TNPRC) in southeastern Louisiana to determine whether the average number of infants produced by a female (GRR) is consistent with previous findings.

The records of 840 Indian-derived and 217 Chinese-derived females spanning a 30-year period were analyzed to establish whether they had given birth while belonging to a specific age group. All of these animals were born at the TNPRC. Results show that the GRR is 7.59 for Indian-derived and 4.48 for Chinese-derived indicating that Indian-derived *M. mulatta* have the highest female fertility not only of any macaque but of any higher primate. The results of this study are consistent with the very high female fertility rates found in the wild *M. mulatta* population in Florida.

Myological estimates of grip strength and dexterity within primates

ADAM HARTSTONE-ROSE¹, MARISSA L. BOETTCHER^{1,2} and EDWIN DICKINSON¹

¹Department of Biological Sciences, North Carolina State University, ²College of Medicine, Medical University of South Carolina

The architecture of primate limb muscles provides insight into ecological adaptation. Over the last several years, we have dissected ~200 primate specimens from dozens of species to determine qualitative differences in the organization of limb muscles and quantitative differences relating to their mass, fascicle length (FL) and physiological cross-sectional area (PCSA). As we have seen in our studies of masticatory muscle architecture, muscle mass and PCSA in the forearm (and leg) of primates tend to scale with positive allometry, while there are discernable ecological correlates of FL (e.g., arboreal primates have significantly greater FL than do terrestrial taxa). We have also studied the ontogeny of these variables in a broad sample of *Microcebus*, observing that FLs attain an earlier plateau than do other architectural variables. Finally, we have explored the myology of highly derived taxa – pottos and aye-ayes. Remarkably, these two taxa are myologically unremarkable; despite their highly specialized digits, the muscles that control them are quantitatively and qualitatively similar to other strepsirrhines. As variability in these muscles has been largely overlooked, we are currently expanding our forearm analyses to examine variation within 1) individuals bilaterally, 2) species, and 3) broader clades, as well as 4) relative to metrics of dexterity. We are also 5) combining myological and osteological data to calculate anatomically-derived grip strengths validated on the few species that

have been directly measured in live animals. We welcome collaborators interested in these or related questions – especially those who wish to combine samples or explore our data.

This work was funded, in part, by the National Science Foundation (IOS-15-57125 and BCS-14-40599).

New 3-D geometric morphometric and dating analyses of the Apidima fossil crania support early dispersal of *Homo sapiens* out of Africa

KATERINA HARVATI^{1,2,3}, CAROLIN RÄDING¹, ABEL M. BOSMAN^{1,2}, FOTIOS A. KARAKOSTIS^{1,3}, RAINER GRÜN⁴, CHRIS STRINGER⁵, PANAGIOTIS KARKANAS⁶, NICHOLAS C. THOMPSON^{1,3}, VASSILIOS KOUTOULIDIS⁷, LIA A. MOULOPOULOS⁷, VASSILIOS GORGOLIS^{10,8,9} and MYRSINI KOULOOUSSA^{3,8}

¹Paleoanthropology, Senckenberg Center for Human Evolution and Palaeoenvironment, Eberhard Karls University of Tuebingen, ²DFG Centre of Advanced Studies 'Words, Bones, Genes, Tools', Eberhard Karls University of Tuebingen, ³Museum of Anthropology, Medical School, National and Kapodistrian University of Athens, ⁴Australian Research Centre for Human Evolution, Griffith University, ⁵Centre for Human Evolution Research, Department of Earth Sciences, The Natural History Museum, ⁶Malcolm H. Wiener Laboratory for Archaeological Science, American School of Classical Studies at Athens, ⁷First Department of Radiology, National and Kapodistrian University of Athens, ⁸Department of Histology and Embryology, Medical School, National and Kapodistrian University of Athens, ⁹Biomedical Research Foundation, Academy of Athens, ¹⁰Faculty of Biology, Medicine and Health, University of Manchester

South East Europe is a major dispersal corridor for both fauna and human populations, and one of the principal European Mediterranean glacial refugia. The region's human fossil record, therefore, has been hypothesized to reflect the complexities of repeated dispersals, late survivals and admixture of human groups. This hypothesis has been difficult to test, as human fossils from S.E. Europe are relatively rare. The fossil human crania from Apidima cave, Mani (Southern Greece), discovered in the late 1970s, are among the most important specimens from the region, yet their affinities and chronology have long remained unclear. In part this was due to taphonomic distortion and breakage, lack of archaeological context and associated faunal remains, and lack of detailed description and comparative analysis. Recently, we obtained CT scans of the two crania and virtually reconstructed them using standard virtual anthropology approaches; we then conducted an exhaustive description and geometric morphometric comparative analysis; and we dated the specimens and associated matrix using the U-series radiometric method. The more complete Apidima 2 dates to >170 ka and conforms to a Neanderthal-like morphological pattern. In contrast, Apidima 1 dates to >210

ka and presents a mixture of modern human and ancestral features. We interpret our results to indicate the presence of an early *Homo sapiens* population, followed by a Neanderthal one, at the Apidima site. Our findings support multiple and geographically far-reaching dispersals of early modern humans out of Africa, and highlight the complex demographic processes that characterized Pleistocene human evolution and dispersals.

Funding by the European Research Council ERC CoG CROSSROADS (724703) and the German Research Foundation (DFG FOR 2237). CS is supported by the Calleva Foundation and Human Origins Research Fund.

A comparison of great ape life histories in captivity

FAYE S. HARWELL and CHERYL D. KNOTT
Anthropology, Boston University

Primates, especially great apes, have slow life histories and long lifespans compared to other mammalian groups. Data pertaining to life history variables can be difficult to collect in the wild considering that species can have longer lifespans than the duration of a field site's existence. Here, we examine life history variables for captive-born great apes housed in the United States. Using studbook data, we investigate stillbirth rates, age at first birth (AFB), interbirth intervals, number of offspring, twinning rates, average lifespan and maximum lifespans. Analyses presented here exclude individuals with estimated birthdates. The oldest maximum lifespan was recorded for gorillas (60.07yrs (female); n= 656) followed by chimpanzees (57.40yrs (female); n= 559), orangutans (54.88yrs (female); n= 660), and bonobos (52.15yrs (female); n= 144). Excluding individuals living ≤10 years of age, average lifespan is similar for all great apes in captivity ($F(3,417)= 0.849$, $p= 0.467$; bonobos: 23.5 ± 9.8 yrs; chimpanzees: 25.2 ± 10.6 yrs; gorillas: 26.2 ± 10.2 yrs; orangutans: 24.2 ± 10.0 yrs). The stillbirth rate is highest in chimpanzees (0.147; n=559) then gorillas (0.144; n=658), bonobos (0.125; n=144), and orangutans (0.010; n=681). Gorillas (11.4 ± 3.7 yrs) have a younger AFB, on average, than chimpanzees (15.9 ± 6.9 yrs), bonobos (14.3 ± 6.9 yrs), or orangutans (14.4 ± 5.1 yrs) ($F(3,377)= 13.97$, $p< 0.0001$). We discuss how our findings are influenced by changes in husbandry practices as well as the captive environment. By examining the life histories of captive populations, we highlight the plasticity these species exhibit in relation to the timing of developmental and reproductive events.

The Past is 3D: using spatial analysis in interpreting an enigmatic mass grave

BRENNAN R. HASSETT¹ and HALUK SAĞLAMTIMUR²

¹Institute of Archaeology, University College London, ²Department of Archaeology, Ege University

ABSTRACTS

Mass graves present a unique challenge in physical anthropology. Their interpretation depends on reconstructing the deposition event(s) that created them— but this can be very challenging where skeletal remains are commingled. Current computational approaches require non-commingled remains and utilise either traditional two-dimensional overlay techniques, or ad-hoc solutions for 3d mapping as simplified shapes. This paper puts forward a new methodology for reconstructing the deposition of the partially commingled remains of ~60 individuals in an approximately 2 by 3.3 meter mass grave from the Early Bronze Age I site of Başur Höyük on the Upper Tigris River. It combines anthropological assessment with novel spatial-analytical approach using broadly available software: 2d Geographic Information Systems (QGIS); 3d GIS (ArcScene); and 3d photogrammetry (PhotoScan Pro).

The results clearly demonstrate the utility of this spatial-analytical approach. We are able to interpret the mass grave as a single deposition event of primary burials over a very limited period of time. We reconstruct the sequence of deposition including events such as moving bodies to make more room, and even the physical act of flinging bodies into the pit by the persons burying them. This offers a potential new methodology for reconstructing mass death events in the past.

This project has received funding from the British Institute at Ankara and the Arts and Humanities Funding Council UK.

Merging biplanar X-ray, 3-D animation, particle simulation, and virtual reality to understand 3-D foot dynamics on deformable substrates

KEVIN G. HATALA^{1,2}, PETER L. FALKINGHAM³, SABREEN MEGHERHI¹, DAVID A. PERRY⁴, SPENCER CHELEDEN⁵, JOHANNES NOVOTNY⁵, DAVID H. LAIDLAW⁵ and STEPHEN M. GATESY⁴

¹Department of Biology, Chatham University,

²CASHP, The George Washington University,

³School of Biological and Environmental Sciences, Liverpool John Moores University, ⁴Department of Ecology and Evolutionary Biology, Brown University,

⁵Department of Computer Science, Brown University

Fossil footprints offer the only direct records of early hominin locomotor behaviors, but present a conundrum to paleoanthropologists. The plethora of experimental data on human and non-human primate foot function are nearly all derived from rigid force-sensing instruments. Little is known about foot function on deformable substrates, and even less about how functional patterns are subsequently recorded in footprints.

We developed a novel variation of X-ray Reconstruction of Moving Morphology to study external foot deformation and motion of seven human subjects walking across four radiolucent

substrates (three deformable muds and rigid carbon fiber), using 70 skin markers applied to their feet and toes. We built and analyzed data-driven 3-D animations of high-resolution surface models of subjects' feet interacting with the substrates. The heel and medial longitudinal arch deform to significantly greater extents on more rigid substrates, and the motion patterns that characterize stance phase consistently vary across substrates. In wetter muds, the morphology of the resulting footprint does not directly match the foot anatomy or kinematic pattern that produced it. To understand why, we simulated subject-specific foot models moving through virtual substrates via the discrete element method. By visualizing particle paths and surface maps, we explored substrate flow as footprints were developed. We found that proximal regions of footprints, specifically areas beneath the arch and heel, are continuously reshaped throughout footprint ontogeny. These results reveal the surprising extent to which foot function varies across deformable substrates, and they expose potential flaws in certain anatomical interpretations derived from fossil hominin footprints.

We are grateful for funding support from the National Science Foundation (SMA-1409612, EAR-1452119, BCS-1825403, BCS-1824821), Chatham University, and the Brown Undergraduate Teaching and Research Awards program.

Enamel hypoplasia and stature in two historic London populations

SARAH M. HAWKS

Graduate Student in Anthropology, California State University, Sacramento

Enamel hypoplasia and stunted stature are non-specific indicators of stress that are often caused by nutritional stress and exposure to disease in adolescence. While many studies have assessed the relationship between stature and hypoplasia in children, few have looked at this relationship in adults. This research examined the relationship between enamel hypoplasia and stature in two historic London populations to determine whether individuals with enamel hypoplasia in their permanent dentition also exhibited shorter than average stature; testing whether the presence of childhood stressors resulting in dental lesions also gave rise to stunted growth or if individuals were able to experience catch-up growth later in adolescence. Data from the medieval East Smithfield Black Death cemetery and the post-medieval St. Bride's lower churchyard cemetery were included in this study. Within each population, average femur lengths between individuals with enamel hypoplasia and those without enamel hypoplasia were compared using t-tests.

Results for the medieval population showed a significantly lower average femur length in individuals with enamel hypoplasia, suggesting that children who developed hypoplasia were unable

to experience catch-up growth later in their development. The post-medieval population did not show a significant difference in height between the two groups. After splitting the post-medieval population into sex-specific subgroups, males did not provide significant results; however, post-medieval females with hypoplasias were significantly shorter than females without hypoplasias from the same population. These results suggest that enamel hypoplasias are a good indicator of frailty in the medieval population, but not in the post-medieval population.

Antimere asymmetry and monozygotic discordance in Carabelli trait: do they reflect common underlying epigenetic factors

SAVANNAH HAY and G. RICHARD SCOTT
Anthropology, University of Nevada, Reno

Twin and family studies indicate nonmetric tooth crown traits have a strong genetic basis. If trait expression is determined entirely by genetic factors, we expect that (1) left and right antimeres should exhibit identical trait expressions and (2) monozygotic twins, who share the same genotype, should exhibit identical phenotypes. We know, however, that in a certain percentage of cases, trait expression is asymmetric between antimeres and discordant between MZ twins. Traditionally, antimere asymmetry and MZ twin discordance were attributed to nonspecific environmental causes. We hypothesize that these two phenomena occur at a similar magnitude and are caused by common underlying epigenetic factors. This analysis is based on direct observations of dental casts and photos from 300 South Australian white twin pairs. For this study, research focused on Carabelli cusp of the upper first molars. The trait was scored on an eight-grade scale from the Turner-Scott Dental Anthropology System (ASUDAS). Carabelli was symmetrical 72.2% of the time in MZ twins and 69.5% of DZ twins with most asymmetry by just one grade (20.6-23.4%). MZ twins were concordant 54.6% of the time with discordance by one grade 29.8% of the time. Presence-absence asymmetry was 5.4% for MZ twins and 9.5% in DZ twins. Presence-absence discordance was 21.3% in MZ twins. Although epigenetic factors may play a role in antimere asymmetry and MZ discordance, the frequency differences are of a magnitude to suggest they operate differently within single individuals and between MZ twins. More crown traits should be analyzed to test this proposition.

Women's responses to climate change in rural Namibia: Subsistence, social ties, and reproductive health

ASHLEY HAZEL

Earth System Science, Stanford University

ABSTRACTS

Sub-Saharan pastoralist subsistence is well adapted to aridity, including occasional drought. However, most climate models project rising temperatures and lower annual rainfall for the region over the coming decades. As droughts increase in frequency and duration, traditional dry-season strategies, including dispersal for better grazing, will increasingly fail. Over the past several years, Namibia has been experiencing the worst drought in living memory and the pastoralist community in the Kaokoveld region are facing an existential crisis: cattle herds are rapidly dying without grass and maize, a staple food, cannot grow. Looking at demographic, livestock, and mobility data I collected from Kaokoveld in 2009 (pre-drought) and 2015–2016 (mid-drought), I identified changes in subsistence, mobility, and social connectivity, particularly with regard to women's resource access in light of climate adaptation. I found that, although livestock mainly pass matrilineally among men, women who owned animals exhibited greater relative resource security. Additionally, goats, which carry less socio-economic value than cows, comprised most of women's livestock ownership; they are also more resilient to drought and thus become a critical resource. I also found evidence that the inequality in livestock ownership between men and women decreased during drought. Finally, women's livestock ownership is neither predicted by marriage status nor sexual-partner number, indicating that, while marriage significantly increases women's overall resource base, it does not shape ability to maintain herds, and, while sexual-partner concurrency may improve social support, it does not influence critical resources directly, suggesting that STD exposure is not an implicit tradeoff for resource security.

This work was funded by a Post-PhD Research Grant from the Wenner-Gren Foundation and an Environmental Ventures Project from the Stanford University's Woods Institute for the Environment.

Sex differences in the brains of capuchin monkeys (*Sapajus [Cebus] apella*), and implications for human brains

ERIN E. HECHT¹, OLIVIA T. REILLY^{2,3}, MARCELA BENITEZ^{2,3,4} and SARAH BROSNAN^{2,3,4,5}

¹Human Evolutionary Biology, Harvard University, ²Psychology, Georgia State University, ³Language Research Center, Georgia State University, ⁴Center for Behavioral Neuroscience, Georgia State University, ⁵Neuroscience Institute, Georgia State University

Human reports on sex differences in brain organization are variable and sometimes conflicting, likely due to the high degree of individual variation and flexibility that occurs in our species. In line with this possibility, much of the reported sexual dimorphism in the human brain occurs in higher-order cortical association regions, which develop late in life and show substantial experience-dependent

plasticity. In contrast, sex differences in rodent brains are consistent and pronounced, and are focused mainly in limbic regions involved in the control of instinctual behavior. What accounts for this disparity, and to what degree is the human pattern of sex-linked neural variation unique? Comparisons with our living primate relatives can help address this question. In the current study, we compared MRI neuroimaging scans from 5 male and 15 female tufted capuchin monkeys (*Sapajus [Cebus] apella*). Voxel-based morphometry identified a number of regions that showed significant sex differences in gray matter volume, including hypothalamus (enlarged in males) and cerebellum, occipital cortex, and occipitotemporal cortex (enlarged in females). Tractography on DTI images revealed that the white matter connectivity of the female-enlarged gray matter regions included a broad network of higher-order association regions. Implications for our understanding of human sex differences are discussed.

* Hecht and Reilly: Co-first authors with equal contribution to this work

Osteobiography of the decapitated Meyer Site (Spencer County, Indiana) Feature 42 Subadult

JENNIFER HEILMANN, GRACE HOLMES, ALEXIS D. MARTINEZ, MACKENZIE VERMILLION, VICTORIA LEAMAN and CHRISTOPHER SCHMIDT

Anthropology, University of Indianapolis

Feature 42 is a decapitated subadult from the ~5,250 y.b.p. (late Middle Archaic period) Meyer Site in Indiana. The site contained 30 burials and included adult males, females and subadults. Feature 42 was a 12-15 year-old probable male; he was likely killed via a blow to the occiput. His head, still articulated with C1 and C2, was found in his right hand. Cut marks were present on C3-5. Cut marks also were present on the right mandibular corpus, including two large cuts on the mylohyoid line. He is the only person in the cemetery with evidence of violence and the only subadult decapitation victim known from this time period in Indiana.

Some Middle/Late Archaic period violence victims had vulnerabilities (such as illness or injury) prior to being killed. Here we sought osteological life history evidence for any circumstance that may have impaired this individual. His sex estimation was based on masculine characters of the cranium and mandible. His age was estimated via his dentition; M3 is unerupted, M2 and P4 are fully erupted but have open apices. His limb lengths were consistent with the lower end of his dental age range; all of his osteometrics were smaller than the adults and comparable to other children at the site. His anterior teeth had a single, roughly

concurrent hypoplastic line. In sum, Feature 42 was not adult-sized. He had no evidence of chronic illness or antemortem injury and is distinguished primarily by his perimortem injuries.

Integrative studies of altitude adaptation: Cross-population genomic and physiological analyses from Tibet and Peru

ERICA C. HEINRICH^{1,2}, JEREMY E. ORR¹, DILLION GILBERTSON¹, CECILIA ANZA-RAMIREZ³, PAMELA N. DEYOUNG¹, JAMES YU¹, ESTEBAN A. MOYA¹, MATEA A. DJOKIC¹, NOEMI CORANTE³, GUSTAVO VIZCARDO-GALINDO³, JOSE L. MACARLUPU³, EDUARDO GAIÓ⁴, FRANK L. POWELL¹, ATUL MALHOTRA¹, FRANCISCO C. VILLAFUERTE³ and TATUM S. SIMONSON¹

¹Department of Medicine, Division of Pulmonary, Critical Care, and Sleep Medicine, University of California San Diego, ²Division of Biomedical Sciences, School of Medicine, University of California Riverside, ³Laboratorio de Fisiología Comparada, Facultad de Ciencias y Filosofía, Universidad Peruana Cayetano Heredia, ⁴Faculty of Medicine, University of Brasília

The integration of genomic and physiological data in high-altitude adaptation studies has become increasingly feasible within the past decade. Our recent genomic analyses, which applied the same test of selection (Composite of Multiple Signals) separately for Tibetan and Andean whole-genome sequence data, identified overlapping selection candidate genes (e.g., in the hypoxia inducible factor pathway: *EGLN1*, *EPAS1*). The genetic variants within these regions appear distinct and likely contribute to variation in traits exhibited between and within populations, as previously shown for hemoglobin concentration ([Hb]), which is linked to adaptive genetic factors in Tibetans exhibiting relatively lower [Hb] but not yet in Andeans. Ventilatory control also varies markedly among highlanders and may be linked to sleep-disordered breathing that further exacerbates hypoxemia at altitude. We measured hematocrit (Hct) and daytime pulse oxygen saturation (SpO₂) in 71 males (M) and 61 females (F), ventilatory chemoreflexes in a subset (M:63; F:46), and sleep parameters in a further subset (M:22; F:23) of Andeans resident at 4300 m. We tested the hypothesis that decreased ventilation and desaturation events during sleep are associated with increased hematocrit (Hct) and Chronic Mountain Sickness (CMS) severity. Our findings suggest differences in ventilatory control, primarily hypoventilation and sensitivity to hypercapnic hypoxia, influence daytime and sleep SpO₂ and are associated with Hct in Andeans. Our ongoing studies aim to compare longitudinal profiles of ventilatory and sleep outcomes, [Hb], and other oxygen transport components across

ABSTRACTS

Tibetan and Andean populations to determine how individual variation contributes to adaptive, or progressively maladaptive, outcomes at high altitude.

Funding for this work was provided by a Wellcome Trust grant 107544/Z/15/Z to FCV, NIH R01HL081823 to FLP, and 1R01HL145470 to TSS.

Relative Faunal Abundance at the KNM-ER 5431 Site in Area 203 of the Koobi Fora Formation

BRI HEISLER¹, MARYSE BIERNAT² and AMANDA MCGROSKY²

¹Department of Anthropology, University of Nevada Las Vegas, ²Institute of Human Origins and School of Human Evolution and Social Change, Arizona State University

The evolution of the earliest Homo species is not well-understood as a result of a relatively poor sedimentary and fossil record between 2.5 and 3.0 million years ago (Ma) in East Africa. KNM-ER 5431 is a set of associated but isolated teeth found in Tulu Bor Member sediments (2.7 - 3.0 Ma) within paleontological Area 203 of the Koobi Fora Formation (KFF). These teeth have been identified as potentially conspecific with LD 350-1, the earliest Homo specimen identified to date. To understand the selective pressures influencing the appearance of Homo and the persistence of Australopithecus at this time, contextual research that characterizes regional paleoecology is crucial. Here we provide a better understanding of the paleoenvironment of Area 203 and the Tulu Bor Member of the KFF more generally. We compare modern mammalian communities with fossil communities and characterize the geology of the region. Results of the initial analysis of recently collected fauna suggest three major conclusions. 1) During the Lokochot and continuing through the Tulu Bor to the Burgi Members, climate becomes more arid. 2) The region around Area 203 during Tulu Bor Member times had relatively greater water availability (more streams, standing water) despite lower rainfall than contemporary sites. 3) Area 203 may have been climatically dissimilar from contemporaneous fossil sites in East Africa, in particular those from the Lee Adayta region in Ethiopia. These results encourage more detailed taxonomic characterization of KNM-ER 5431 and refinement of the geological context of the site.

This research was supported by the National Science Foundation (OISE-1358178), NSF Archaeology Technological origins archaeology grant (1624398), and supplemental REU (1930719).

A mixed-methods approach to identify factors influencing non-human primate genomic sequence data generation

MARGARITA HERNANDEZ¹ and GEORGE PERRY^{1,2}

¹Department of Anthropology, Penn State University, ²Department of Biology, Penn State University

Massively-parallel genomic sequencing methods have facilitated powerful investigations into the phylogenetic relationships, population dynamics, and evolutionary biology of diverse species. Yet for non-human primates (NHP), the availability of genomic data appears to be unevenly distributed among taxa, perhaps limiting subsequent developments of knowledge on these topics across the order. Our goal was to test whether variables including publication history, geographic range, and IUCN Red List status were significantly correlated with publicly-available genomic sequence data in the NCBI Sequence Read Archive. We also conducted a qualitative analysis, where we interviewed 33 authors of genomic data-producing publications to learn their motivations when selecting species for study. Of the 180 terabases (Tb) of publicly-available genomic sequence data for 519 NHP species, 135 Tb (~75%) are from only five species: rhesus macaques, olive baboons, green monkeys, chimpanzees, and crab-eating macaques. We also found that total number of publications focusing on each species ($R^2=0.37; P=6.15 \times 10^{-12}$) and representation in the medical literature ($R^2=0.27; P=9.27 \times 10^{-9}$) were the strongest predictors of the amount of genomic sequence data available. Evaluating the most common themes to emerge across interviews (grounded theory analysis), authors frequently mentioned that their choices of species were motivated by sample accessibility, extent of prior published work, and perceived relevance (especially health-related) to humans. Our mixed-methods approach identifies and contextualizes driving factors regarding the decisions made when devising research studies. Through this, we hope to bring about an awareness of these processes for consideration when aligning research goals with species data generation where it is needed most.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship Program under Grant No. DGE1255832 to M.H.

Variation in nasal and paranasal structures in adults from Cambodia, France, and Russia

YANN HEUZÉ¹, LAURA MARÉCHAL¹, TAISIA SYUTKINA², ANNA RASSKAZOVA², NATALIA BEREZINA³ and ANDREJ EVTEEV³

¹PACEA UMR5199, CNRS, MCC, University of Bordeaux, Pessac, France, ²Institute of Ethnology and Anthropology, Russian Academy of Science, Moscow, Russia, ³Anuchin Research Institute and

Museum of Anthropology, Lomonosov Moscow State University, Moscow, Russia

Computational fluid dynamics has been recently used to simulate nasal airflows in Neanderthals and discuss specific adaptations to cold environments in this group. To do so, nasal soft tissues covering the nasal cavity (NC) might be reconstructed and data from anatomically modern humans are used. However, the intra- and inter-population variation of the negative volume defined by the nasal soft tissues, the nasal airways (NA), remains poorly studied, and so does its covariation with NC and paranasal sinuses. Here, we propose to quantify the variation of these anatomical units through the study of *in vivo* CT images from adults living in Cambodia (N = 40), France (N=40), and Russia (N = 40). Individuals from France have significantly smaller NA and NC volumes, while no significant differences were found between the three groups for the volumes of the paranasal sinuses. NC height is significantly larger in individuals from France. NC length is significantly shorter in individuals from Cambodia. Individuals from Russia have significantly larger anterior NC width and individuals from Cambodia have significantly larger posterior NC width. Regarding interpopulation differences, males have larger volumes of the nasal and paranasal structures and larger NC dimensions. The intensity level of the sex differences is the highest in the Cambodian sample and the lowest in the French sample. Finally, though the correlation between NC and NA volumes is significant ($p = 0.0001$), its intensity remains relatively low ($R^2 = 0.2218$). This study highlights the necessity to better quantify intra- and inter-population NA variations.

This study was partially supported by (1) the CNRS and RFBR (project number 18-56-15001), and (2) the French National Agency for Research (ANR) with the program ANR-10-LABX-52

Gut microbiota and fecal stable isotopic values for bonobos (*Pan paniscus*) of the Lomako Forest, Democratic Republic of Congo

ALEXANA J. HICKMOTT¹, JAMES E. LOUDON², DIANA M. CHRISTIE^{1,5}, COLIN M. BRAND¹, MONICA L. WAKEFIELD³, MICHEL T. WALLER^{1,4}, FRANCES J. WHITE¹ and NELSON TING^{1,5}

¹Department of Anthropology, University of Oregon, ²Department of Anthropology, East Carolina University, ³Department of Sociology Anthropology & Philosophy, Northern Kentucky University, ⁴Department of Anthropology, Central Oregon Community College, ⁵Institute of Ecology and Evolution, University of Oregon

Primate gut microbiome communities are of increasing interest due to their important role in nutrition, development, health, and disease. While many factors shape the relationship between the gut microbiomes and primate dietary strategies, these interplays are complex and poorly

ABSTRACTS

understood. Stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope values can be used to supplement observational data to quantify diets, given that these values reflect dietary behavior. Here we describe the gut microbiomes, $\delta^{13}\text{C}$, and $\delta^{15}\text{N}$ data for 18 bonobo (*Pan paniscus*) fecal samples, from separate individuals, collected in June 2014 at Iyema, Lomako Forest, Democratic Republic of Congo. To characterize the gut microbiome, DNA was extracted and 16S rRNA libraries prepared, and sequenced on a partial Illumina NextSeq run. For the isotopic data, samples were desiccated in the field, ground, weighed, and combusted in an elemental analyzer to measure the carbon and nitrogen abundances. To examine the relationship between stable isotope values on bonobo gut microbiome we ran PERMANOVAs with social group, sex, relative age, food item, $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values as predictors. The results of the PERMANOVAs found that $\delta^{13}\text{C}$ were significant [PERMANOVA $F_{1,17} = 0.17261$, $P = 0.023$] in explaining beta diversity in gut microbiota but only when sex was a predictor in the model. These results suggest that there may be sex-specific differences in gut microbiota, perhaps due to dietary differences in feeding behavior. Incorporating stable isotope data with gut microbiomes can provide a more robust understanding of how diet and dietary shifts impact the gut microbiomes of primates.

Age-related and culturally specific causes of depression underdiagnosis among older adults: Results from the Study on global AGEing and adult health

JOAN HICKS, ALICIA M. DELOUIZE and J. JOSH SNODGRASS

Anthropology, University of Oregon

Cultural competency should be prioritized when dealing with any issue surrounding mental health. Older adult populations are growing rapidly in lower and middle-income countries (LMICs) and depression is a neglected form of disability that is especially pronounced in older adults. The current study analyzes data among older adults collected in Wave 1 of the World Health Organization's Study on global AGEing and adult health (SAGE) in order to examine the underlying factors related to underdiagnosis of depression in Ghana, Mexico, India, China, South Africa, and Russia. These countries were compared to observe the societal and individual influences that lead to patterns of depression diagnosis. We test two hypotheses: 1) lower rates of underdiagnosis of depression being associated with easily accessed and utilized healthcare facilities; and 2) the underdiagnosis of depression being associated with higher levels of stigma. Functional quality of life was a consistent predictor of the underdiagnosis of depression in all countries tested ($B's = 0.02$ to 0.04 , $p's < 0.001$). Other predictors of underdiagnosis varied greatly

by country but include age ($p's < 0.05$ in China and Russia), gender ($p's < 0.05$ in China and India), income ($p's < 0.05$ in China and India), memory status ($p's < 0.05$ in China and India), healthcare quality ($p's < 0.05$ in India and Ghana), social cohesion ($p's < 0.05$ in Mexico, India, and Ghana), and stigma ($p's < 0.05$ in India and Ghana). Both age-related stressors and cultural differences should be considered when addressing the underdiagnosis and, therefore, treatment of depression.

NIH NIA Interagency Agreement YA1323-08-CN-0020; NIH R01-AG034479; WHO; Ministry of Health in Mexico; Shanghai CDC in China; NDH in South Africa; University of Ghana Medical School; USAID; UO Bray Fellowship.

An examination of the frequency and etiology of cribra orbitalia and porotic hyperostosis using computed tomography (CT) scans of a contemporary sample from New Mexico

ETHAN C. HILL¹, LEXI O'DONNELL^{1,2,3}, AMY S. ANDERSON⁴ and HEATHER J.H. EDGAR^{1,5}

¹Anthropology, University of New Mexico,

²Sociology & Anthropology, University of Mississippi, ³Laboratory of Human Osteology, Maxwell Museum of Anthropology, ⁴Anthropology, University of California, Santa Barbara, ⁵Office of the Medical Investigator, University of New Mexico

In the bioarchaeological literature, most individuals reported to have active cribra orbitalia (CO) and porotic hyperostosis (PH) are between six months and five years old at death. CO and PH lesions are associated with nutritional deficiencies or other insults that occurred during growth and development, thus they are often reported as linked indicators of systemic stress. Based on skeletal observations and radiography, these lesions have also been linked to anemia, especially when they co-occur. However, there are few studies that have examined the potential underlying causes of CO and PH lesions in contemporary people. The purpose of this study is to examine the etiology of CO and PH lesions using high-resolution CT scans and associated data for individuals who died in New Mexico from 2011–2019. Our sample consists of 204 individuals ≤ 15 years of age with recorded manner and cause of death, information about their illnesses during life, as well as their sex, age, height, weight, and ethnicity. We find that CO has a higher frequency (26.7%) than PH on the parietals (11.4%), PH on the frontal (21.1%), or PH on the occipital (5.1%). These results are in keeping with studies of these lesions in archaeological skeletal assemblages. Additionally, our results show a significant correlation ($X^2=10.6$, $p=0.00$) between the presence of CO and lung infections connected to individuals' cause of death. CO may be a reliable indicator of pulmonary disease, but may not be a reliable indicator of anemia, at least in contemporary populations.

Variation in the arrangement of the foot interosseous muscles in great apes

EISHI HIRASAKI¹ and MOTOHARU OISHI²

¹Primate Research Institute, Kyoto University,

²School of Veterinary Medicine, Azabu University

The dorsal interossei of the human foot are arranged to abduct the digits around the second digit, whereas those of non-hominoid anthropoid primates are mostly arranged around the third digit. This might be associated with the medial shift of "the functional foot axis" in humans, which makes the interossei "the most interesting muscles of the foot" (Manter, 1945). However, these muscles have been scarcely studied, and their results on apes are not necessarily in accord. In this study, we examined the arrangement of the dorsal interosseous muscles of the foot in ten chimpanzees, a bonobo, six gorillas, and eight orangutans. Results showed that in two chimpanzees, a bonobo, and a gorilla, the dorsal interossei were arranged around the second digit, whereas in the remaining specimens (except for one orangutan) the third digit had two insertions of the dorsal interossei. Interestingly, one orangutan specimen had its foot axis on the fourth digit. The variation found in the African ape specimens suggests that they are in a transitional condition from the monkey-type to the human type in terms of the arrangement of the interosseous muscle. Considering that the osteological studies support the idea that the foot axis is on the second digit in great apes (Wunderlich, 1999), it seems that osteological change in the foot axis phylogenetically preceded the change in the arrangement of the interosseous muscles.

Japan Society for the Promotion of Science 15H04428, 19K22454

They came, they saw, they masticated: Mandible morphology, mastication and diet in Roman Britain

CARA S. HIRST

Anthropology Department, University College London, Institute of Archaeology, University College London

Mandible morphology has been demonstrated in numerous studies to be influenced by masticatory behaviour and diet. Large scale dietary changes such as the Agricultural and Industrial Revolution are associated with a softer diet and significant reductions in mandibular robusticity. There has however been little research investigating morphological changes associated with smaller dietary changes. During the Romano-British period new flora and fauna were introduced, along with food processing technology and other dietary changes. The aim of this study was to determine how mandible morphology from Romano-British sites differed from the preceding period, as well as within and between Romano-British assemblages and what this may indicate about dietary

ABSTRACTS

changes during Roman occupation. The sample included 178 mandibles (84 Bronze/Iron Age and 94 Roman). The Roman sample were from 18 sites in Britain. Mandibles were digitised using a NextEngine 3D scanner, 46 landmarks were placed on these digitisations and data were analysed using principal component and canonical variate analysis. Results indicated that compared to the Bronze and Iron Age mandibles from Romano Britain were more robust, however when considering sex estimation, it was determined that only among those estimated as male was mandible morphology significantly more robust compared to the preceding period. While no significant difference was reported between Romano British sites which included a range of rural, urban and military sites. These reported morphological changes in Roman-British assemblages are consistent with males consuming a more masticatory demanding diet that has not previously been indicated in archaeological or anthropological research.

N/A

Variation in health-protective sexual behavior may be influenced by individual differences in self-perceived health, immunity, and disgust: A cross-cultural examination

JESSICA K. HLAY¹, GRAHAM ALBERT¹, CARLOTA BATRES², STEVAN A. AMOCKY³ and CAROLYN R. HODGES-SIMEON¹

¹Anthropology, Boston University, ²Psychology, Franklin & Marshall College, ³Psychology, Nipissing University

Previous researchers have hypothesized that the behavioral immune system functions to limit exposure to potentially infectious contexts and persons. Several studies have shown that higher disgust is associated with lower sociosexuality; however, no studies have yet shown whether self-reported and/or biological measures of health regulate this association. We predict that individuals in poorer health (i.e. low self-reported health, low mucosal immunity) will show greater health-protective behavior (i.e. greater disgust levels and lower sociosexual attitude, desire and behavior). We explore these relationships in three populations: a US university sample (N=119), a global online sample (N=520), and a Salvadorean sample (N=100). All participants answered questions related to health, disgust, and sociosexuality; however, US men also contributed saliva, from which secretory IgA (sIgA; a measure of mucosal immunity) was assayed. In the US, both sIgA and self-reported general health predicted pathogen disgust, while pathogen and sexual disgust predicted domains of sociosexuality. In the global online sample, general health predicted sexual disgust, and both general health and sexual disgust predicted two domains of sociosexuality. In El Salvador, general health

did not predict disgust; however, sexual disgust predicted all domains of sociosexuality—providing the first evidence of this association outside of a Western context. Across samples, our results provide support for the hypothesis that individual differences in health and disgust are related to sociosexuality. Overall, these findings add to the literature on the behavioral immune system; that is, variation in health-protective behavior may be influenced by individual differences in self-perceived health, immunity, and disgust.

None.

Is dental morphology in *Paranthropus* the result of drift or selection?

NOMAWETHU HLAZO^{1,2,4}, LAUREN DR. SCHROEDER^{2,3} and REBECCA R DR. ACKERMANN^{1,2}

¹Archaeology, University of Cape Town, ²Human Evolution Research Institute, University of Cape Town, ³Department of Anthropology, University of Toronto Mississauga, ⁴Evolutionary Genomics Section, Globe Institute, University of Copenhagen

Cranial and dental robusticity in the genus *Paranthropus* has traditionally been characterized as resulting from a shared dietary adaptation resulting in a robust “hyper megadont” morphology. However, recent morphological studies of the cranium and mandible suggest that species-specific adaptations do occur and, moreover, that the highly variable *Paranthropus* morphology is not only the result of adaptation, but that non-adaptive processes play much more of a role than previously appreciated. Furthermore, many of the morphological differences identified across species are not the direct result of selection acting to differentiate those differences *per se*, but rather are correlated responses to selection acting on other variables. In light of this, here we expand on our earlier work by examining inter and intra-specific variation in the teeth of *Paranthropus* and other australopithecines using Elliptical Fourier Analysis. We also apply a hypothesis testing framework developed from evolutionary quantitative genetics to test whether this variation is a result of selection versus genetic drift. This study includes samples of *Paranthropus* (n=25) *Australopithecus africanus* (n=12), *Australopithecus sediba* (n=2) and *Australopithecus Promethus* (n=1). Extant taxa i.e., *Homo sapiens*, *Pan troglodytes* and *Gorilla gorilla* (n=300) act as models of within species variation for *Paranthropus* variance/covariance (V/CV). Results indicate that *Paranthropus* teeth are highly variable; shape differences do not always correspond to accepted taxonomic categories. As

seen for the maxilla selection plays a major role in shaping variation in the teeth of *Paranthropus*. The Drimolen molar appears to be adaptively different, distinct in both size and shape.

Funded by the National Research Foundation, the Centre of Excellence in Palaeosciences (CoE-Pal), Human Evolution Research Institute, Villum Fonden and the Australian Research Council Future Fellowship hosted by La Trobe University, Australia.

A holistic approach to student engagement in field settings

SARAH K. HLUBIK¹, MARYSE BEIRNAT², KATHRYN L. RANHORN², EMMANUEL K. NDIEMA³, PURITY KIURA³ and DAVID R. BRAUN¹

¹Anthropology, George Washington University, ²Anthropology, Arizona State University, ³Earth Sciences, National Museums of Kenya

The Koobi Fora Research and Training Program (KF RTP) has brought undergraduate and graduate student researchers to remote northern Kenya to learn field methods for nearly 35 years. Over this time the host institution and programmatic focus have varied. Presently, the field school is an immersive research-intensive program that focuses on field research and design, while still providing a solid foundation in human paleontology, archaeology, and anthropology. Instructional design has shifted from lectures to activities, and students complete a research project in collaboration with an instructional mentor. Mentor staff range in experience from advanced undergraduate through graduate students, postdoctoral researchers, and early career and senior researchers. Students and research staff come from institutions throughout North and South America, Europe, and Africa. This creates an inclusive environment and distinct tiered-mentoring structure which encourages the participation of both students and researchers from underrepresented communities who may have been discouraged from more traditional STEM coursework. Over the past five years, KF RTP has trained over 60 women from the US, Canada, and African nations, and over 30 men and women from the African continent. Over half of these students are currently enrolled in graduate programs. Continued collaboration with students has resulted in more than 40 conference presentations and multiple journal publications with student co-authorship. KF RTP has supported data collection for 18 senior undergraduate, Masters, and PhD dissertation theses. We have worked with students, interns, and instructional staff to develop a range of practices and policies to create a safe environment for learning and research.

KF RTP is funded in part by the NSF Archaeology program #1624398 and supplemental REU #1930719.

ABSTRACTS

Middle Archaic Human Bone Trophies: Embodiment of Giving

SHANNON CHAPPELL HODGE

Sociology and Anthropology, Middle Tennessee State University

Human trophy-taking is well-established bioarchaeologically, represented by perimortem cut-marks reflecting soft-tissue removal, or removal of skeletal elements by dismemberment at joint surfaces or score-snap breaks. Proposed reasons for such behaviors include defaming or shaming the trophy victim, self-aggrandizement, revenge, or face-saving by the trophy taker, intimidating enemies, or violently disabling or destroying the soul of the trophy victim. This research discusses previously unreported limb trophies from a Middle Archaic (7500-5000 BP) cave cemetery in Tennessee. This cave bears the archaeological signature of a special-purpose locus in the regional settlement pattern, is positioned on the landscape in an auspicious relationship to the western horizon and the Milky Way (Path of Souls), and features a domestic dog burial on the western margin of the site, perhaps a spirit guide or guardian of the dead. In this context, it is unsatisfying to apply traditional models for trophy-taking, which reflect violent encounters with meaning or significance only to the trophy-taker. It is compelling instead to focus on the purpose of the trophy-giver. In smaller scale societies such as those of the Middle Archaic in the American midcontinent, interpersonal violence is argued to have been typically individualized and homicidal. While anonymized violence may fit trophy-taking in later eras, I argue that trophy-taking in smaller-scale communities may not fit a violence model at all. Perhaps instead the trophy represents a gift of the deceased, as postmortem embodiment of a beloved community member or trusted elder, and a materialized representation of the transition to revered ancestor.

Testosterone, cortisol, and secretory IgA in cis- and transgender men: Evidence for the dual hormone hypothesis

CAROLYN R. HODGES-SIMEON¹, GRAHAM GRAIL², GRAHAM ALBERT¹, NICHOLAS LANDRY³, TRIANA L. ORTIZ³, JUSTIN M. CARRE³, TIMOTHY S. MCHALE^{1,4} and STEVEN A. ARNOCKY³

¹Anthropology, Boston University, ²Forensic Sciences, George Washington University, ³Psychology, Nipissing University, ⁴Anthropology and Museum Studies, Central Washington University

Previous research on the association between testosterone (T) and immunity has produced conflicting results. Here, we address two potential reasons for these inconsistencies. First, results may depend on the measure of immunity employed. Here, we examine secretory IgA (sIgA), a measure of mucosal immunity functionally related to respiratory infection risk. Second, the

effect of T on immunity may depend on levels of cortisol; previous research indicates that cortisol may interfere, suppress, or antagonize T's action on target tissues in the body, including immunity. For this research, we target two populations of men: (1) cisgender (i.e., born and identifying as male), (2) transgender (i.e., born female but identifying as male) undergoing T therapy for gender realignment. One hundred and forty-eight young men (transgender $n = 29$) provided saliva samples at three time points: (1) upon waking, (2) before sleep on the same day, and (3) upon waking the following day. Samples were assayed in duplicate for sIgA, T and cortisol. For cisgender males, path models revealed that sIgA was significantly related to T within samples, and that changes in sIgA and T across samples were positively related. Further, positive relationships were found between sIgA and the interaction between T and cortisol across the two populations. Overall, stronger associations between T and sIgA were found for those low in cortisol. We interpret findings in light of the dual-hormone hypothesis.

Taphonomy or targeting? Re-examining trauma patterns in skeletons from medieval European battlefields

RUSSELL T. HOGG

Rehabilitation Sciences, Florida Gulf Coast University

It is largely unknown the degree to which our interpretations of trauma patterns present in human skeletal remains from medieval European battlefield excavations are skewed by taphonomic processes. For example, multiple battlefield sites display unusually low axial trauma frequencies, and studies have suggested this may result from taphonomy, armor, or target preferences (irrespective of bodily protection). The effect of taphonomy here remains an open question due to a lack of comprehensive analysis of battlefield samples overall, and a lack of evidence as to targeting patterns of medieval combatants, though we hypothesize that taphonomy is having a major effect on preserved trauma patterns. Therefore, this study has two objectives: 1) provide the first broad analysis of trauma across major medieval battlefield skeletal samples, and 2) compare these data to evidence on trauma from medieval combat treatises. We compiled reported trauma frequencies from the literature on four major battlefield skeletal samples, and compared them to frequencies of injuries depicted in contemporary manuscripts. Battlefield sites are largely consistent in injury patterns, with the exception of Visby, which exhibits an anomalously high frequency of lower limb injuries. In both skeletal and manuscript datasets, there is a prevalence of injuries to the head, followed by the upper limb. However, the manuscripts display far more targeting of the torso than we encounter in the archaeological record; due to the lack of

difference between armored and unarmored sequences depicted in the manuscripts, we conclude that absence of axial wounds osteologically is likely a taphonomic artifact.

Gut Function, Immune Function Tradeoffs, and Infant Growth among High Altitude Andeans

MORGAN K. HOKE¹ and KIMBERLY M. MCCABE²

¹Anthropology, University of Pennsylvania,

²Anthropology, Northwestern University

Life history theory suggests that a tradeoff exists between immune function and growth in setting with high disease burdens. Several studies have shown that energetic costs of mounting immune responses and/or chronic HPA activation may draw energy away from growth using markers such as CRP, EBV, and IgG. What has been less well studied is the role of gut function and enteric inflammation in growth disturbance. The study sample is made up of 62 infants between the ages of 2 months and 24 months at the time of enrollment from the highland community of Nuñoa, Peru. Anthropometric measures were conducted at two time points approximately six months apart. Anthropometric measures were accompanied by a household survey and the collection of dried blood spots (DBS), which were tested for C reactive protein (CRP) and endotoxin core antibodies (endoCAb) a marker of intestinal permeability and enteric inflammation. Multiple regressions were used to test for relationships between change in height, weight, and triceps skinfold for age z-scores and CRP and EndoCAb. Analyses were stratified by infectious status at the time of DBS collection. We found no relationships between CRP or EndoCAb and HAZ, WAZ or TSAZ within rounds. Among children without active infection, both EndoCAb ($\beta = -1.40$, $p = 0.007$) and CRP ($\beta = -0.31$, $p = 0.003$) were negatively associated with change in HAZ between rounds. We found no significant associations between CRP and EndoCAb and WAZ. CRP, but not EndoCAb, was negatively associated with the change in TSAZ between rounds in children without active infection ($\beta = -0.35$, $p = 0.05$).

This research was supported by The Fulbright Hays and the Wenner Gren Foundation.

Marching on their Stomachs: Reconstructing Dietary Life Histories of Napoleonic Soldiers through Stable Isotope Analysis

SAMMANATHA HOLDER¹, LAURIE J. REITSEMA¹, TOSHA L. DUPRAS², RIMANTAS JANKAUSKAS³ and KATEY MARI⁴

¹Department of Anthropology, University of Georgia, ²Department of Anthropology, University of Central Florida, ³Department of Anatomy, Histology, and Anthropology, Vilnius University,

ABSTRACTS

⁴Department of Anthropology, University of Pennsylvania

Dietary life histories can provide valuable insight into the impact of military service during warfare on soldier biology. Dietary life histories are reconstructed through stable isotope analysis of multiple skeletal tissues that capture different periods of time in an individual's life. Military and long-term diets were reconstructed through stable carbon and nitrogen isotope analysis of Napoleonic soldier rib and femoral bone collagen (n=43) from the mass gravesite of šiaurės miestelis in Vilnius, Lithuania. Mean femoral and rib $\delta^{13}\text{C}$ ratios are $-17.15\text{‰} \pm 1.69\text{‰}$ and $-19.17\text{‰} \pm 0.91\text{‰}$, and mean femoral and rib $\delta^{15}\text{N}$ ratios are $10.46\text{‰} \pm 1.39\text{‰}$ and $10.95\text{‰} \pm 1.15\text{‰}$. There were statistically significant differences in mean $\delta^{13}\text{C}$ ratios ($t=6.88$, $df=64.74$, $p<2.80\text{e-}09$), but not $\delta^{15}\text{N}$ ratios ($t=-1.80$, $df=81.33$, $p=0.08$). There were also statistically significant differences in variance in $\delta^{13}\text{C}$ ratios ($F=5.03$, $df=84$, $p=0.03$), but not $\delta^{15}\text{N}$ ratios ($F=1.13$, $df=84$, $p=0.29$). These results indicate that soldier diets canalized around C_3 plants later in life with animal protein consumption remaining similar over the life course. Canalization around C_3 plant foods is likely due to the provisioning of rations, whereas differences in animal protein consumption maintained during military service are likely an artifact of access. Historic evidence indicates officers and imperial guardsmen received higher quality rations and high socioeconomic status soldiers had the ability to supplement rations by purchasing animal products. Canalization of plant protein resources and maintenance of differences in animal protein consumption highlight the tension between military control over soldier bodies through provisioning and soldier agency through supplementation.

This research was supported by the University of Georgia's Innovative and Interdisciplinary Research Grant for Doctoral Students, Dean's Award, and Melissa Hague Field Study Award, and Sigma Xi's Grants-in-Aid-of-Research.

A morphometric analysis of Pliopithecoid maxillary molar cusp peripheralization

ANDREW C. HOLMES, JACQUELINE GARNETT and DAVID R. BEGUN

Anthropology, University of Toronto

Pliopithecoidae are a widespread clade of primates that inhabited Eurasia during the Miocene from approximately 18 to 8 million years ago. The two most prominent pliopithecoid families, Crouzeliidae and Pliopithecidae, are each defined by their own distinct suite of dental characters. One of these characters is cusp peripheralization. Crouzeliids are described as having molar cusps that are significantly more peripheralized compared to pliopithecids. In the literature this observation has remained largely qualitative. Our research employs a methodology

that allows us to quantify it. We collected our data by taking digital occlusal photographs of original fossil specimens. We then took linear, angle, and area measurements of the upper first and second molars from these photographs using image-processing software. We used univariate and multivariate statistical tests to evaluate the differences between crouzeliid and pliopithecoid upper molar occlusal morphology. Our results show that there are significant differences in cusp peripheralization between the two pliopithecoid clades, and that crouzeliids have upper molars with more peripheralized cusps.

Department of Anthropology, University of Toronto Natural Sciences and Engineering Research Council of Canada

Fiber phenotype of the temporalis muscle in *Papio anubis*

MEGAN A. HOLMES¹ and ANDREA B. TAYLOR²

¹Family Medicine and Community Health, Duke University SOM, ²Department of Basic Science, Touro University

The "high-occlusal bite force" hypothesis asserts that the jaw adductors of mammals that feed on mechanically challenging items should comprise disproportionately more fast fibers. Previous work on baboon temporalis found larger proportions of fast fibers in the superficial anterior (SAT) compared to the deep anterior (DAT) temporalis. These differences were found to correlate with variation in EMG activation amplitudes between the SAT (strong) and DAT (weak) during hard/tough feeding. However, mammalian jaw adductors show large amounts of hybrid fibers and previous immunohistochemistry (IHC) on baboon temporalis applied only two antibodies (NOQ7.5.4, MyHC I; MY32, MyHC II) to identify fiber-types. Here we use IHC to further evaluate the high-occlusal force hypothesis by comparing the presence and distribution of slow (MyHC-I and MyHC α -cardiac; fatigue resistant) and fast (MyHC-II and MyHC-M; fatigable) myosin proteins in *Papio anubis* (n=4) superficial (ST) and deep (DT) temporalis. Cells were counted and scored based on staining intensity and cross-sectional area (CSA; μm) was measured to calculate the %CSA attributed to each fiber type. The majority of cells were hybrid (co-expressed multiple MyHCs); MyHC-I/ α -cardiac-II and MyHC α -cardiac-II/M were the most common combinations. ST was dominated by fibers expressing majority fast MyHC (71%) in contrast to the DT which expressed majority slow fibers (64%). Chi-square analyses of fiber-type frequency confirmed significant differences between ST and DT expression patterns ($p<0.0001$). Results further support the high-occlusal bite force hypothesis. However, the high percentage of hybrid fibers indicates a more complex relationship between the fine-tuning of feeding and fiber-type expression.

This research was funded in part by a grant from the National Science Foundation (BCS1719743).

The spring in the arch of the human foot, revisited

NICHOLAS B. HOLOWKA^{1,2}, ALEXANDER RICHARDS², BENJAMIN E. SIBSON² and DANIEL E. LIEBERMAN²

¹Anthropology, University at Buffalo, ²Human Evolutionary Biology, Harvard University

Humans are the only living animals that possess a longitudinal arch in their feet. One frequently cited evolutionary explanation for this unique structure is its purported capacity to store and release elastic energy like a spring during running. However, support for this notion comes mainly from studies of cadaveric feet, which cannot account for the actions of foot muscles on arch function. Furthermore, the effects of anatomical features like arch height on the spring-like properties of the foot are unknown. Here we present the first *in vivo* investigation of the spring function of the arch in humans with varying arch heights. We recorded 27 adult participants running on a force-plate-instrumented treadmill using 3-D motion capture, and used inverse dynamics to calculate arch stiffness. To test for the possibility of active muscular contributions to the spring mechanism, participants ran at different stride frequencies, which is known to cause changes in overall leg spring stiffness. Across conditions we found that arch compression increases and decreases nearly linearly with bending forces on the arch, strongly supporting a spring-like function during running. Additionally, we found that arch stiffness changes by nearly 50% across running frequencies, suggesting a major role for foot muscles in modulating the stiffness of the arch spring. Finally, we found positive correlations between arch height and stiffness during running across participants. These results suggest that the evolution of a well-defined, fully modern longitudinal arch would have enhanced the hominin foot's capacity to function as a stiff spring during running.

Genetic Contributions to Individual Variation in Cortical Organization and Cognition in Chimpanzees

WILLIAM HOPKINS

Comparative Medicine, MD Anderson Cancer Center

Advances in quantitative genetic and molecular biological methods has increasingly allowed for analysis of individual and phylogenetic variability in brain and behavioral phenotypes. Specifically, using source-based morphometry, we quantified 19 gray matter covariation networks in a sample of 225 captive chimpanzee MRI scans. Quantitative genetic analysis based on the extant pedigree revealed significant heritability in gray matter covariation networks in 16 of the 19 regions (h^2 ranging from .235 to .851, all $p < .05$). We also quantified social and physical cognition in 218 chimpanzees using the Primate Cognition

ABSTRACTS

Test Battery (PCTB) as well as tool use skill for a simulated termite fishing task. Overall chimpanzee intelligence was found to be significantly heritable ($h^2 = .435, p < .05$) as was their tool use skill ($h^2 = .544, p < .01$). Lastly, we found significant phenotypic but not genetic correlations between overall intelligence and three of the gray matter covariation networks. In contrast, for tool use skill, significant phenotypic and genetic correlation for two gray matter regions including visual cortex and portions of the superior and inferior parietal lobe. The collective results suggest that genes play a significant role in accounting for tool use skill in chimpanzees but this is less so the case for intelligence, suggesting a greater role of non-genetic factors such as social learning, as accounting for performance

Supported by grants NS-42867, NS-73134, NSF-INSPIRE SMA-1542848

Effect of gait and velocity on in-vivo tibial loading in humans

MARTIN HORA^{1,2}, HERMAN PONTZER³, LOUIS E. DEFRATE^{3,4,5}, HAL C. CHARLES⁶, VLADIMIR SLADEK¹ and AIDAN MCGINNIS²

¹Anthropology and Human Genetics, Charles University, Czech Republic, ²Evolutionary Anthropology, Duke University, ³Biomedical Engineering, Duke University, ⁴Mechanical Engineering and Materials Science, Duke University, ⁵Orthopaedic Surgery, Duke University School of Medicine, ⁶Radiology, Duke University School of Medicine

Lower limb bone cross-sectional geometry is widely used to infer about subsistence behavior and mobility of past populations in bioarchaeology and paleoanthropology. However, our knowledge about variation in human bone loading – within the shaft cross-section and across gaits and velocities – is limited due to invasiveness of the measuring procedure. Here we aim to explore the effect of gait and velocity on tibial loading in humans during locomotion in-vivo using a non-invasive approach.

We collected kinematic and kinetic data for five healthy adults while walking and running barefoot at eight velocities (Froude number 0.1–0.9) on an instrumented treadmill. We used 3D musculo-skeletal modeling (OpenSim) to estimate bending moments acting on tibial midshaft during early stance phase of step. We obtained magnetic resonance images of our subjects' lower limbs to determine the orientation of maximum bending strength at tibial midshaft. We analyzed the effect of gait and velocity on two parameters: 1) maximum bending moment, and 2) difference between the orientation of maximum bending moment and maximum bending strength.

Our results indicate that maximum bending moment increases with velocity in walking and then levels off at the transition to running. Difference between the orientation of maximum

bending moment and maximum bending strength also increases with velocity in walking while no further increase was observed throughout our range of running speeds. Our findings are counterintuitive as the orientation of bending moments matches bone structure better during slower locomotion – in which the bone loads are lower – than during faster locomotion.

This work was supported by the Czech Science Foundation, grant number 18-16287S. M.H. has been supported by the Czech Fulbright Commission and Charles University Research Centre program No. 204069.

A comparison of knee replacement hardware dimensions to natural femoral anatomy

HALEY E. HORBALY and BENJAMIN M. AUERBACH
Anthropology, University of Tennessee, Knoxville

Orthopedics companies have recently pursued sex-specific total knee replacement (TKR) designs that account for sexual dimorphism to improve post-operative outcomes for females. Variance in human skeletal morphology associated with sexual dimorphism is well-documented, but prior research on knee anatomy has shown no significant differences in morphology between the sexes when controlling for size. For knee replacements to be effective they must functionally mimic natural skeletal anatomy, yet the variance in TKR appliances in relation to skeletal variation has not been studied. The question remains if scaling knee replacement appliances to the individual sufficiently reflects the functional variation of knee morphology, or if additional variation in shape must be taken into account. This research analyzes 14 bilateral landmarks on the distal femur and orthopedic hardware for 18 individuals who received unilateral TKRs and 36 individuals with no TKRs. Procrustes-transformed data indicate that 5 of 8 posterior condylar landmarks exhibit the greatest variance among individuals; however, sex-specific *t*-tests conducted on interlandmark distances indicated a significant difference only in left and right side medial condyle breadths for men with TKRs ($p = 0.02$), and no significant differences in measurements for women with TKRs or individuals with no TKR. Mann-Whitney U tests confirmed there are no significant differences in bilateral femoral asymmetry between individuals with TKR hardware and those without ($p > 0.05$). This indicates that bilateral asymmetry in individuals with unilateral TKR is not outside the range of normal human variation. Thus, implant size is likely not contributing to reduced post-operative outcomes for females.

Our Daily Bread: Intersections of Dental Health, Social Status, and Religious Identity in Early Medieval Central Europe

LAUREN HOSEK
Anthropology, Syracuse University

This study is a bioarchaeological examination of dental health in two early medieval skeletal samples from contemporary burial locations. The dental remains of 115 adults and 84 subadults were examined from the Akropole and Kanin cemeteries at the 9-11th century site complex of Libice nad Cidlinou in what is now the Czech Republic. Carious lesions, attrition, antemortem tooth loss, and abscessing were assessed. Despite traditionally recognized status differences between the mortuary contexts of these two cemeteries, few statistically significant differences in dental health were found between the two cemetery samples. Furthermore, adult males from both cemetery samples exhibit higher rates of attrition than females, suggesting gendered differences in diet that transcend status groups. Finally, macroscopic dental indicators suggest variation in infant weaning patterns between the two cemetery samples. In the Akropole sample, 77% of infants over six months in age exhibit carious lesions and attrition on deciduous teeth, suggesting the commencement of solid food consumption for most infants. In contrast, only 20% of Kanin infants exhibit potential weaning signatures. This project integrates skeletal data with archaeological and historical sources to offer insight into how dental health is also informed by social factors, including status, gender, and religious identity. For example, these data may be indicative of variation in adherence to early medieval Christian prescriptions for diet and weaning. This work has implications for our understanding of dental health in early medieval contexts, as well as how religious transitions might be accessed bioarchaeologically.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship under Grant No. 2012142383, and the Moynihan Institute Center for European Studies at Syracuse University

Soft and hard tissue relationships of the mouth in a southern African population

TOBIAS M.R. HOULTON¹, NICOLENE JOOSTE², JASON HEMINGWAY¹, ANDRE UYS³ and MARYNA STEYN¹

¹School of Anatomical Sciences, University of the Witwatersrand, ²Department of Human Anatomy and Physiology, University of Johannesburg, ³School of Dentistry, University of Pretoria

The South African Police Service frequently depends on craniofacial approximation (CFA) and superimposition (CFS) for purposes of personal identification, but limited standards exist for determining mouth morphology from the skull. Cone-beam computerised tomography (CBCT) scans comprising 124 black (72 male, 52 female; mean age 35.1 years) and 39 white (19 males, 20 females; mean age 36.1 years) southern

ABSTRACTS

African adults were utilised to examine patterns in mouth shape, size and position. This involved the assessment of linear craniofacial dimensions and geometric morphometrics (GM).

Comparative hard and soft tissue dimensions were recorded using OsiriX. Significant differences between ancestry, sex and age groups were tested, and regression analysis performed using SPSS version 25. In ImageJ, hard and soft tissue landmarks were also assigned to anterior CBCT stills of the skull/face in Frankfurt position, for GM analysis using MorphoJ.

Generated equations utilising skeletal face height, inter-canine width, and central incisor inter-alveolar width, performed best in lip height, mouth width and Cupid's bow estimation, respectively. Inclusion of ancestry, sex and age group (20-39 and 40+ years) significantly improved regression performance. These regression models outperformed mean models and existing approximation standards in validation tests, using a hold-out sample of ~30. GM visually elucidated key hard and soft tissue landmark relationships between groups; e.g. the stomion was roughly two-thirds down the maxillary central incisors in white individuals, but positioned close to the occlusal line in black individuals.

These new guidelines support the advancement of CFA and CFS practice, improving their reliability within law enforcement.

This research was funded by the Leverhulme Trust (Grant Number: SAS-2017-005).

Understanding evolutionary changes in gene expression through the development of a comparative primate skeletal cell culture model

GENEVIEVE HOUSMAN¹ and YOAV GILAD^{1,2}

¹Section of Genetic Medicine, University of Chicago, ²Department of Human Genetics, University of Chicago

Comparative skeletal anatomy is integral in anthropological research. While the functional consequences of skeletal morphologies have been readily examined, the underlying mechanisms that drive the development and evolution of complex skeletal traits are less well characterized. Assaying the impact of gene regulation in primate skeletal tissues has been particularly challenging because samples are difficult to obtain, often have preservation issues, and contain heterogeneous populations of cells. Thus, we have established a comparative primate skeletal cell culture model as an alternative and more accessible way of evaluating gene expression in the skeleton. Specifically, we optimized protocols for differentiating four human and four chimpanzee induced pluripotent stem cells (iPSCs) into mesenchymal stem cells (MSCs) and subsequently into osteoblasts (bone cells) and chondrocytes (cartilage cells). Standard

FACS, staining, and candidate gene qPCR assays were performed to validate cell differentiation. Additionally, single-cell RNA-seq data are being collected from samples and replicates (n=20). These high-resolution gene expression data allow us to identify interspecific variation in gene expression among skeletal cell types while accounting for variations in cell composition across samples and replicates. Preliminary results indicate that humans and chimpanzees share several cell-specific gene markers that denote pluripotency in iPSCs, commitment to the mesodermal lineage in MSCs, osteogenic potential in osteoblasts, and chondrogenic potential in chondrocytes. These data also reveal distinct patterns of gene expression between species. Overall, these findings provide novel insight into gene regulation of primate skeletons, and continued work with this cell culture system will further increase our understanding of skeletal gene regulation.

A Longitudinal Study of Habitat Use among Primate and Non-Primate Mammals at the La Selva Biological Station, Costa Rica

SUE M. HOWELL¹, MELISSA SCHAEFER SEABOCH² and ORLANDO VARGAS RAMIREZ³

¹Department of Anthropology, University of Colorado Colorado Springs, ²Department of History, Anthropology and Political Science, Salt Lake Community College, ³La Selva Biological Station, Costa Rica

This study considers the association between natural resource types and habitat use for mammals at the La Selva Biological Station, Costa Rica (1994-2017). Mammal species were censused each December by traversing routes throughout the station. Data were summarized by species and route. Habitat use was identified by forest types (Old Growth, Secondary Forest, Pasture, and Swamp) and water resources (Rivers, Streams, and Creeks). ArcGIS and R Studio were used for analyses ($p < 0.05$). Multiple regression methods were used to test whether routes, forest types and/or water resource types predicted habitat use. Results indicate primates routes and forest types did not predict habitat use but the river water resource types explained most of the variation ($R^2 = 0.127$, $F(3,351) = 2.288$, $p = 0.017$) (Mean(SD): River=8.4(4.13), Stream=6.4(2.17), Creek=5.18(2.77)). Further, *Alouatta palliata* habitat use was predicted by old growth forest type and river water resource type (Forest type: $R^2 = 0.022$, River type: $F(3,185) = 4.309$, $p = 0.039$) (Mean(SD): Forest Old 4.94(1.62), Secondary 4.53(1.91), Pasture 1.17(0.408), Swamp 1.45(0.93) (Mean(SD) River 6.11(2.50), Stream 2.89(0.96), Creek 2.54(0.97)). Predictions did not reach significance for most non-primate mammals including artiodactyls, carnivores, and edentates and there were insufficient data for marsupials and lagomorphs. However, forest type did predict rodent habitat

use with a preference for old growth forest types ($R^2 = 0.02$, $F = (3, 242)$, $p = 0.024$), particularly among squirrel genera (*Sciurus granatensis*, *Sciurus variegatoides*, and *Sylvilagus brasiliensis*) ($R^2 = 0.073$, $F(1,96) = 7.545$, $p = 0.007$). Maintaining old growth forests and river water resources are critically important to conservation management plans for primates, particularly *Alouatta palliata*, and other mammals in this Neotropical rainforest.

Effects of Energetic Need on Human-Macaque Interactions and Access to Anthropogenic Food in the Urban Environment

JOSEPHINE HUBBARD^{1,2}, NADINE RUPPERT⁴, KRISHNA BALASUBRAMANIAM², BRIANNE BEISNER^{2,5}, PASCAL MARTY², STEFANO KABURU³ and BRENDA MCCOWAN^{2,5}

¹Animal Behavior Graduate Group, University of California, Davis, ²School of Veterinary Medicine, University of California, Davis, ³Biomedical Science & Physiology, University of Wolverhampton, ⁴School of Biological Sciences, Universiti Sains Malaysia, ⁵Neuroscience & Behavior Unit, California National Primate Research Center

As human encroachment on wildlife increases, assessments of these effects are increasingly important. Human-wildlife interactions provide benefits and risks to wildlife, such as increased access to anthropogenic food (AF) or receiving aggression. This study explores individual differences among urban rhesus (*Macaca mulatta*) and long-tailed (*Macaca fascicularis*) macaques in India and Malaysia. We investigate how females balance the risks of human interactions under different requirements of energetic need, defined as late pregnancy (LP: 3 months pre-birth), early lactation (EL: 1-3 months post-birth) and late lactation phases (LL: 3-6 months post-birth). We observed five groups and collected data on infant births and human-macaque interactions from 2016-2018.

Due to higher energetic needs during lactation compared to pregnancy, we hypothesize that females will interact more with humans during lactation to receive AF. Since interactions with humans can be risky, we hypothesize that females will interact with humans less during EL, when infants are vulnerable, compared to LL. We used GLMs to assess the effects of phase on human-macaque interactions and AF consumption. Using an IT approach, the best model for human-macaque interactions included an interaction between phase and the percentage of AF females consume. This model showed that during LP and EL, females interact significantly less with humans as consumption of AF increases, whereas during LL, females show the opposite ($b = 1.97$, $p = 0.05$). These results illustrate the

ABSTRACTS

importance of human-macaque interactions on macaque behavior and is the first to link these changes with energetic need and risk mitigation in urban environments.

This work was supported by the National Science Foundation Grant # 1518555, and was awarded to Brenda McCowan.

Standing ground against entropy: The history of the osteological collections from San Pedro de Atacama, Chile

MARK HUBBE^{1,3} and CHRISTINA TORRES-ROUFF^{2,3}

¹Department of Anthropology, Ohio State University, ²Department of Anthropology and Heritage Studies, University of California, Merced, ³Instituto de Arqueología y Antropología, Universidad Católica del Norte

The curation of skeletal collections has been among the most important roles biological anthropologists have assumed in the last century, not only for their scientific value but also given their importance in discussions about ethnic identity and the relationship between living and past native communities. However, despite their importance, the long-term maintenance and care of these collections is challenging due to the loss of institutional memory and the regularly shrinking number of professionals in charge of these vast collections. Here, we present our experience working with the human skeletal collections housed at the Instituto de Arqueología y Antropología (San Pedro de Atacama, Chile) as a case study on the challenges that curators commonly face and how to improve our responsible and ethical care for osteological collections in general. Between the 1950s and 1970s Father Gustavo Le Paige excavated one of the largest osteological collections in Latin America, recording in his field notes the excavation of 5,482 skulls and human bodies. However, cumulative processes of abandonment and the lack of preventive conservation resulted in a substantial loss of context and a decrease in the quality of preservation of a significant portion of this skeletal collection. Our research has shown that over 35% of these burials currently lack adequate information to be included in scientific studies due to preservation issues and/or loss of contextual and provenience information. Our work with this collection has helped open space to debate mid and long-term ways to minimize its future deterioration.

Patterns of Changes in Cranial Capacity in Asia

AUTUMN HUDOCK¹ and SANG-HEE LEE²

¹Department of Anthropology, University of North Carolina at Charlotte, ²Department of Anthropology, University of California at Riverside

It has been argued that hominin cranial capacity shows an increasing trend over time during the Pleistocene, followed by a decrease during

the Holocene. Several hypotheses have been proposed to explain the decrease, including self-domestication with agriculture in the Holocene. The cranial capacity data, however, impose a challenge in the uneven distribution of data points. African data are concentrated in the Early Pleistocene, European data are concentrated in the Late Pleistocene, with substantially more data for the Holocene.

Recent decades have seen an increase in the Pleistocene Asian data, and more reliable dates associated with previously uncertain fossils. With a relatively even distribution of data points across the Early, Middle, and Late Pleistocene, Asia provides a unique opportunity to test the hypothesis of a single pattern of increase throughout the Pleistocene. In this paper, we ask how human brain size has changed in the Pleistocene, using 60 hominin specimens from Asia, with dates ranging from 1.66 Ma to 10 Ka. We use a resampling algorithm using a distribution of increments to test the null hypothesis that a single process generated the observed increase pattern, developed in a previous study. Results do not reject the hypothesis of a single process of brain size change during most of the Pleistocene but a change in the direction from 50 Ka. It is concluded that the decreasing trend in hominin brain size began during the terminal Pleistocene, before the onset of the Holocene.

This research was supported by University of California, Riverside.

Methods to infer the timing of admixture and selection in high altitude populations

EMILIA HUERTA-SANCHEZ¹, XINJUN ZHANG², KELSEY WITT¹, AMY KO⁴, RASMUS NIELSEN⁴, SHUHUA XU⁵, ASAN ASAN³ and XIN JIN³

¹Ecology and Evolutionary Biology, Brown University, ²Ecology and Evolutionary Biology, UCLA, ³BGI, BGI, China, ⁴Integrative Biology, UC Berkeley, ⁵Chinese Academy of Science, Max Planck Partner Institute of Computational Biology

Living at more than 3500 meters above sea level, Tibetans provide one of the classical examples of human adaptation to extreme environments. One of the genes involved in this adaptation is the Endothelial Pas Domain Protein1 gene (EPAS1) which encodes a transcription factor that regulates the response to variation in oxygen level. This gene exhibits not only a striking signature of positive selection, but it also harbors a haplotype that matches most closely with the Denisovan sequence, suggesting that admixture between Denisovans and the ancestral population of Tibetans facilitated this adaptation. We leverage the patterns of introgression and selection at this locus to infer the archaic admixture time and the timing of selection. We find that like other East Asian populations, Tibetans show evidence for two introgressions from Denisovans. We find

that the putative beneficial alleles were likely introduced by the East Asian-specific Denisovan introgression between 30-40kya. We also find that selection acted on standing archaic variants suggesting that selective variants were not immediately beneficial but instead lingered neutrally in the population and then more recently became beneficial.

E.H.-S. is funded by NSF award grant no. 1557151 and NIH award grant no. 1R35GM128946-01.

Implications for Identifications: Exploring How Collaborative Efforts Mitigate Structural Vulnerabilities of Missing Migrants along the Arizona-Mexico Border

CRIS E. HUGHES¹, ROBIN C. REINEKE², BRIDGET F.B. ALGEE-HEWITT³ and BRUCE E. ANDERSON⁴

¹Anthropology, Institute for Genomic Biology, University of Illinois at Urbana-Champaign, ²The Southwest Center, Latin American Studies, University of Arizona, ³Center for Comparative Studies in Race and Ethnicity, Stanford University, ⁴W.H. Birkby Forensic Anthropology Laboratory, Pima County Office Of the Medical Examiner

Hughes et al. (2016) concluded that structural vulnerabilities linked to indigeneity reduced the success of identifying deceased migrants along the Arizona-Mexico border. Mexican migrants with more Native American ancestry were less often successfully identified in recent years as compared to individuals with more European ancestry. The authors hypothesized that this "identification bias" could be mitigated by collaboration between forensic practitioners and nongovernmental organizations working closely with affected communities. Pima County Office of the Medical Examiner (PCOME) has been at the forefront of establishing these NGO partnerships, drawing upon the combined strengths of biological and cultural anthropologists.

To test whether the identification bias is reduced by NGO collaborations, we compared migrant cases from PCOME for which an NGO-collaboration played a critical role in the identification (N = 52) and those for which it did not (N = 77). CODIS STR data were used to estimate ancestry via STRUCTURE. Our results show for cases without NGO collaboration, migrants with increased Native American ancestry were identified less frequently in more recent years ($r = -0.28, p=0.011$). In contrast, we found that when NGO collaboration played a critical role in case-work, migrants with increased Native American ancestry were identified *more* frequently in recent years ($r = 0.38, p=0.006$).

These preliminary findings suggest that NGOs mitigate the identification bias. They play a vital role, ensuring that the overall identification

ABSTRACTS

trends at state entities involved in migrant death investigations, like PCOME, attend to the shifting demographics of Latin American migrants crossing and dying on the Border

Bio-anthropological practice in contemporary South Africa: engaged critical approaches to research on human remains

ROBYN A. HUMPHREYS^{1,2}, WENDY BLACK^{2,3}, JUNE BAM HUTCHISON⁴ and REBECCA R. ACKERMANN^{1,2}

¹Archaeology, University of Cape Town, ²Human Evolution Research Institute, University of Cape Town, ³Archaeology Unit, Research & Exhibitions Department, Iziko Museums of South Africa, ⁴Centre for African Studies, University of Cape Town

The Prestwich Street colonial-era informal burial ground was discovered in 2003 in Cape Town during real estate development. Its discovery and the subsequent decision to exhume the >2000 underclass skeletons (including slaves) resulted in socio-political contestation. For many, these remains became the material embodiment of the history of colonialism and the impact of racial science in South Africa. Exhumation of the remains highlighted the entanglement of biological anthropology, heritage management, historical knowledge production, contemporary issues such as gentrification, and resulted in further erasure of the history of slavery and forced removals. This happened despite South African legislation democratising the process around exhumation/management of human remains. No research has been done on these remains in the 15 years since their discovery; they remain entombed in a poorly-equipped and managed memorial facility. Here we discuss the history of this site, current biological anthropological practice as it relates to human remains from archaeological sites in Cape Town, as well as current practice around management of such human remains by local heritage agencies, and their practice regarding engagement with communities. We further report the results of a dialogue hosted jointly by the University of Cape Town and Iziko Museums in April 2019 called 'Discussing change of disciplinary practice in Archaeology and Human Remains work.' This dialogue occurred between academics, heritage practitioners, descendant communities (e.g. San and Khoe), and other interested parties, and revolved around community perception of research, and exploring how researchers might more effectively engage with communities regarding custodianship and research of remains.

National Research Foundation of South Africa, the National Institute for Humanities and Social Sciences of South Africa and the KW Johnston Bequest award from the University of Cape Town

ELUCIDATING THE PERPETUATION OF SYSTEMIC VIOLENCE IN BIOARCHAEOLOGICAL PRACTICES: An examination of postmortem violence through the lens of historic Eastern Cemetery

CASSIDY M. HURT and CODI N. GOODWYN
Anthropology, University of Louisville

Structural violence is a form of systemic oppression against marginalized people causing harm both physically and mentally. Although this term was initially applied to living populations, it has since been adopted into the bioarchaeological theoretical corpus, considering violence in past life histories. However, structural violence arguably can also be observed *after* death in the burial, excavation, and curation of human remains. We propose that individuals from the criminally overburied site of Eastern Cemetery (1843-1993) in Louisville, Kentucky represent a case of post-mortem structural violence. By comparing rates of preservation and unnecessary/excessive modification (excavation, destructive sampling, or curatorial damage) to evidence of antemortem periosteal lesions (PL) and osteoarthritis (OA), we show the continuation of violence to this marginalized community beyond death.

Due to the fragmentary state of remains, observations and statistical analyses focused exclusively on tibiae (n=19). Each tibia was recorded for preservation score, excavation damage, unnecessary modification, PL, and OA. On a preservation scale of 0 (<25%) to 3 (>75%), the average preservation score was 1.47. Of the tibiae observed, 84.2% displayed damage from shovel and trowel cuts, sawing, and gluing. 89.5% of the tibiae presented PL and OA. Although these data derive from a singular element, antemortem and postmortem traumata were observed throughout the fragmentary Eastern Cemetery sample.

Results indicate that those individuals who were marginalized and oppressed in life often experience the same treatment in death. Recognizing postmortem structural violence as a form of oppression is an important step toward more ethical treatment of marginalized people after death.

Funding provided by University of Louisville Executive Vice President for Research and Innovation Internal Grant Program, Undergraduate Research Grant.

Evaluating the Symptomatic Expression of a Prehistoric Case of North American Blastomycosis from North Carolina

DALE L. HUTCHINSON¹, SOPHIA C. DENT¹, ABIGAIL S. GANCOZ², MARY GLENN KRAUSE¹, CHRIS LAMACK³ and ASHLYN M. WHITE⁴

¹Anthropology and Research Laboratories of Archaeology, University of North Carolina Chapel Hill, ²Anthropology, Pennsylvania State University,

³Anthropology, University of Pennsylvania, ⁴School of Medicine, Duke University

North American Blastomycosis is a respiratory tract fungal infection caused by breathing *Blastomyces dermatidis* spores, which are normally found in rotting wood or soil. In contemporary North America, the disease is distributed primarily in the Mississippi and Ohio river valleys and in North Carolina. When blastomycosis affects bone (roughly 25-50% of cases), the lytic lesions are typically expressed on the vertebrae, ribs, skull, tibia, and feet. The disease is symptomatic between the ages of 20-50. A 25-35 year old female from the Upper Saratow archaeological site in North Carolina has lesions consistent with blastomycosis. She lived during the Middle Contact period (AD 1650-1670). Lesions indicative of blastomycosis include focal lytic lesions on the lumbar vertebrae and right tarsal bones, remodeled porous new bone on the posterior sacrum, and remodeled smooth new bone on the rib heads. Co-morbidities include lesions indicative of nutritional deficiency (porosity in the region of foramen ovale and on the posterior zygomatic bones), periodontal disease, and sinusitis. Together, these lesions indicate active, chronic infection and inflammation. Linear enamel defects of both the anterior and posterior teeth suggest that this individual experienced stress during development, which may have predisposed her to chronic adult morbidity. As with tuberculosis, immune suppression makes blastomycosis more likely to be symptomatic than asymptomatic. We argue that symptomatic expression of diseases like blastomycosis may act as an important indicator of biocultural stress - in this case, immune suppression compounded by the stress of the colonial landscape.

This research was supported by NSF grant BCS 1450633.

Insights into Native American adaptations to high altitude from modern and ancient genomes

TÁBITA HÜNEMEIER¹, CAINÁ M. COUTO-SILVA¹, RENAN B. LEMES¹ and COSIMO POSTH²

¹Genetics and Evolutionary Biology, University of São Paulo, ²Archaeogenetics, Max Planck Institute for the Science of Human History

The Andean Altiplano has been occupied since the Late Pleistocene, ~12,000 years ago, making the Andes one of the first high altitude regions in the world to be permanently settled by modern humans. In the present study, we analyzed published genomic data from ancient Native American individuals (n=15) who lived during different periods at Andean high altitude. We have identified ten candidate genes - *CPNE4*, *FAM213A*, *ACAD10*, *CNTNAP5*, *NGF*, *PRDM5*, *HLA-G*, *OCA-2*, *SLC7A6*, and *DDX10* - with evidence of positive selection for altitude adaptation in the Late Ancient Andeans (4,200-900 YBP) when compared to the Early Ancient Andeans (9,000-5,800 YBP). Three

ABSTRACTS

of these *loci* were already described as under selection in present-day Andeans or other high-altitude populations (*CPNE4*, *FAM213A*, *ACAD10*). The other genes are mainly involved in response to hypoxia (*CNTNAP5*, *NGF*, *PRDM5*), functions at the fetus-maternal interface (*HLA-G*, *SLC7A6*) and skin pigmentation (*OCA2*). Our results pointed to essential physiologic pathways related to contexts of long-term adaptation to high altitudes. However, this complex combination of genes is not found when only modern-day Andeans populations are studied, likely due to recent demographic events that could be acting as confounding factors.

This project has been supported by FAPESP and CAPES.

Fertility and survivorship in Jomon and Yayoi populations

YURIKO IGARASHI¹, KUNIO SHIMIZU² and SHOGO MIZUTAKA³

¹School of Dentistry at Matsudo, Nihon University, ²School of Statistical Thinking, The Institute of Statistical Mathematics, ³Department of Mathematics and Informatics, Ibaraki University

Fertility and survivorship in Jomon hunter-gatherers and Yayoi agriculturalists of Japan were reconstructed by examining human skeletal remains from Jomon and Yayoi sites, in order to see whether there were differences among populations. Fertility was estimated using pregnancy and parturition scars (PPS) in the preauricular area (Igarashi et al. 2019). PPS include three categories: TS0 indicates “no pregnancies and parturitions”, TSL indicates “fewer pregnancies and parturitions” and TSH indicates “more pregnancies and parturitions”. The percentages of TS0, TSL and TSH in a population can be regarded to be the fertility of the group. Survivorship was based on the ages of individuals estimated by the morphology of the auricular surface (Igarashi et al. 2005). Results show that fertility and survivorship were different among populations. In the northern Jomon population, fertility was high and survivorship was low; in southern Yayoi populations, fertility was low and survivorship was high. In central and western Jomon populations, fertility and survivorship fell in the middle between the extremes of the other two groups. We cannot currently determine whether these differences are caused by the difference of area: climate or subsistence system, or by the era: subsistence system or genes. We would like to examine the fertility and survivorship of southern Jomon populations and of central and northern Yayoi populations in order to better identify the cause of the differences in fertility and survivorship among the populations.

How good are ASUDAS traits for assessing population relatedness? An answer—from comparisons of African dental and genetic data

JOEL D. IRISH, ADELIN MOREZ and LINUS GIRDLAND FLINK

Anthropology and Archaeology, School of Biological and Environmental Sciences, Liverpool John Moores University

Arizona State University Dental Anthropology System (ASUDAS) nonmetric traits are often considered the “gold standard” for estimating phenetic affinities at individual through global scales. Beyond user-friendliness, high observer replicability, low cost, and non-destructive sampling, these traits are largely selectively neutral with a high genetic component in expression. Thus, they are deemed expedient proxies for genetic markers. But are they really?

In answer, several recent studies compared ASUDAS and genetic (SNPs, STRs) data via model-free and model-bound methods at local, regional, and global levels among recent peoples. The consensus is that the nonmetric data yield dependable results, although some authors are less convinced than others.

We assess further the utility of ASUDAS traits—here on a continental scale. Using a model-free approach for matched samples of 12 North and sub-Saharan African populations, mean measure of divergence (MMD) distances from 36 traits were compared with those of Hudson *F*_{st} based on high density SNP (>300,000) data. These matrices are strongly correlated ($rm=0.786$, $p=9.999e-05$). After trait editing, described elsewhere by the first author, a 25-trait MMD and *F*_{st} correlation increased ($rm=0.838$, $p=9.999e-05$). This concordance is notably better than in the abovementioned studies. Of further interest, the correlation for both 36- and 25-trait MMD with geographic distances is higher ($rm=0.700$, $p=9.999e-05$) than for *F*_{st} and geography ($rm=0.486$, $p=0.001$).

These findings suggest ASUDAS traits are valuable for assessing relatedness, and several explanations for the improved concordance are presented. This and our current global level research continues to address just how good these traits are.

Data collection by the first author was funded by the National Science Foundation (BNS-9013942, BNS-0104731, BCS-0840674), the ASU Research Development Program, and the American Museum of Natural History.

Folivore rules and frugivore rules: Variation in diet and food chemistry in sympatric frugivorous and folivorous lemurs

MITCHELL T. IRWIN^{1,3}, VOLOLONIRINA RAHALINARIVO², JEAN-LUC RAHARISON³, BRUNO RAMORASATA², JEAN-FREDDY RANAIVOARISOA²,

JEANNOT RANDRIANASY² and JESSICA M. ROTHMAN^{4,5}

¹Anthropology, Northern Illinois University, ²Anthropobiology and Sustainable Development, University of Antananarivo, ³Research, ONG Sadabe, ⁴Anthropology, Hunter College, ⁵Graduate Center, CUNY

Primates are traditionally categorized into broad dietary guilds (frugivores, folivores, insectivores) but these are “fuzzy” boxes and primatologists have rarely explored actual nutritional divergence among species, which nutrients drive foraging choices, and how this varies across guilds and clades.

We analyzed food chemistry for folivorous sifakas (*Propithecus diadema*, $n=61$ foods) and frugivorous brown lemurs (*Eulemur fulvus*, 69 foods) at Tsinjoarivo, Madagascar (overlapping home ranges). Considering fruit (81% of brown lemur diet, 37% for sifakas), the two lemurs rarely ate the same foods, yet there was no evidence of nutritional divergence (no significant differences in available protein, fiber, sugar, or nonstructural carbohydrates). For leaves (14% of brown lemur diet, 54% for sifakas), dietary overlap was again minimal. Brown lemur leaves were higher in available protein and sifaka leaves were higher in nonstructural carbohydrates; brown lemur leaves were also higher in simple sugars than leaves selected by neither species. Brown lemurs thus appear to select leaves for protein (their leaves average 10.0% vs just 3.9% in their fruits) and simple sugars (well-suited to fast gut passage and cathemerality), while sifakas select for nonstructural carbohydrates (an energy source well-suited to slow gut passage) but not protein (leaves average 7.1%, similar to non-selected leaves).

Further research is necessary to examine how selection rules vary seasonally, the interaction between nutrient absorption and gut retention times, and the effects of PSMs. These advances will elucidate the physiological constraints that cause divergence in food selection, which will aid in better understanding feeding competition and guiding conservation efforts.

Funded by National Geographic Society, Eppley Foundation for Research, and Northern Illinois University.

Opening a can of worms: Elucidating parasite transmission patterns among non-territorial social groups of Grauer's gorillas in the Democratic Republic of Congo

NEETHA S. IYER¹, CHRISTOPHER A. PAGAN², ALAIN MUNDOLA³, URBAIN NGOBOBO-AS-IBUNGU³, STEVEN A. NADLER² and DAMIEN CAILLAUD^{1,3}

¹Department of Anthropology, University of California Davis, ²Department of Entomology & Nematology, University of California Davis, ³The Dian Fossey Gorilla Fund International

ABSTRACTS

Group living is a fundamental, adaptive feature of many primate societies. Yet with increased sociality comes a greater risk of exposure to infectious disease. Previous field-based research has revealed that primate social groups share many of the same parasites. However, territorial behavior and increased spatial segregation between social groups should minimize parasite transmission among groups. This has elicited efforts to model the spread of environmentally-transmitted parasites among social groups with varying degrees of territoriality. We sought to investigate this idea empirically in wild Grauer's gorillas (*Gorilla beringei graueri*) endemic to the Democratic Republic of Congo. Gorillas live in family groups that have partially-overlapping home ranges and are infected by a number of parasites species. We hypothesized that because gorilla groups encounter their own past, contaminated trails more often than those of other groups, social groups serve as islands for parasite transmission despite the lack of territoriality exhibited by gorillas. We examined the genetic diversity of gastrointestinal nematode worms from five social groups (n=72 gorillas) in a high-altitude population of gorillas. We collected dung at gorilla nests, cultured nematode larva from each sample, and sequenced ribosomal RNA of at least 10 worms per sample. Our results suggest that there are more unique nematode haplotypes found within a social group than between groups. This study provides empirical evidence for the relative importance of within- versus between-group transmission of nematodes and other pathogens, and adds to our understanding of the costs and benefits of sociality.

This research was supported by the Morris Animal Foundation (D18ZO-831), and the University of California, Davis (Department of Anthropology and Institute of Social Sciences).

Assessing matrilineal genetic diversity in Mexico through the analysis of ancient mitogenomes spanning 2,300 – 500 YBP

ALAN IZARRARAS-GÓMEZ¹, VIRIDIANA VILLAS-
ISLAS¹, MIRIAM BRAVO-LÓPEZ¹, MARCELA
SANDOVAL-VELASCO², ELIZABETH M. PÉREZ-
CAMPOS³, ALBERTO HERRERA-MUÑOZ³, EUGENIA
VILLANUEVA-MEDINA⁴, RAMIRO AGUAYO-
HARO⁴, CRISTINA VALDIOSERA⁵ and MARIA C.
ÁVILA-ARCOS¹

¹International Laboratory for Human Genome Research (LIIGH), Universidad Nacional Autónoma de México (UNAM), ²Natural History Museum of Denmark, University of Copenhagen, ³INAH-Querétaro, Instituto Nacional de Antropología e Historia, ⁴INAH-Michoacán, Instituto Nacional de Antropología e Historia, ⁵Department of Archaeology and History, La Trobe University, Melbourne, Australia

The loss of Native genetic diversity due to Spanish colonization has been acknowledged by several disciplines. One approach to assess this loss is through the use of ancient DNA (aDNA) to contrast mitochondrial DNA (mtDNA) diversity between pre and post contact individuals. MtDNA is present in high copy numbers in virtually any cell type, which makes it amenable for (aDNA) studies. Additionally, its maternal mode of inheritance and non-recombining nature make it attractive for assessing changes in matrilineal genetic diversity through time. In this study, we recovered and sequenced new ancient mitogenomes from ancient human remains from Central and Northern Mexico spanning Pre-Hispanic to Colonial times (~2,300 – 500YBP). We integrated these data with publicly available ancient and present-day mitogenomes from Mexico and the rest of the Americas to assess the extent of genetic continuity of ancient mtDNA Native American lineages in the contemporary Mexican population. We carried out haplotype network analyses and estimated past female effective population sizes using a Bayesian Skyline approach. Results show that all Mexican samples are part of the four major Native American haplogroups (A2, B2, C1, and D1). Interestingly, the vast majority of sub-haplogroup variants found are unreported in present-day samples and in the current Phylotree (build 17), suggesting either that these lineages have gone extinct after European contact or at the very least rare among present-day Mexican populations and not yet reported.

Cortical neuromorphology in large mammals

BOB JACOBS

Neuroscience, Colorado College

In the last three decades, we have quantitatively documented the variety of neocortical neurons in humans (n = 2,500+) and in a broad collection of relatively large brained mammals (n = 2,200+) that have seldom, if ever, been examined previously. Here, we summarize the major findings of these investigations and provide a brief overview of neuronal types across several of these 20+ species: African elephant, Florida manatee, humpback whale, giraffe, Siberian tiger, and cheetah. Comparative analyses reveal some similarities in neuronal types across species, but also some striking differences, both qualitatively and quantitatively. In particular, the poster will highlight two broad observations: (1) neurons in the African elephant neocortex are the most distinctive and represent a fundamentally different organizational architecture than observed in other mammals, including humans; moreover, although the overall complexity of elephant pyramidal neurons is similar to that in humans, the dendritic branches in elephants tend to be longer and less branched. (2) motor gigantopyramidal neurons in non-domestic felids (e.g., African lion, African leopard,

caracal, cheetah, clouded leopard, Siberian tiger) are disproportionately large compared to those in other mammals, including human Betz cells, presumably due to specializations in felid musculoskeletal systems and hunting behavior. Although pyramidal neurons remain the dominant cortical cell in mammals, morphological variation exists across taxonomies. In addition, there is variation in neuron types across species, suggesting that the prototypical primate/rodent model of cortical organization does not extend to all mammals.

Database bias hinders functional analysis of non-industrial populations' gut microbiomes

DAVID K. JACOBSON^{1,2}, THERESE S. KAGONE³,
NICOLAS MEDA⁴, HELENE CARABIN⁵, TANVI
HONAP^{1,2}, KRITHIVASAN SANKARANARAYANAN⁶
and CECIL M. LEWIS, JR.^{1,2}

¹Department of Anthropology, University of Oklahoma, ²Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, ³Department of Biological Sciences, Centre MURAZ, Burkina Faso, ⁴Ministry of Health, Burkina Faso, ⁵Department of Pathology and Microbiology, University of Montreal, ⁶Department of Microbiology and Plant Biology, University of Oklahoma

Non-industrial populations have higher gut microbiome taxonomic diversity than industrial groups and gene/functional diversity are expected to fit a similar profile; however, little is known about functional diversity in non-industrial gut microbiomes. Here, we explore functional diversity of gut microbiomes from industrial (North America, Europe), pastoral (Mongolia), rural agricultural (Burkina Faso, Madagascar), and hunter-gatherer populations (Peru, Tanzania), each of which meet the criteria for inclusion: >10 million metagenomic reads post quality filtering, >20 samples, distinct lifestyle). Each sample was taxonomically profiled, then taxonomy-specific and overall gene abundance data were generated by mapping metagenomic reads to microbial pangenomes and protein databases, respectively. Overall, we find tremendous discrepancies in our ability to functionally characterize gut microbiomes. After normalization, a significantly higher number of genes are found in industrial populations compared to hunter-gatherers and agriculturalists (p-value < 1x10⁻¹³). Additionally, an average of 66% of genes were matched to a species encoding that gene in industrial populations but only 47%, 37%, and 29% of genes were species-classified in pastoral, rural agricultural, and hunter-gatherers, respectively (p-value < 2.2x10⁻¹⁶). Performance does not improve for genes at high abundance in non-industrial populations, as short chain fatty acid synthesis enzymes have a significantly lower classification percent at all taxonomic levels in non-industrial compared to industrial populations (p-value < 1x10⁻⁶). These results mirror human genome research, where ascertainment bias

ABSTRACTS

impacts our understanding of genetic diversity and health risk. Diverse microbiome database representation is necessary to more accurately capture biological variation and mitigate ascertainment bias in microbiome research.

Investigating Vegetation Structure within Abandoned Dassanach Bomas

HANNAH JACOBSON¹, VENANZIO MUNYAKA², HUSNA MASHAKA², ELLA BEAUDOIN³, CHRIS SSEBUYUNGO⁴, RAHAB KINYANJUI⁵, EMMANUEL NDIEMA⁵ and MATT DOUGLASS⁶

¹The Department of Anthropology, The George Washington University, ²Paleobotany, Koobi Fora Field School, ³Human Origins, National Museum of Natural History, ⁴Archaeology, Uganda National Museum, ⁵Archaeology, National Museum of Kenya, ⁶College of Agricultural Sciences and Natural Resources, University of Nebraska

The land use practices (grazing, bush clearing) of nomadic pastoralists populations have historically been considered detrimental to the local ecology and the natural landscape of the areas they inhabit. However, recent research has suggested that the alterations made to the landscape by pastoralists have the effect of contributing to landscape heterogeneity and that areas of former homesteads (bomas) produce nutrient hotspots that increase vegetation health and species abundance. The Inkoria Section of the broader Dassanach ethnic group are pastoralists who inhabit the eastern basin margins of Lake Turkana in far northwestern Kenya. Ongoing research by the Koobi Fora Field School has investigated the hotspot phenomenon in abandoned Dassanach bomas. Here we present a pilot study on methods to measure both vegetation health, species abundance, and soil fertility in abandoned bomas of varying ages. The data collected suggests that certain plant species are characteristic of abandoned bomas and there is a correlation between vegetation type and distance from the center of the boma. Future efforts may be needed to determine whether drone NDVI imagery can be successful at identifying abandoned bomas based on vegetation health.

Life-history tradeoffs and fertility transitions in a historic population (1896-1939)

ADRIAN V. JAEGLI¹, JORDAN S. MARTIN¹, JOEL FLORIS^{1,2}, NICOLE BENDER¹, MARTIN HÄUSLER¹ and KASPAR STAUB¹

¹Evolutionary Medicine, University of Zurich, ²Department of History, University of Zurich

Life-history theory (LHT) has been very successful in explaining variation in schedules of fertility and mortality across species. A fundamental tenet of LHT is that organisms face a series of allocation decisions resulting in tradeoffs between competing demands. Specifically, organisms face a tradeoff between (i) continued growth and the onset of reproduction, which should accelerate

under improved conditions, as well as between (ii) reproduction and future survival for the mother (the "cost of reproduction") or for the offspring (quantity-quality tradeoff). These tradeoffs are reduced for individuals with greater access to resources, who can afford to invest more across domains. While some of these predictions are well supported in humans, evidence for others is mixed. Here we test a series of predictions directly derived from LHT using a dataset of N=13'663 birth records from the Basel maternity hospital (1896-1939). We use Bayesian multivariate models allowing us to simultaneously analyze related outcomes, appropriately model non-linear effects (year, SES), and impute missing data. We find the predicted and well-known secular decline in age at menarche as conditions improve but increase in age at first reproduction as fertility norms change; however, there was no tradeoff between height and age of menarche or first reproduction. Similarly, taller and higher-SES women produced bigger babies, but there was no evidence for quantity-quality tradeoffs. This study provides an important test of LHT in a period of improving conditions and demographic transitions, which complements other populations typically studied by evolutionary demographers.

Direct Identification of Neanderthal Introgressed Genetic Variation Affecting Gene Expression in Modern Human Immune Cell Lines

EVELYN JAGODA¹, JAMES XUE², STEVEN REILLY^{2,3}, MICHAEL DANNEMANN⁵, FERNANDO RACIMO⁴, EMILIA HUERTA-SANCHEZ⁷, SRIRAM SANKARARAMAN⁶, JANET KELSO⁵, LUCA PAGANI^{8,9}, PARDIS SABETI^{2,3} and TERENCE D. CAPELLINI^{1,3}

¹Human Evolutionary Biology Department, Harvard University, ²Department of Organismic and Evolutionary Biology, Harvard University, ³Broad Institute of Harvard and MIT, Broad Institute, ⁴Lundbeck GeoGenetics Centre, The Globe Institute, University of Copenhagen, ⁵Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, ⁶Department of Computer Science, Department of Human Genetics, University of California Los Angeles, ⁷Department of Ecology and Evolutionary Biology and Center for Computational Molecular Biology, Brown University, ⁸Estonian Biocentre, Institute of Genomics, University of Tartu, ⁹Department of Biology, University of Padova

Since the discovery of Neanderthal-human interbreeding, researchers have wondered what adaptive impact introgression may have had in the modern human gene pool. Studies have identified putative cases of adaptive introgression (AI). However, broader functional characterization of AI regions has been limited as most variants reside in non-coding portions of the genome. This challenge is compounded because AI regions consist of many linked genetic variants, further obscuring discovery of the true driver variant(s) underlying

each positive selection signal. Identifying such driver variants in introgressed portions of the genome is paramount to understanding the phenotypic and, potentially, adaptive consequences of interbreeding with archaic hominins.

Adaptation through changes in gene expression may explain why positive selection targeted non-coding AI variation. We used the Massively Parallel Reporter Assay (MPRA) system to simultaneously test ~6,000 introgressed Neanderthal variants and their non-introgressed orthologs for their ability to modulate gene expression. We selected Neanderthal AI variants from geographically diverse human populations and tested them in two human immune cell lines. Out of all tested variants, ~5% significantly modulated gene expression. We further investigated the set of candidate driver variants and found their activity to be functionally enriched in certain immune pathways, particularly in the signaling pathways of certain Interleukins. We are continuing to investigate the most promising of these potential driver variants using other *in vitro* assays. Overall, this research identifies some of the most likely driver variants of adaptive introgression and illustrates the ability of next generation laboratory methods to contribute to this field of study.

Age-associated changes in the microbiome of rhesus macaques on Cayo Santiago

MAREIKE C. JANIAK^{1,2}, MICHAEL J. MONTAGUE³, CATALINA VILLAMIL⁴, MICHALA K. STOCK⁵, AMBER E. TRUJILLO⁶, ALLEGRA DEPASQUALE¹, JOSEPH D. ORKIN⁷, SAMUEL E. BAUMAN SURRET⁸, OLGA GONZALEZ², MICHAEL L. PLATT³, MELWEEN MARTINEZ⁹, SUSAN C. ANTÓN⁶, GLORIA DOMINGUEZ-BELLO¹⁰, AMANDA D. MELIN^{1,2} and JAMES P. HIGHAM⁶

¹Anthropology & Archaeology, University of Calgary, ²Alberta Children's Hospital Research Institute, University of Calgary, ³Department of Neuroscience, University of Pennsylvania, ⁴School of Chiropractic, Universidad Central del Caribe, ⁵Department of Exercise Science, High Point University, ⁶Department of Anthropology, New York University, ⁷Institut de Biologia Evolutiva, Universitat Pompeu Fabra-CSIC, ⁸Caribbean Primate Research Center, University of Puerto Rico, ⁹Disease Intervention & Prevention, Southwest National Primate Research Center, ¹⁰Department of Biochemistry and Microbiology, Rutgers University

An animal's microbiome changes over the course of its lifetime, especially during infancy, and again in old age. Confounding factors such as diet and healthcare make it difficult to disentangle the interactions between age, health, and microbial changes in humans. Here, we analyze a large dataset of oral, rectal, and genital swabs collected from 105 rhesus macaques (*Macaca mulatta*, aged <1-26 years) from Cayo Santiago. We sequenced 16S V4 rRNA amplicons for all samples. Microbial communities differed significantly between the

ABSTRACTS

three body sites (PERMANOVA $r^2=0.4$, $p=0.001$). Infant gut microbial communities had significantly higher relative abundances of *Bifidobacterium* (\log_2 fold change = 8.79, $p<0.001$) and lower abundances of *Ruminococcus* (\log_2 fold change = -23.84, $p<0.001$) compared to other age groups, consistent with a diet high in milk rather than solid foods. Infants also had much lower abundances of *Helicobacter* than adults of all ages (\log_2 fold change = -22.4, $p<0.001$). Genital microbial communities were comparatively more uniform across age groups, with only *Corynebacterium* being relatively more abundant in adults than in infants ($p=0.03$). Oral microbiome composition was associated with age ($r^2=0.12$, $p=0.001$), and was most distinctive for infants. Across all three body regions, while infant microbiomes were distinctly different from other age groups, those of adults were relatively invariant, even in advanced age. This finding is contrary to findings in humans and suggests that at least some of the microbial changes observed in aged humans may be due to age-related changes in diet and lifestyle rather than aging itself.

AAPA Cobb Award (MCJ), ACHRI Postdoctoral Fellowship (MCJ), NSERC (ADM), UCalgary (ADM), Leakey Foundation (JPH, SCA), NIH R01MH096875 (MM, MP), National Center for Research Resources #8-P40-OD012217-25 (Cayo Santiago)

Sex determination of human deciduous teeth from three millennia via amelogenin isoform identification

LUKAS JANKER¹, ANNA HADOBAS², DINA SCHUSTER¹, CHRISTOPHER GERNER¹, KATHARINA REBAY-SALISBURY³ and FABIAN KANZ²

¹Department of Analytical Chemistry, University of Vienna, ²Center for Forensic Medicine, Medical University of Vienna, ³OREA, Austrian Academy of Sciences

Archaeological, anthropological and forensic research relies on the secure identification of the biological sex of human remains. Morphological sex determination of juveniles is notoriously difficult, and genetic sexing is costly, destructive and limited by the preservation of nuclear DNA. In recent years, however, a new nano-LC-MS-based method of sex determination via sexually dimorphic amelogenin peptides in dental enamel of permanent teeth has been introduced. Our aim was to test if this method can successfully be applied to deciduous teeth of modern, medieval and Bronze Age origin.

Recently replaced deciduous teeth were collected from 10 female and 9 male children. Ten deciduous teeth from 13th century children and 10 deciduous teeth from Bronze Age (2200-1600 BC) children of unknown sex were extracted from the jaws.

Based on a modified protocol from Stewart et al. 2017, we established a robust nano-LC-MS/MS method for the analysis of dimorphic peptides. To

avoid false negative interpretation, an unbiased and automated data analysis via MaxQuant software was employed. The sex of all modern girls and boys was identified correctly by the applied method; the biological sex of all medieval (4 girls and 6 boys) and Bronze Age (5 girls and 5 boys) children was determined.

Furthermore, we identified an additional 220 peptides, which demonstrates the analytical potential of this method for opening up new avenues of research. As it is minimally destructive, it has the potential to significantly advance studies in which a reliable sex determination of subadults is crucial, even in ancient populations.

What what in the... A case of interpersonal violence from the Early Neolithic grave from Smilčić, Croatia

IVOR JANKOVIĆ¹, MISLAV ČAVKA², BRUNISLAV MARIJANOVIĆ³, MARIO CARIĆ¹ and MARIO NOVAK¹

¹Center for Applied Bioanthropology, Institute for Anthropological Research, Zagreb, Croatia,

²Department of Diagnostic and Interventional Radiology, Chair of Social Medicine and Organisation of Healthcare, School of Medicine, University of Zagreb, ³Department of Archaeology, University of Zadar

Archaeological excavations at the Early/Middle Neolithic site at Smilčići-Barice, led by B. Marijanović (University of Zadar) in 2016/2017, revealed skeletal remains of several people. Of particular interest is the skeleton from Grave 2, directly dated to 5574-5484 cal BCE. The skeleton was positioned on its left side, in a crouched position with bended knees and its right arm flexed at the elbow. Based on metric and morphological observations, the skeleton belongs to a young male, aged between 25 and 35 years. The most interesting feature is a penetrating trauma located at intertrochanteric crest on the posterior proximal side on the left femur. A 15x4x3 mm lithic fragment is still embedded in the bone. Slight osteogenic reaction around the fragment is noted on CT, indicating survival for a longer period. This is the earliest example of interpersonal violence recorded on the eastern Adriatic coast.

This work was supported by the Croatian Science Foundation [grant number HRZZ IP-2016-06-1450].

Comprehensive phylogenetic analysis of early Miocene catarrhines reveals the assembly of the hominoid body plan

RUTGER J.W. JANSMA^{1,2} and KIERAN P. MCNULTY²

¹College of Medicine - Phoenix, University of Arizona, ²Department of Anthropology, University of Minnesota

The early Miocene catarrhines are key taxa for elucidating the evolutionary history of the living apes and Old World monkeys. The two living lineages exemplify two divergent adaptive

strategies among a diverse and complex evolutionary history. However, insight into the adaptive processes that led to these living catarrhine clades is obscured because of confusion over the systematic affinities within key early Miocene groups. This study undertakes a new phylogenetic analysis using maximum parsimony sampling 64 taxa and 243 characters from the skull, dentition, and postcranium. The analysis finds a well-resolved consensus tree that supports monophyly of Cercopithecoidea and Hominoidea. Within Hominoidea, Pliopithecidae, Dendropithecidae, and Proconsulidae are identified as successively more derived monophyletic clades that reflect the initial assembly of the hominoid body plan. A monophyletic Oreopithecidae clade containing *Oreopithecus* and the nyanzapithecines is also well supported within Hominoidea. However, the positions of both Pliopithecidae and Oreopithecidae are strongly influenced by the morphology preserved within single species in these clades. These results demonstrate both the importance of comprehensive taxonomic sampling and the impact of missing data on phylogenetic results. The analysis also reveals that suspensory adaptations documented in living apes appeared independently in four hominoid clades (Pliopithecidae, Oreopithecidae, Hylobatidae, and Hominidae). Finally, a general perspective on catarrhine evolution emphasizes that the adaptations and appearance of the ancestral hominin ca. 6 - 8 Ma cannot be properly interpreted without making reference to the entire Miocene ape radiation.

Support for this project received from the Leakey Foundation and the University of Minnesota Department of Anthropology.

Are there any reliable biomarkers of early fetal development in humans?

GRAZYNA JASIENSKA, MAGDALENA KLIMEK, ANDRZEJ GALBARCZYK and ILONA NENKO

Department of Environmental Health, Jagiellonian University

Early fetal development is crucial for life-long biological condition and health of the individual. Studies that investigate relationships between pre-natal and post-natal periods of life rely on various biomarkers that are thought to reflect environmental conditions during fetal development. We hypothesized that if biomarkers of early period of fetal development are to be reliable indicators of that environment, their values should be highly correlated.

In 236 women, aged 40-92 (mean 59.4), from the Mogielica Human Ecology Study Site in southern Poland three different biomarkers were assessed: finger ridge-counts, digit ratio and level of facial fluctuating asymmetry. Several different simple indices were constructed and analysed for each biomarker. Further, principal component analysis

ABSTRACTS

was used to obtain a composite variable for each biomarker. Neither correlations between individual simple indices of biomarkers, nor between composite variables, were statistically significant.

The lack of statistically significant relationships among biomarkers widely used to reflect early pre-natal development suggests that: 1) they are not reliable as indicators of fetal developmental conditions, 2) they are sensitive only to very short time of developmental conditions, 3) their values are not as stable during post-natal life as is often assumed. This implies that our ability to detect a comprehensive signal about developmental conditions in humans may be limited. We also point out that there is a need for designing precise models that would allow for better understanding of critical windows, sensitive periods and plasticity during early human development.

This study was supported by National Science Centre: grant no. UMO-2017/25/B/NZ7/01509

Age assessments based on DNA methylation signatures in vervet monkeys

ANNA J. JASINSKA^{1,2}, JOSEPH ZOLLER^{3,4}, MICHAEL THOMPSON^{3,4}, KYLIE KAVANAGH^{5,6}, MATTHEW J. JORGENSEN⁵, KEVIN WOJTA^{1,7}, OI-WA CHOI¹, JOSEPH DEYOUNG¹, XINMIN LI⁸, MIKE FACIO⁹, GIOVANNI COPPOLA^{1,7}, NELSON FREIMER^{1,3}, ROGER P. WOODS^{1,7} and STEVE HORVATH^{3,4}

¹Center for Neurobehavioral Genetics, Semel Institute for Neuroscience and Human Behavior, Department of Psychiatry and Biobehavioral Sciences, David Geffen School of Medicine, University of California, University of California Los Angeles, ²Department of Molecular Genetics, Institute of Bioorganic Chemistry, Poznan, Poland, ³Department of Human Genetics, David Geffen School of Medicine, University of California Los Angeles, ⁴Department of Biostatistics, School of Public Health, University of California, Los Angeles, Los Angeles, California, USA, ⁵Department of Pathology, Section on Comparative Medicine, Wake Forest School of Medicine, Medical Center Boulevard, Winston-Salem, 27157-1040, USA, ⁶Department of Biomedicine, University of Tasmania, Hobart Australia, ⁷Department of Neurology, Department of Neurology, University of California, Los Angeles, Los Angeles, CA 90095, USA, ⁸Technology Center for Genomics & Bioinformatics, Department of Pathology & Laboratory Medicine, University of California, Los Angeles, Los Angeles, CA 90095, USA

The process of aging is associated with epigenetic changes in the methylation status of CpG sites in the genome. The DNA methylation (DNAm) signatures based on age-associated CpG sites can be leveraged to construct an epigenetic clock, which is a universal molecular biomarker of so-called biological age. DNAm clock from human and mouse proved to be an accurate predictor of chronological age and all-cause mortality, and showed an acceleration in response to factors causing biological aging (e.g., diseases, exposure to environmental factors). We created the

first DNAm clock from a non-human primate species, the vervet monkey (*Chlorocebus aethiops sabaeus*), to facilitate aging studies in this species. We characterized DNAm profiles in vervets with known chronological age accurate to one day that represented the entire vervet lifespan, from neonate to senile stage. We studied a total of 240 samples: 144 samples from peripheral blood, 48 samples from liver, and 48 samples from brain area BA10. We measured DNA methylation on a mammalian methylation chip assessing ~37K CpG sites, highly conserved across the mammalian evolution. We constructed highly accurate epigenetic clocks for the individual tissues. We also created a multi-tissue clock, which shows a high correlation between the chronological age and epigenetic age ($r=0.98$, median absolute error of 0.43 years) based on a leave-one-sample-out analysis. We anticipate that the epigenetic clock will facilitate identification of genetic and environmental impacts on age acceleration in vervet and open a new avenue for age assessment in natural vervet populations.

This work was supported by the following grants from the US National Institutes of Health: P40RR019963/OD010965; R01RR016300/OD010980; R37MH060233.

Possible Evidence of Termite Osteophagy of Skeletonized Human Remains in Ecuador

NICOLE A. A. JASTREMSKI¹ and ALEJANDRA SÁNCHEZ-POLO²

¹Department of Anthropology and Museum Studies, Central Washington University,

²Departamento de Prehistoria, Antigua, y Arqueología, Universidad de Salamanca

Taphonomic activity caused by insects is common in decaying human remains and is a source of forensic significance. Less common is insect osteophagy or modification of bone tissue on prehistoric remains. Of the insect orders that are known to modify human remains, only four have been found to consume osseous material: termites (*Isoptera*), beetles (*Coleoptera*), flies (*Diptera*), and wasps and bees (*Hymenoptera*). A recent analysis of a human skeleton from the Ecuadorian Amazon associated with the Napo Culture (A.D. 1188–1480) displays taphonomic characteristics consistent with necrophagous activity. The likely culprit is believed to be termites since the remains lack both a skull and os coxa (two areas highly favored by termite osteophagy), boring, cavities, tunneling, and sub-circular perforations, among other traits. However, beetles cannot be ruled out since they also display deep pit borings on skeletal material. The skeletal remains were found within an urn typical of the Amazon Polychrome Horizon Style and was radiocarbon dated to A.D. 1021–1152. Since little is known of the funerary practices of the Napo Culture, identifying the type of insect modification

may enlighten mortuary practices within this group, as burial urns from some African groups are found to be placed intentionally within termite mounds.

Functional anatomy of the caudalmost sacrum in *Australopithecus afarensis*, *Australopithecus sediba* and *Homo erectus*

SAMANTHA JAYE¹, VALERIA CORTEZ², MARC R. MEYER² and SCOTT A. WILLIAMS^{3,4}

¹Anthropology, Cal State Los Angeles,

²Anthropology, Chaffey College, ³Center for the Study of Human Origins, Department of Anthropology, New York University, ⁴New York Consortium in Evolutionary Primatology

While much research has been devoted to the cranial aspect of the sacrum, because of a paucity of fossils, little work has been conducted on the caudalmost anatomy of the sacrum, the S5. Here we utilize 2D geometric morphometric (GM) and linear analyses to analyze this understudied anatomic region of the axial skeleton in *A. afarensis* (A.L. 288), *A. sediba* (MH2) and *Homo erectus* (KNM-WT 15000).

Our extant comparative sample consists of extant hominoid taxa from 5 genera (N = 213). PCA and linear regression successfully partition *H. sapiens* from non-human apes using 11 landmarks on the S5. Analyses reveal a more medial position of the terminal cornua in non-human apes producing a transversely restricted sacral hiatus relative to *H. sapiens* and each fossil hominin. As is the case in the cranial elements of the sacrum, the S5 of *A. afarensis*, *A. sediba* and *Homo erectus* present an overall S5 anatomy similar to *H. sapiens*, although we highlight some aspects of transitional morphology in *Australopithecus*.

Despite some variation between *H. sapiens* and the fossil sample, all three hominins present an expanded attachment site for the gluteus maximus muscle relative to non-human apes, as well as an expanded origin for the sacrotuberous ligament and perineum. These derived features are germane to understanding the evolution of human postural and locomotor behaviors and are diagnostic of an adaptation to bipedality at the caudalmost region of the axial skeleton.

Partial funding for this project was provided by a Leakey Grant (to SAW)

Spatial-Packing & Ontogeny of the Hypermuscular Mouse Skull

NATHAN JEFFERY, DYLAN SARVER and CHRIS MENDIAS

Institute of Ageing & Chronic Disease, University of Liverpool

The human skull has a finite capacity to accommodate competing spatial and functional demands, leading to pleiotropic trade-offs that manifest as intraspecific phenotypic plasticity and

ABSTRACTS

provide capacity for life-course physical as well as behavioural adaptation. The challenge is detecting these effects among the many other sources of human population variance. Here we examine certain fundamental aspects of the spatial trade-offs at the intraspecific level using a hyper-muscular mouse model (MSTN^{-/-}). We focus on the spatial requirements of the enlarged masticatory muscles in relation to those of the brain, and document associated variations of skull form at 1, 7, 14 and 30 postnatal days. A total of 48 mice (6 control & 6 MSTN^{-/-} per age group) were studied post-mortem in accordance with ethics granted by the University of Michigan IACUC. Heads were removed fixed in PBFS, microCT imaged to capture skull geometry using landmarks then stained with I₂KI solution and microCT imaged again to measure the volume of the masseter and endocranium. Landmark configurations (n=18) were analysed using geometric morphometrics. Results suggests that the masseter was slightly larger in controls at P1, but that MSTN^{-/-} muscle growth quickly accelerated to become 17% larger by P30. By contrast MSTN^{-/-} endocranial size started and remained smaller (7-30%). Form changes that coincided with this relative expansion of the masseter included: enlargement of infratemporal fossa by lateral displacement of the zygomatic arches and narrowing of the face; elongation of the palate; dorsoventral shortening and mediolateral narrowing of the calvarium; and flattening of the basicranium.

Living conditions of the Korean people did not improve during the Japanese colonization period (1910 – 1945): Based on the secular changes of stature and body mass

YANGSEUNG JEONG¹, EUNJIN WOO², SIMON PERGANDE³ and OMAR ALY⁴

¹Biology, Middle Tennessee State University, ²History, Sejong University, ³Biology, Middle Tennessee State University, ⁴Chemistry, Middle Tennessee State University

There has been a long debate on whether the living condition of Korean people deteriorated or improved during the Japanese colonization period (1910-1945). The purpose of this study is to examine the secular changes of Korean people's body size during this time period to assess the living standard in the colonized Korea.

Korean anthropometric data on stature and body mass were obtained from 26 surveys published between 1901 and 1956. Additionally, stature and body mass of 567 Korean skeletal samples, who were deceased in the mid-20th century, were reconstructed following Jeong and Jantz (2016) and Jeong et al. (2017), respectively.

Results show that female stature increased significantly between the early and mid-20th century (from 149.8cm to 155.1cm), while male stature remained nearly unchanged (from 163.1cm to

162.8cm). Body mass showed a similar pattern with a greater increase in females (from 46.8kg to 53.2kg) than males (from 56.6kg to 56.9kg) during this time period.

Given the biological fact that male size is more plastic/sensitive to the quality of environments than females, the stagnant trend of male size indicates that there was not an improvement in the living conditions of Korean people under the Japanese rule. The positive trend in female size is more likely attributed to the advanced women's right and status as a result of modernization of Korean society since the late 19th century.

This study stresses that an insight into both the biological and cultural aspects of the individuals is necessary to evaluate the living quality of a society.

Changing student misconceptions about evolution in an introductory biological anthropology course using an inquiry-based approach

SUSAN L. JOHNSTON¹, MAUREEN KNABB², JOSH AULD² and LORETTA RIESER-DANNER³

¹Anthropology & Sociology, West Chester University, ²Biology, West Chester University, ³Psychology, West Chester University

College students demonstrate persistent misconceptions about evolution even after instruction in the life sciences, including biological anthropology. Studies suggest that student-centered approaches have been more successful than standard curricula in teaching evolution concepts at the college level. An innovative, introductory biological anthropology laboratory curriculum focused on correcting misconceptions about evolution was developed between 2013 and 2016 at West Chester University (WCU) and is in current use at that institution. This inquiry-based approach challenges students to engage actively in solving problems using the scientific method. During development of the curriculum, a 25-item, pre-post course evolution concepts survey was administered at WCU and three other US universities offering introductory biological anthropology courses with more standard laboratory curricula. Data are available for all four universities for three semesters (fall 2014, spring 2015, and fall 2015). While students at all schools showed improvement in understanding of evolution concepts over each semester, there was a significant effect of institution on post-course percent items correct, after controlling for pre-course percent items correct ($p < .001$). Post-hoc tests demonstrated significant differences between post-course scores at WCU and at all three other institutions. Moreover, there was clear improvement in post-course scores over time when comparing the development phase to the pre-development phase at WCU ($p < .05$). Formative and summative assessment measures

were collected during development to identify the most effective approaches and activities. In this paper, we discuss features of the inquiry-based curriculum that we believe are associated with this greater improvement in understanding of evolution concepts.

Supported by an NSF TUES Award (DUE-1245013) and West Chester University.

Time Preferences, Risk Preferences, and Climate Change Adaptation

JAMES HOLLAND JONES

Earth System Science, Stanford University

Human livelihood adaptations involve investments in the present that yield payoffs in the future. Food production, for example, involves a substantial delay from the time of investment to the time of consumption. People value payoffs differentially depending on their time of payoff and delayed payoffs also entail risks (e.g., the resource may disappear, an exchange partner might die). Understanding adaptation therefore requires that we consider people's preferences for both time and risk. However, a growing literature in behavioral economics suggests that people aren't very good at managing either risk or time. This presents a paradox: How is it that *Homo sapiens* emerged as the globally ecologically-dominant species when our capacity to manage these two crucial features of adaptation is apparently faulty? I present evidence that both the observed inconsistencies in time and risk preferences have been mis-interpreted and that an explicitly evolutionary approach helps resolve the paradox. For example, present bias arises in people with otherwise time-consistent preferences in the presence of uncertainty, whereas the observed distortions in people's risk preferences arise from selection acting indirectly on economic preferences by way of their effect on fitness. I discuss these results in light of livelihood adaptations to anthropogenic climate change. The evolutionary perspective on human time and risk preferences turns several pieces of conventional policy wisdom on their head and suggests that social discount rates should be far lower than they are typically set and that more aggressive mitigation policies are optimal.

Interpreting ancient human migration in the Peruvian Andes with co-evolutionary insect genetics

KELSEY C. JORGENSEN¹, CHUANZHU FAN², JESÚS ALCÁZAR³, NORMA MUJICA³, CLORINDA V. COBIÁN³ and JULIE J. LESNIK¹

¹Anthropology, Wayne State University, ²Biological Sciences, Wayne State University, ³Entomology, Universidad Nacional Agraria La Molina

ABSTRACTS

Multispecies anthropology lends fresh perspective to studies of ancient human migration where fossil and archaeological evidence is sparse. In the Peruvian Andes, the spread of potato domestication led to the co-evolutionary development of its primary pest, the *Andean Potato Weevil* (APW). Unique geographic and biological constraints exist for the APW, suggesting that external facilitation would have been necessary for its present-day diversification. After humans began to domesticate the potato (*Solanum tuberosum*) about 8,000 to 10,000 years ago, APW speciation likely occurred when ancient humans carried the potato with this tiny hitchhiker to new locations. Samples of all (11) Peruvian species of APW were collected throughout the Andes. Candidate genes from nuclear (*18S*, *28S rRNA*) and mitochondrial (*COI*, *16S rRNA*) genomes were chosen since they are standard markers for taxonomic identification. DNA sequences using Sanger termination methods were used to reconstruct a phylogenetic tree. Sequence alignment was conducted using higher-accuracy MUSCLE program. Phylogenetic trees were constructed and implemented using MEGA with a best-fit model determined with jModelTest2.1.1. Evolutionary divergence of APW species was calculated with the cross-platform program BEAST 2v2.5.2, based upon Bayesian analysis of molecular sequences using the MCMC method. Phylogenetic trees were compared to relevant archaeological settlements and present-day niches of APW species. Results were used to visualize the directions (phylogenetic tree), and the timing (molecular clock), of ancient human migration after potato domestication. This research furthers biocultural contributions to multispecies anthropology by applying the proxy of insect genetics towards exploring ancient human migration in the Peruvian Andes.

Dietary reconstruction of *Australopithecus africanus* using dental microwear features

CHRISTINA R. JOSEPH and FRANK L. WILLIAMS
Anthropology, Georgia State University

Terrestrial foraging may have figured prominently in the evolution of bipedality. In addition to underground storage organs and terrestrial herbaceous vegetation, scavenging for ground-level fermented fruits could have prompted *Australopithecus* to leave the safety of arboreal habitats, particularly after the evolution of alcohol dehydrogenase 4 (ADH4) permitted the metabolism of ethanol. The consumption of felled fruit in *Australopithecus* should result in a higher instance of light, refractive pits and scratches from terrestrial grit on the surface of the food. Stereomicroscopy at 35x and a movable external light source was used to manifest microwear features which were tallied within a 0.4mm² ocular reticle on the paracone and protoconid of *Australopithecus africanus* molars from Sterkfontein Member 4 (Sts 1, Sts 17, Sts 36, Sts 52a, Sts 71 and TM 1512), *Pan troglodytes*

(n = 7) and *Gorilla gorilla* (n = 7). Tukey's test demonstrates *Au. africanus* and *P. troglodytes* significantly differ in fine scratches. Canonical scores axes show a separation of the 95% confidence ellipses for the centroids of *Au. africanus* and *P. troglodytes*, but some overlap between *Australopithecus* and *Gorilla* on the first axis, where fine scratches, small pits, and large pits differentiate taxa. On the second axis, the confidence ellipse for *Au. africanus* largely overlaps those of the apes, and Sts 17 is polarized from TM 1512. Felled fruit could have been an essential dietary item in early hominins, and *Au. africanus* appears to exhibit evidence for the consumption of at least some foods laden with fine grit.

Re-evaluating Forced Migration in a Population of Enslaved Africans from a Revolutionary War Era cemetery in Charleston, SC with a new Revolutionary era strontium baseline

CHELSEY A. JUAREZ

Anthropology, Fresno State University

Objectives: This study has two objective 1) to identify a time appropriate strontium faunal for revolutionary war era Charleston and 2) to re-evaluate migrants of the international slave trade among 35 individuals of African ancestry buried in a Revolutionary War era cemetery in Charleston, South Carolina.

Materials and Methods: Strontium, isotopes were analyzed in tooth enamel samples of 18 *Sus scrofa* individuals from revolutionary war era Charleston and Strontium, carbon and oxygen isotopes were analyzed in tooth enamel and bone in 28 individuals, and in bone only from 7 individuals (for these individuals there was no enamel present).

Results: The ⁸⁷Sr/⁸⁶Sr ratios of the human enamel ranged from 0.7106 to 0.7329. The ⁸⁷Sr/⁸⁶Sr ratios of the human bone samples range from 0.7096 to 0.7177. The ⁸⁷Sr/⁸⁶Sr faunal range for (N=18) samples from revolutionary era Charleston is 0.7086 to 0.7130. Strontium, carbon and oxygen isotope analysis from enamel have shown that 9 of 35 individuals uncovered in a downtown Charleston burial ground were enslaved Africans from the international slave trade. Seven individuals have no tooth enamel and their place of birth is indeterminant. The data on tooth enamel provide conclusive evidence that (N=7) were consistent with West African origins. For the remaining 2 individuals with enamel samples, the data demonstrated a range of possible regions of origin including Cameroon, Namibia, Angola, Zambia, Morocco, Niger and Madagascar.

Discussion: ⁸⁷Sr/⁸⁶Sr values in enamel suggest that 9 out of 35 individuals show isotope values that are not consistent with birth in Charleston.

no funding support

Suicidal Thoughts and Suicide Attempts in Depressed Older Adults Globally

TYRA R. JUDGE¹, ALICIA M. DELOUIZE¹, PAUL KOWAL^{1,2,3}, NIRMALA NAIDOO², SOMNATH CHATTERJI² and J. JOSH SNODGRASS¹

¹Anthropology, University of Oregon, ²(Switzerland), World Health Organization, ³(Australia), University of New Castle Research Centre for Generational Health and Ageing

It is estimated that suicide accounts for 800,000 deaths per year and rates tend to increase in older adulthood. While 79% of global suicides occur in low- and middle-income countries (LMICs), most studies on suicide have been done in wealthy nations. Here, we examine the prevalence of suicidal thoughts and suicide attempts in people who are depressed and show that there is great variation among LMICs in the Study for global AGEing and adult health (SAGE). Suicidality was high, with different countries having 25% (in China) to 53% (in South Africa) of people who were depressed having suicidal thoughts and 4% (in Mexico) to 26% (in South Africa) of people who were depressed having attempted suicide. Predictors of suicidal thoughts and attempts varied widely by country and gender, with poor health being the most common predictor (*B*'s = 0.10 to 2.20, *p*'s < .01 in China, Russia, India, and Ghana), followed by wealth (*B*'s = -2.71 to 1.03, *p*'s < .05 in China and Ghana), age (*B*'s = -0.14 to 0.03, *p*'s < .05 in Mexico and Ghana), declines in cognitive functioning (*B*'s = -0.78 to 0.53, *p* < .05 in South Africa), being single, divorced, or widowed (*B*'s = -1.85 to 1.77, *p* < .05 in India), and a lack of social cohesion (*B*'s = -0.16 to 0.11, *p* < .05 in South Africa). Our results demonstrate that while these predictors vary widely, they appear to be primarily driven by socioeconomic and cultural factors.

Support: NIH NIA Interagency Agreement YA1323-08-CN-0020; NIH R01-AG034479; Ministry of Health in Mexico; University of Oregon Bray Fellowship.

Home range estimations and site fidelity of western lowland gorillas (*Gorilla gorilla gorilla*) in the Ndoki Forest

KATHRYN JUDSON¹, DAVID MORGAN², JEAN MARIE MASSAMBA³, FABRICE EBOMBI³, PROSPER TEBERD³, GASTON ABEA³, ESPOIRE MAGEMBA³, GAETON MBEBOUTE³, JUAN ORTEGA³, IVONNE KIENAST³ and CRICKETTE SANZ^{1,3}

¹Anthropology, Washington University in St. Louis, ²Lester E. Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo, ³Congo Program, Wildlife Conservation Society

There are few studies on western lowland gorilla (*Gorilla gorilla gorilla*) ranging patterns and most are descriptive, single group investigations. We calculated home range size and fidelity of three groups from two field sites in northern Republic of Congo to implement comparative averages for western lowland gorillas. GPS coordinates were collected at the start of each gorilla group

ABSTRACTS

follow from 2015 to 2018. Range estimations were calculated using 90% Kernel Density Estimations, with site fidelity measured by general percent overlap among years for each group. The average home range was 5.82+1.88km² with a range of 2.98-8.89km². The overall percent range overlap year to year was 87.22+12.78%. Overall, the ranges of these groups was smaller than previously published ranges for western lowland gorillas, including an estimate from one of our study groups assessed earlier in the silverback's tenure. Year to year overlap was higher in our study compared to those published for mountain gorillas, which fits previous findings that western lowland gorillas have higher site fidelity than their mountain counterparts. Toward explaining differences between studies, we compare reported range estimates and methodologies. Our study provides a preliminary framework to understand general patterns of gorilla ranging as well as intra-specific variation across different habitats in the Congo Basin.

Arcus Foundation, Cincinnati Zoo, Indianapolis Zoo, Houston Zoo, Columbus Zoological Park, Nouabale-Ndoki Foundation, U.S. Fish and Wildlife Service

Who and when? Dental modification in coastal Ecuador

SARA L. JUENGST¹ and BRITTANY HUNDMAN²
¹Anthropology, University of North Carolina Charlotte, ²Archaeological Services, DirectAMS Radiocarbon Dating

Dental modification has been previously identified from several pre-Hispanic Ecuadorian burials, interpreted as an important marker of wealth and identity. However, most known cases are from museum collections or other circumstances without clear provenience or cultural affiliation. We sampled four individuals with dental modification from the Museo Arqueológico y Arte Contemporáneo in Guayaquil, Ecuador, in order to obtain more data on the practitioners and antiquity of coastal dental modification. Specifically, we tested four teeth for radiocarbon dates, and collected demographic and pathological skeletal data to identify patterns in dental modification. We identified three distinct types of dental modification (gold alloy insets, gold alloy appliques, and grooved cross-hatching). One probable male, two probable females, and one indeterminate individual presented some form of dental modification. All individuals were adults above the age of 20. Radiocarbon dates returned a range of 1065-352 radiocarbon years, suggesting this was an enduring practice over time. One calibrated range extends into the colonial period, perhaps indicating that people continued to practice dental modification even throughout Spanish presence. All individuals presented diffuse cranial porosity (indicating malnutrition or systemic bodily stress) and one individual had a well-healed maxillary

fracture. We interpret these results as suggestive that dental modification was not restricted to elite individuals but may have been accessible to many coastal Ecuadorians over time.

Funding for this project was provided by a UNC Charlotte Faculty Research Grant.

Prezygopophyseal articular facet shape of the first post-transitional (lumbar) vertebra in anthropoids

HYUNWOO JUNG and NOREEN VON CRAMON-TAUBADEL

Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo (SUNY)

This study aims to explore shape variation in the prezygopophyseal articular facet (PAF) of the anthropoid first post-transitional (lumbar) vertebra, the function of which is important as PAF shifts from having a coronal to a sagittal orientation, thus allowing movement in the sagittal plane but limiting lateral flexion. It was hypothesized that humans have divergent PAF shape among anthropoids due to the functional distinction of bipedalism from other locomotor strategies. 3D surface scans of the first post-transitional vertebra of a sample of anthropoids (n = 215) across ten genera (two atelids, two cercopithecines, one colobine, five hominoids, including humans) were captured using Macro and HDI structured-light scanners. Thereafter, configurations of 19 landmarks capturing the shape and relative position of the PAF were digitized and subjected to Generalized Procrustes analysis (GPA). A principal component analysis (PCA) based on a pooled within-sex covariance matrix was used to explore patterns of PAF shape variation among anthropoid taxa.

Overall, hominoids and Old World monkeys were separated from atelids on PC1 (29% variance) and PC2 (16% variance). On PC1, *Hylobates*, *Alouatta*, and *Ateles* showed more coronally oriented PAF, while *Colobus* and *Chlorocebus* showed more sagittally oriented PAF. *Pan*, *Pongo*, and *Cercopithecus* showed intermediate PAF orientation. Humans and gorillas occupied broadly similar ranges, which overlapped with Old World monkeys and atelids on PC1. In conclusion, humans showed highly variable but not distinctive PAF orientation among anthropoids. Moreover, there may be convergent characteristics in PAF between *Hylobates* and atelids due to functional similarities in suspensory behavior.

This research is supported by a National Science Foundation Grant (NSF BCS - 1830745) and the Mark Diamond Research Fund (SU-19-12 SUNY Buffalo).

The first voyagers in East Asia: Peopling of the Japanese islands in the Late Pleistocene

YOUSUKE KAIFU

Department of Anthropology, National Museum of Nature and Science, Tokyo

Recent geographic, tectonic, oceanographic, biogeographic, and paleontological evidence clearly indicate that many islands of Japan have been isolated from the Asian continent during and after the Late Pleistocene. There are no secure evidence for the presence of archaic humans or Lower-Middle Paleolithic culture among more than 10,000 Paleolithic sites so far recorded from these islands. This situation, like in the case of Australasia, would allow us to have a useful yardstick to define the timing of modern-human dispersal as well as the origin of seafaring in this area of the world. By integrating currently available information from skeletal anthropology, archaeology, palaeogeography, genetics, and various other sources, here I construct a synthetic view about migration history in the Japanese Islands, and discuss Late Pleistocene seafaring in insular East Asia. Different parts of the Japanese Islands were colonized probably by different populations from the south and north around and after 38,000 years ago. Colonization of the long Ryukyu island chain in southwestern Japan was not easy. In some parts on their ways people had to voyage for long distances without seeing land, and in other parts they confronted ocean current. Combined with evidences from Wallacea and central Japan, this underlines not only purposive but also some level of advanced voyaging capability of MIS-3 modern humans in the West Pacific.

This work was supported by JSPS KAKENHI (grant number JP18H03596)

Sociality and Longevity in wild white-faced capuchin monkeys

KOTRINA KAJOKAITE^{1,2,3}, ANDREW WHALEN^{4,5,6} and SUSAN PERRY⁷

¹The Department of Human Behavior, Ecology and Culture, Max Planck Institute, ²The Department of Human Behavior, Ecology and Culture, Max Planck Institute, ³The Department of Human Behavior, Ecology and Culture, Max Planck Institute, ⁴Lomas Barbudal Monkey Project, Costa Rica, ⁵Lomas Barbudal Monkey Project, Costa Rica, ⁶Lomas Barbudal Monkey Project, Costa Rica, ⁷Department of Anthropology, UCLA

The assumption that sociality is consequential to fitness outcomes is ubiquitous in the primatological literature, but direct evidence that variation in sociality between individuals explains variation in fitness related outcomes is still scant, particularly in Neotropical primates. In long-lived species, lifespan is one of the main fitness components. In this study, we investigated whether more social adult female capuchin monkeys live longer than less social females. We used 17 years of the

ABSTRACTS

long-term data from Lomas Barbudal Monkey project to quantify sociality in 11 capuchin social groups using three separate interaction types: grooming, support in coalitionary aggression, and foraging in close proximity. To estimate adult female interaction rates and to take into account the variation in observation time between individuals, we used the Social Relations Model (SRM). This approach enabled us to estimate individual rates of giving and receiving interactions and the uncertainty due to varying amounts of observations per each individual. We modeled adult females' survival as a function of their sociality, rank, age, group size, and maternal kin presence using a Bayesian Cox proportional hazard model. We found that females who give and receive more grooming and support in coalitionary conflicts tend to have higher survival rates, but rates of foraging in close proximity to others do not have a considerable effect on survival rates.

MPI-EVAN, UCLA and grants to S. Perry; NSF (1638428, 0613226, 848360), National Geographic Society (7968-06, 8671-09, 20113909, 9795-15), Templeton World Charity Foundation (0208), Leakey Foundation (20152777, 20112644, 20082262, 20060592)

Enamel Thickness in Lower Third Premolars of the Early and Middle Pleistocene Hominins from Atapuerca, Spain

M SHRUTI KAMATH^{1,2}, MARÁA MARTINÓN-TORRES^{1,2}, CHRISTOPHE SOLIGO¹, LAURA MARTÂN-FRANCÉS^{1,2,3}, CLÉMENT ZANOLLI³, JUAN LUIS ARSUAGA⁴ and JOSÉ MARÁA BERMÚDEZ DE CASTRO^{1,2}

¹Department of Anthropology, University College London, UK, ²CENIEH, National Research Centre for Human Evolution, Burgos, Spain, ³PACEA Laboratory, University of Bordeaux, France, ⁴Mixed Centre (UCM-ISCI) for Human Evolution and Behaviour, Complutense University of Madrid, Spain

The Atapuerca sites continue to figure prominently in our understanding of European hominin evolution. Dental studies of these Early Pleistocene (EP) (*Homo antecessor*) and Middle Pleistocene (MP) (Sima de los Huesos – SH) hominins are particularly useful in providing phylogenetic contexts, and micro-computed tomography (μ CT) has offered opportunities to examine the tissue proportions of their molars and canines. Considering most Pleistocene hominins exhibit thick to hyper-thick enamel and Neanderthals demonstrate relatively thin enamel, the Atapuerca groups show affinities with Neanderthals for both dental classes. This study characterises the tissue proportions of the lower third premolar (LP₃) crowns of the Atapuerca hominins to establish if they present the primitive or derived (Neanderthal-like) condition.

We applied μ CT methods to the LP₃s to extract a set of 3D variables, measuring complete crown and lateral (LET) enamel thickness. The samples comprised *H. antecessor* (n=2), SH (n=13), Early *Homo* from Africa and Asia (n=2), MP hominins from Tighenif, Africa (n=2), Late Pleistocene Neanderthals (n=12), Bronze Age and contemporary *Homo sapiens* from Africa and Europe (n=54).

Despite their close phylogenetic relationship with Neanderthals, our study indicates that the SH hominins are more similar to modern humans than they are to Neanderthals. *Homo antecessor* is more comparable (for LET) to the Tighenif hominins and Neanderthals than to any other group. Currently, *Homo antecessor* and SH hominins are the only known populations of the genus *Homo* to exhibit a combination of primitive and derived conditions for the enamel thickness trait, highlighting the mosaic evolution of dentition.

This research is supported by the Wadsworth International Fellowship, Wenner Gren Foundation (Gr. WIF-251). MINCIU-FEDER (PGC2018-093925-B-C31 and C33). The Leakey Foundation and British Academy (PM160019).

Climatic predictors of primate hair length

JASON M. KAMILAR^{1,2}, AMANDA N. SPRIGGS³, ALYSE MAKSIMOSKI⁴ and BRENDA J. BRADLEY^{5,6}

¹Department of Anthropology, University of Massachusetts, ²Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts, ³Department of Anthropology, University at Albany, State University of New York, ⁴Department of Integrative Biology, University of Wisconsin, ⁵Center for the Advanced Study of Human Paleobiology, George Washington University, ⁶Department of Anthropology, George Washington University

Although hair structure and growth is well-studied, particularly in humans, we know relatively little about the functional evolution of hair variation across primates and other mammals. Thermoregulation has been argued to be an important driver of hair morphology but there is little evidence for this effect in a broad comparative context. Here, we test the idea that primate species living in cold habitats will have relatively longer hair than those living in warm regions. We obtained scaled photographs via digital microscopy from museum research skins representing 58 species from all major primate clades. We measured hair length and width from five body regions using ImageJ and Photoshop. We used phylogenetic generalized linear models to examine the association between mean temperature and temperature variability and hair length, while accounting for body size, hair width, and precipitation. We found a strong negative association between mean temperature and tail hair length and a moderate negative association between mean temperature and ventral torso hair length. We found no relationship between temperature

and crown, back, or cheek hair length. Our results support the hypothesis that variation in primate hair length for some body regions are a function of temperature. In particular, it is interesting to note that we found the strongest association between temperature and hair length for the body region with the highest surface area to volume ratio. We will discuss these results in the context of human and nonhuman primate evolution.

Funded by National Science Foundation (BCS #1546730, BCS #1606360), the Wenner-Gren Foundation, The George Washington University, the University of Massachusetts Amherst

The Influence of Fruit Availability on Energy Allocation in Infant and Juvenile Bornean Orangutans

ERIN E. KANE¹, TRI HAYU SUSANTO² and CHERYL D. KNOTT^{1,3}

¹Department of Anthropology, Boston University, ²Department of Biology, National University of Indonesia, ³Department of Biology, Boston University

The juvenile risk aversion hypothesis suggests an extended life history is an adaptation to unpredictable environments, such as those that characterize Bornean orangutans. We examined how changes in infant and juvenile activity budgets changed over time and with varying periods of food availability. We hypothesized that during periods of low food availability juvenile orangutans would trade-off developmentally important behavior, such as play, in order to conserve energetic resources. We tested this hypothesis using 924 follows of infant (0-4 years) and juvenile (5-8 years) orangutans, collected over a 25 year period, encompassing period of high and low food availability at Gunung Palung National Park, Indonesia. Using a GLMM to control for individual and examining both age and food availability we found that overall, infant and juveniles played less during period of low food availability compared to medium and high food availability (b= -14.3, p < 0.0001) and that play behavior varied significantly by age (b= -5.9, p < 0.0001). Infants in the 1-2 age category showed the highest percentage of play, comprising 42% of their overall activity budget, with play dropping to 14% by age 4. We also found significant interaction effects between age and food availability on play behavior (b=2.1, p < 0.0001). We discuss the ways that infants and juvenile trade off energetically expensive behavior through different development periods as well as the role that maternal behavior may play in buffering infants and juveniles of coping with periods of low food availability.

NSF (9414388, BCS-1638823, BCS-0936199); National Geographic; USFish/Wildlife (F18AP00898, F15AP00812, F13AP00920, 96200-G-249, 96200-9-G110); Leakey; Disney Conservation Fund; Wenner-Gren; Nacey-Maggioncalda; Conservation-Food-Health; Orangutan Conservancy; Woodland Park Zoo

ABSTRACTS

Paleodemographic representation indices of a large, single-site graveyard excavation

FABIAN KANZ¹, BARBARA RENDL¹, RONALD RISY², STEPHANIE WINTER¹ and KARL GROSSSCHMIDT³

¹Center for Forensic Medicine, Medical University of Vienna, ²City Archaeology, Municipal Department of Culture and Education St. Pölten, ³Center of Anatomy and Cell-Biology, Medical University of Vienna

The demographic representativeness of cemeteries has been described and tested on skeletal series using various estimators or indices (Angel 1969, Brothwell 1971, Masset 1973, Weiss 1973, Bocquet and Masset 1977, MacFadden 2017). We applied these methods to the largest skeletal collection from a single-site cemetery excavation in Europe, the Cathedral Square of St. Pölten. The site functioned as the main burial site of the town from the 9th century to 1779.

Archeological excavations between 2010 and 2018 unearthed 19856 individuals, which were subject to basic anthropological investigations; 91% individuals were buried in single graves and 9% in multiple, collective or mass graves. In an area of ~5600m², at least 50% of the former graveyard cubature has been excavated, although excavations stopped at various depths for conservation reasons. We rendered an abridged life table and calculated numerous demographic estimators and indices.

Most calculated values passed the criteria for a good sample representation, but calculations failed in two respects: First, the D(5-9)/D(10-14) ratio was 1.469 and therefore below the ≥ 2.0 recommended by Masset 1973. An overrepresentation of 10-14-year-olds is more likely than an underrepresentation of 5-9-year-olds, taking into account that the Weiss 1973 rejection criteria do not apply [$Q(10) > Q(15)$, $Q(0) < Q(15)$]. Second, the $D(<1) \times 10 / D(20+)$ ratio is 1.104 and therefore not in the representative range of 5.0-8.0 after Angel 1969. This indicates a significant deficit of under-one-year-olds. With a total of 1024 fetal and perinatal individuals recovered in perfect preservation, a bias caused by acid soil properties or poor excavation skills appears unlikely.

Population Dynamics at the Late Copper Age site of Budakalász (Hungary)

AMY N. KARABOWICZ

Department of Anthropology, University of Pittsburgh

The examination of demographic features of populations refines our understanding of trends and variations that impact the demographic profiles of individuals. Holistic projects investigating cultural (e.g., sociocultural, economic, and political), ecological, or evolutionary topics can then integrate these findings. This study explores the dynamics of a Late Copper Age (3500-2700 B.C.) population using skeletal data from the

Budakalász site, a prehistoric cemetery located in Hungary in the Carpathian Basin. More than 450 individuals associated with the Baden culture were recovered during mid-20th century excavations. The cemetery includes both inhumations and cremations; however, some Baden graves (~10%) lack the skeletal data necessary for inclusion in this study.

At the Budakalász site, individuals range in age from neonate to 50+ years. Subadults, individuals aged 0 to 15 years, comprise approximately 42% of the 438 individuals sampled. Preliminary analysis of some overarching trends of the Baden population at Budakalász includes a relatively high level of early childhood mortality, a low growth rate for the population per the D30+/D5+ proportion, and that the proportion of 5 to 19 year olds over the age of 5 was around 30%. The cultural impacts of these trends are considered as is their role in evaluating and interpreting more complex demographic models. Potential biases in the Baden skeletal series and their effects on paleodemographic reconstructions are briefly addressed. This study aligns with other projects reconstructing prehistoric population dynamics, particularly projects within and around the Carpathian Basin in Europe.

Reconstructing manual physical activity in an early high-altitude Paleoindian settlement of the Peruvian Andes

FOTIOS ALEXANDROS KARAKOSTIS¹, HUGO REYES-CENTENO², MICHAEL FRANCKEN¹, KURT RADEMAKER³ and KATERINA HARVATI^{1,2}

¹Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoecology, ²DFG (Deutsche Forschungsgemeinschaft) Center for Advanced Studies "Words, Bones, Genes, Tools", Eberhard Karls University of Tübingen, ³Department of Anthropology, Michigan State University

Cuncaicha is a rockshelter site in the southern Peruvian Andes, which has yielded the oldest known (12.5 to 11.2 cal BP) high-altitude (4480 m asl) human occupation in the Andes. One of the excavated human individuals (15-06), a middle-aged female of relatively small body size dated to 8536-8386 cal BP, was found in association with three small tools. Importantly, she demonstrated a distribution of osteoarthritic lesions across her skeleton that might reflect body postures associated with crafting activities requiring precise manual labor. We tested this hypothesis through the application of a novel multivariate methodology for the analysis of muscle attachment surfaces (entheses). This new approach has been previously validated on the basis of uniquely documented anthropological samples, histological research, as well as blind experimental analyses using different animal species. Results show that individual 15-06 exhibits a distinctive enthesal pattern associated with precision grasping via thumb-index finger coordination, which is found

exclusively in documented lifelong precision workers (e.g. tailors). Our geometric morphometric analysis found that the enthesal area of *opponens pollicis* has an extremely high proportional projection, similar to hunter-gatherers from entirely distinct geo-chronological contexts (i.e., other early modern human hunter-gatherers from Eurasia). Overall, these results confirm that the lifestyle of this early high-altitude forager involved habitual and forceful precision grasping. Such hand movements would have been facilitated by her remarkable enthesal projection, which is naturally associated with greater moment arm and force-producing capacities for the attaching muscle.

This work was supported by the German Research Foundation (DFG-INST-37/706-1 FUGG and DFG-FOR-2237: "Words, Bones, Genes, Tools: Tracking Linguistic, Cultural, and Biological Trajectories of the Human Past").

The shape of the shape response of the human cranium to temperature

DAVID C. KATZ¹, MARK N. GROTE² and TIMOTHY D. WEAVER²

¹Cell Biology & Anatomy, University of Calgary Cumming School of Medicine, ²Anthropology, University of California, Davis

It is well established that in humans, genetic distances are correlated with distances based on cranial shape and form, indicating a substantial role for population structure in global skull diversity. Studies controlling for population structure have demonstrated underlying associations between cranial distances and ecological distances derived from some temperature variables. Typically, these correlations are stronger when populations from frigid climates are incorporated into the analysis, suggesting that the response of the skull to temperature variation may increase at the colder margin of human inhabitation. Here, we estimate the nature of the response to temperature variation in a global sample of recent human crania using a Bayesian mixed model for highly multivariate data to disentangle the effects of temperature and population structure. In preliminary analysis, we evaluated whether the temperature response was constant over the ecological range of the sample populations by fitting the model twice—once for the full sample ($n = 559$ from 25 groups), and once excluding the three coldest-climate groups from the analysis. The direction of the temperature effect is broadly similar with both samples. However, with the full sample, shape change per unit change in temperature is approximately 15% greater, and effect uncertainty is notably reduced. The current findings support the inference that the cranial shape response to temperature increases

ABSTRACTS

in magnitude in colder climates. We will also model these effects with a polynomial temperature predictor in order to capture the shape of the response.

This study was funded with generous support from the Wenner Gren Foundation (Dissertation Fieldwork Grant) and the National Science Foundation (DDIG; Award No. BCS-1232590).

A skeleton of *Homunculus patagonicus* Ameghino, 1891 from the Santa Cruz Formation (Early Miocene, Patagonia)

RICHARD F. KAY¹, JONATHAN M. G. PERRY², SERGIO F. VIZCAÍNO³ and M. SUSANA BARGO³

¹Evolutionary Anthropology, Duke University, Durham NC, ²Center for Functional Anatomy and Evolution, The Johns Hopkins University, Baltimore MD, ³División Paleontología Vertebrados, Museo de La Plata, La Plata, Argentina

Fossil platyrrhine postcranial bones are rare, usually fragmentary, and unassociated with cranial material. We report here the first skeleton with associated cranium and jaws of *Homunculus patagonicus*. The specimen, from ~17.5 Ma deposits of the Santa Cruz Formation, is the most completely preserved Early Miocene platyrrhine.

The skeleton resembles many similar-sized strepsirrhines and Eocene-Oligocene African anthropoids, but is unlike extant platyrrhines. The sacral canal suggests a long tail. The humerus and femur are more robust than in extant platyrrhines. Hip extensors reconstructed from the pelvis suggest rapid extension. The hip joint demonstrates modest capabilities for abduction; a deep and narrow knee joint suggests rapid extension. The humerus has a pronounced deltopectoral crest, a strong supinator crest, and a broad brachialis flange reaching almost halfway up the shaft, features especially resembling African early anthropoids. The mobile glenohumeral joint allowed substantial abduction. Collectively, the skeleton indicates that *Homunculus* was an arboreal quadruped with some leaping abilities, but limited suspensory abilities.

The type specimen of *H. patagonicus* is a mandible whereas that of the contemporaneous type of the former species *Killikakei blakei* is a cranial fragment. The new association of maxillary and mandibular teeth demonstrates unequivocally that the former *K. blakei* specimens are *Homunculus*. Many of the postcranial features enumerated above combined with previously known cranial and dental features support the conclusion that *Homunculus* was a stem platyrrhine not belonging to the extant Pitheciidae or Cebidae, as some propose.

PIP-CONICET 00781 to JCF and SFV, UNLP N867 to SFV and MSB, PICT 2013-0389 to SFV, and PICT 2017-1081 to MSB. Also NSF BCS 1348259 to RFK.

Evolution Education is not a (W)Rap: Creative Methods for Engaging the Public in Evolution Education Aren't Always Effective

CHLOE M. T. KECK¹, CHRISTOPHER D. LYNN² and WILLIAM EVANS³

¹Biological Sciences, The University of Alabama, ²Anthropology, The University of Alabama, ³Journalism & Creative Media, The University of Alabama

In this study, we tested a creative method of presenting evolution concepts and applications for a general public. We hypothesized that a creative approach (e.g., hip-hop performance) in teaching these concepts would be more effective than a traditional lecture. We randomly assigned a group of 44 undergraduate participants (ages 18 to 25) one of two conditions. Condition 1 was a hip-hop performance by Baba Brinkman, an artist specializing in educational concepts using creative settings. Condition 2 was a lecture by Jerry Coyne, an American biologist specializing in evolutionary principles. Before and after each condition, the participants completed a modified version of the Evolution Attitudes and Literacy Survey (EALS) in order to assess changes in knowledge and comprehension of evolutionary principles. During each condition, we measured emotional arousal via skin conductance using electrodermal sensors. To test our hypothesis, we conducted multiple linear regressions on post-test EALS factors (e.g., Knowledge of the Scientific Enterprise, Intelligent Design Fallacies, Evolutionary Misconceptions) with pre-test measures, condition, and emotional arousal as independent variables. We found that, after the Baba Brinkman performance, Knowledge of the Scientific Enterprise decreased, and Evolutionary Misconceptions increased ($p < 0.05$). After the Jerry Coyne lecture, Knowledge of the Scientific Enterprise increased, and Evolutionary Misconceptions decreased ($p < 0.05$). These results contradict our hypothesis, suggesting that more factors affect evolution education than simply format.

Anthropological study of the Bañolas mandible (Girona, Spain)

BRIAN A. KEELING¹ and ROLF QUAM^{1,2,3}

¹Anthropology, Binghamton University, ²Evolución y Comportamiento Humanos, Centro UCM-ISCIII, ³Anthropology, American Museum of Natural History

The Bañolas mandible was the first fossil hominin specimen ever discovered in Spain and has received sporadic attention ever since its discovery in 1887. Researchers have tended to emphasize the presence of generally archaic features in this specimen or closer affinities with Neandertals, mainly based on the perceived absence of chin structures. Recently, the mandible has been dated to the Late Pleistocene (66 ± 7 kya). The present study re-examines the Bañolas mandible relying

on 3D geometric morphometrics (GM), including 22 landmarks that capture overall mandibular shape, and the comparative analysis of 15 morphological features. Bañolas is compared with Middle and Late Pleistocene members of the genus *Homo* as well as a recent *H. sapiens* sample. The results of the 3DGM analysis demonstrated that Bañolas falls slightly closer to the centroid of the pooled *Homo sapiens* sample (i.e. Pleistocene and recent) than to the Neandertals. Regarding the morphological features, Bañolas shows a regular (i.e. non-truncated) gonial profile, a mental foramen placed under the P_4 and an absence of a retromolar space. The anterior symphysis is largely vertical (94°) and shows a slight degree of curvature (incurvatio mandibulae), but lacks other structures (e.g. mental trigone, symphyseal tubercle) associated with the modern human chin. The results of the present study suggest a need to reconsider the taxonomic affinities of this enigmatic fossil specimen.

Genetic ancestry and demographic history of a rural Caribbean village

MONICA H. KEITH¹, HARLY J. DURBIN², TROY N. ROWAN², GREGORY E. BLOMQUIST¹, MARK V. FLINN³, JERRY F. TAYLOR² and JARED E. DECKER²

¹Department of Anthropology, University of Missouri, ²Division of Animal Sciences, University of Missouri, ³Department of Anthropology, Baylor University

The Caribbean is a genetically diverse region with distinctive local histories of admixture related to European colonization and the transatlantic slave trade. The Commonwealth of Dominica is a small, mountainous island historically known to have unique pockets of ancestry and population structure. Using high-density genotype data from 160 people, we characterize genetic structure and historical admixture in a relatively isolated, rural village in the most remote part of the island along the eastern coast. Variational Bayesian inferences in fastSTRUCTURE indicate that there are 4 genetically distinct family clusters in this village of approximately 500 current residents, each with a unique pattern of admixed haplotypes and ancestry proportions. Global comparisons with the Human Genome Diversity Project data show that the majority of genetic variation for most villagers is of recent West African origin, with varying admixture from French colonists and indigenous Caribbean ancestry. Analyses in fastSTRUCTURE, TreeMix, ALDER, and principal component analysis support historical accounts that some of the most isolated interiors of the Lesser Antilles were settled by people fleeing enslavement on sugar plantations in the 18th century. Our localized analyses show how migrations, demography, and island ecology have interacted to shape current patterns of genetic variation. Additionally, detailed knowledge of the village's population structure provides essential

ABSTRACTS

context for interpreting patterns of genetic variation as they relate to phenotypic variation. Future genotype-phenotype and genetic mapping analyses will address how genetic variation influences health phenotypes of local concern in this Caribbean village.

This research was funded by the University of Missouri Research Board.

A “trophy” head individual found at the Middle Horizon site of Huaca del Loro in the Las Trancas Valley of Nasca, Peru (A.D. 600-1000)

CORINA M. KELLNER¹, CHRISTINA A. CONLEE² and ALDO NORIEGA³

¹Anthropology, Northern Arizona University,

²Anthropology, Texas State University, San Marcos,

³Proyecto Huaca del Loro, Las Trancas, Nasca, Peru

Huaca del Loro was the largest site in the entire Nasca drainage of southern Peru during the Middle Horizon (A.D. 600-1000). Recently, modern excavations were undertaken to understand the role Huaca del Loro played in the Nasca-Wari relationship. Wari and Nasca were well known to each other and shared ceramic styles and possibly ideology. The Wari entered the Nasca drainage during the Middle Horizon and built at least three compounds: Pacheco, Pataraya, and Inkawasi. Excavations in the 1950s and earlier suggested that Huaca del Loro could have been a local site of resistance or a Wari imperial outpost. In summer 2019, we uncovered a D-shaped temple, which is one of the first identified in coastal Peru. Material culture associated with the Wari architecture consists of local Loro ceramics, Wari style offerings, and limited amounts of Wari imperial ceramics. In the large habitation area, excavations uncovered *quincha* (cane) architecture in the local style along with Loro ceramics, suggesting this area was occupied by local people although future excavations are necessary to assess the nature of this sector. In a communal tomb in the elite area of the site, we found a “trophy” head individual buried with at least three other adults. This individual is stylistically aligned with local Nasca people and suggests that even with significant Wari influence at the site, the Nasca were able to continue and control an important cultural behavior.

National Science Foundation Senior Archaeology Award 1758084 to CMK and CC

Being Nose-y: Dissecting out the influences of climate and energetics on human nasal anatomy

ALEXA P. KELLY¹, CARA OCOBOCK² and SCOTT D. MADDUX¹

¹Center for Anatomical Sciences, UNT Health Science Center, ²Department of Anthropology, University of Notre Dame

Narrower nasal airways enhance inspiratory air-conditioning in cold-dry climates. Yet, cold-dry environments are also metabolically expensive, demanding greater oxygen intake than tropical environments. Thus, it has been hypothesized that climate-mediated nasal narrowing may necessitate a compensatory increase in nasal height to ensure the airways remain large enough to transmit a metabolically adequate volume of oxygen. To test this, we collected 17 linear measurements from the nasal skeleton of modern humans from 10 climatically diverse geographic areas (Arctic Circle, Europe, Iran, Australia, North Africa, Khoisan, South African Bantu, East Africa, West Africa, Papua New Guinea). Measurements of associated postcranial elements were then used to estimate body mass and basal metabolic rate (BMR) for each individual. Climatic data were similarly collected for each geographic provenance and employed with morphological data in multivariate analyses. Our results indicate that most measurements of nasal complex breadth are significantly correlated with climate (all r -values >0.45 , all p -values <0.009), but not BMR. Conversely, nasal height is more strongly correlated with BMR ($r=0.47$, $p=0.02$) than climate. Additionally, overall nasal passage area demonstrated a positive association with BMR ($r=0.74$, $p=0.0007$), while nasal passage shape exhibited a significant relationship with climate ($r=0.52$, $p=0.0017$) with taller/narrower airways found in colder-drier environments. Our results support assertions that nasal narrowing necessitates an increase in airway height to meet energetic demands. These results are also consistent with established ecogeographic patterns of body size/shape. Thus, future research employing larger and more diverse samples appears poised to provide far-reaching insights regarding climatic adaptation during human evolution.

Correlative Relationships between Dental Metrics and Primate Life History

CHRISTA D. KELLY

Anthropology, University of Arkansas

Across primates, dental development is correlated with life history traits. Phylogenetic least squares models were computed to determine if a relationship exists between relative tooth size and nine life history traits (time to sexual maturity, gestation length, weaning age, litter size, number of litters per year, interbirth interval, birth weight, adult weight, and maximum longevity). Tooth size of each mandibular tooth was collected from adult specimens ($n = 1234$; 22 genera; seven families). A ratio of tooth size to a geometric mean of three cranial interlandmark distances was used to calculate relative tooth size; males and females were considered separately. Life history traits are found to be highly conserved phylogenetically, with most relationships between relative tooth size and life history traits explained by the

phylogenetic relationships (i.e., most feature λ values above 0.9). However, gestational length (males, $p = 0.04$; females, $p = 0.01$), number of litters per year (males, $p = 0.03$; females, $p = 0.03$), and birth weight (males, $p < 0.001$; females, $p < 0.001$), were significantly associated with the relative size of the second molar in both sexes. Additional significant relationships were observed but only in one sex or the other. These results indicate that relative tooth size, like dental eruption sequence, is phylogenetically conserved. However, correlative relationships with life history traits persist, indicating the possible use of relative tooth size in the reconstruction of fossil life histories.

Sub-regional Variability in East Turkana Mammalian Communities

MADELEINE G. KELLY¹, MARYSE D. BIERNAT², AMANDA MCGROSKY², DAVID R. BRAUN³, NEIL T. ROACH¹ and DAVID R. PILBEAM¹

¹Human Evolutionary Biology, Harvard University,

²Institute of Human Origins, School of Human

Evolution and Social Change, Arizona State

University, ³Center for Advanced Study of Human

Paleobiology, The George Washington University

Reconstructing East African paleoenvironments is important for contextualizing hominin evolution and improving our understanding of the selective pressures that drove the unique adaptations of the hominin lineage. One widely used proxy for inferring East African paleoecology is faunal assemblages. Previous analyses have indicated a general trend towards increasingly open, seasonally arid environments, which is thought to be driven by greater climatic variability and a general pattern of cooling in the Pleistocene. However, evidence also suggests that environments, especially around the Turkana Basin, were regionally variable in the proportion of open grassland to closed woodland ecosystems. To infer aspects of regional variability in East African paleoenvironments, we compared three sub-regions within the Koobi Fora Formation – Ileret, Karari, and Koobi Fora – using the fossil mammal record of the Upper Burgi, KBS, and Okote Members. Faunal data were collected from the Turkana Basin Public Database and supplemented with original collections from 2019 field research. Ancient faunal communities were reconstructed through two correspondence analyses – one using faunal abundances and a second incorporating dietary and locomotor functional traits – to determine the ecological context of East Turkana fossil mammals based on comparisons to extant African mammal communities. Results suggest that mean annual precipitation is the primary impetus of community variation between East Turkana sub-regions. Karari was slightly drier than both Ileret and Koobi Fora. This supports the

ABSTRACTS

hypothesis that hominins are adapted to living in highly variable environments and suggests that water availability may have played a role in mammal community evolution.

This research was supported by NSF REU #1930719 and NSF ARCH #1624398.

Markets and mycobacteria – a bioarchaeological analysis of the influence of urbanization on leprosy and tuberculosis in Denmark (AD 1200-1536)

SAIGE KELMELIS¹, VICKI R. KRISTENSEN², METTE ALEXANDERSEN² and DORTHE DANGVARD PEDERSEN^{2,3}

¹Anthropology, University of South Dakota, ²ADBOU, University of Southern Denmark, ³Anthropology, The National Danish Museum

Tuberculosis (TB) and leprosy are two infectious diseases often associated with urbanization that can be observed in archaeological samples through systematically examined skeletal indicators and statistical probabilities. To test whether TB and leprosy frequencies were influenced by growing trends of urbanization in medieval Denmark, skeletons from thirteen cemetery samples (n = 1546) were examined and characterized into varying urban levels based on historic and archaeological evidence. Disease frequencies were estimated using a probabilistic approach based on sensitivity and specificity measures of six lesions associated with TB and six associated with leprosy. There were statistically significant differences in leprosy frequencies between urban levels with rural and transitional urban sites having the highest frequencies. While TB frequencies were higher overall, there were no significant differences between urban levels. Leprosy lesion counts showed that facial lesions were observed less than post-cranial lesions among the samples, while TB lesions were more often observed in the hip and vertebrae. For individual sites, leprosy was highest in rural Sct. Alberts (28%), rural Sejet (18%), and transitional urban Ole Wormsgade (22%) with other sites ranging from zero to six percent. For TB, sites with the highest frequencies were rural Sct. Alberts (100%) and urban Sct. Drotten (73%) with remaining sites from seven to 59 percent. The findings suggest the presence of leprosaria in urban settlements may have led to fewer individuals with visible lesions being buried non-leprosaria cemeteries. Comparatively higher TB frequencies may reflect increased contact through widening economic networks between urban and rural communities.

This research was financed by the NSF Biological Anthropology DDIG (#1825362), the Wenner-Gren Foundation (Gr. 9604), the American-Scandinavian Foundation, the Velux Foundation (VELUX 32089), and the Independent Research Fund Denmark.

Mechanics of leaping between vertical supports in a small arboreal quadruped (*Cheirogaleus medius*)

ADDISON D. KEMP, GABRIEL S. YAPUNCICH and ANGEL ZEININGER

Evolutionary Anthropology, Duke University

Specialized vertical clingers and leapers achieve long leaps via anatomical adaptations that increase their velocity at take-off and the use of take-off angles (mean ~45°) that maximize horizontal leap distance relative to downward displacement. Studies of leaping in more generalized arboreal quadrupeds have not evaluated how these species approach leaps between vertical supports, though less specialized primates also engage in this behavior. Here we test the hypothesis that when leaping between vertical supports, species lacking vertical clinging and leaping adaptations will increase take-off angle and/or exhibit leap trajectories characterized by increasing downward displacement to achieve longer leaps. Five captive *Cheirogaleus medius* were recorded leaping self-selected distances (30-75cm) using a high speed camera (n=40 leaps) at the Duke Lemur Center. Leap distance, velocity, take-off angle, trajectory and landing posture were then analyzed using DLT data viewer.

C. medius take-off angles (5-38°) were significantly lower than those recorded by other studies for VCL specialists, though individuals did use higher angles when leaping longer distances (p<0.05). Take-off angle, but not initial velocity, also significantly affected leap trajectory (p<0.05). While specialized leapers land with their hindlimbs, *C. medius* landed with their forelimbs in all trials analyzed. The exclusive use of forelimb first landing on vertical supports has not been reported during leaping in other primates. These results suggest that small generalized primates may employ a different strategy for leaping between vertical supports involving lower take-off angles and, perhaps as a function of that low angle, forelimb first landing.

This work was funded by NSF BCS-1650734.

Global variation in dental crowding

DORI E. KENESSEY, TATIANA VLEMINCQ-MENDIETA, G. RICHARD SCOTT and MARIN A. PILLOUD

Department of Anthropology, University of Nevada, Reno

Pilloud (2018) recently defined crowding as a deviation in the ideal alignment of teeth as a result of rotation and/or displacement. In this investigation, a scoring system for crowding was devised using a 3-point scale for the anterior teeth (incisal and lateral). However, data were not provided as to population variation in dental crowding. Here, we expand on this work to investigate the global variation of this defined trait. Data were collected from four modern major world regions (Africa,

Australia, Asia, and North America) and nine samples (Australian White, US White, US Black, US Hispanic, South African Coloured, South African Black, Japanese, Chinese, and Native American; n=990). Crowding data were collected from casts of living individuals and skeletal remains; photographs were also consulted. Grade 2 was used as the breakpoint to obtain frequencies representative of regional patterns. A chi-square analysis was run to test for population differences.

Results of maxillary crowding show Australian Whites, US Whites, US Blacks, US Hispanics, South African Coloured, and South African Black groups displayed low crowding frequencies (0-14%). Conversely, the Chinese, Japanese, and Native American samples exhibited high frequencies of crowding (15%+). In the mandible, Australian Whites showed low crowding frequencies, while all other samples exceeded the frequency of 15%. Statistical tests indicate the sample differences are significant. While there is population variation observed in dental crowding, the assessment of more populations from the archaeological record (pre-orthodontic treatment) will help to establish a more comprehensive picture of global crowding variation.

The taxonomic efficacy of the macaque innominate

BRITTANY KENYON-FLATT and NOREEN VON CRAMON-TAUBADEL

Department of Anthropology, University at Buffalo

Recent research suggests that the innominate is a particularly reliable region of the primate postcranium for assessing taxonomic relationships. However, much of this work has assessed inter-generic taxonomy, leaving open the question of the accuracy of intra-generic taxonomic assessment. The genus *Macaca* provides a good model for testing this question, given that macaques are highly speciose and have the widest geographic range of any primate genus aside from humans. Here, we tested the hypothesis that the innominate accurately predicts intra-generic taxonomy in macaques using a large sample (n=230) representing nine species; *M. fascicularis*, *M. mulatta*, *M. fuscata*, *M. arctoides*, *M. radiata*, *M. nigra*, *M. nemestrina*, and *M. sylvanus* and a Colobine outgroup (*Trachypithecus cristatus*). 3D scans of the innominate were taken using an HDI structured light scanner and 28 landmarks were applied to the scans to capture overall form. Following Procrustes superimposition, Canonical Variates Analysis (CVA) was performed and a Procrustes distance matrix was extracted and subjected to 2D multidimensional scaling (MDS) to visualize average group affinities. The results of both analyses showed clear differences between the *Trachypithecus* outgroup and macaques, as well as between *M. sylvanus* and *M. nigra* and all other macaques. While there was substantial overlap

ABSTRACTS

in shape variation among macaques, the pattern of among-species affinity broadly matched that expected based on their phylogenetic history. In general, therefore, the results support the hypothesis, although it remains to be tested to what extent convergent behaviors or environmental factors might influence the pattern of morphological variation among macaque species.

This research is supported by a National Science Foundation Grant (NSF BCS-1830745), Field Museum Visiting Researcher Fellowship, Primate Research Institute Cooperative Research Grant, and the Mark Diamond Research Fund (SP-18-13).

A comparative analysis of CT and surface scan 3D models of fossil primate dentition using dental topographic metrics

WAQQAS KHALID, ANDREW C. HOLMES and DAVID R. BEGUN

Anthropology, University of Toronto

Three-dimensional (3D) models of primate dentitions are useful for learning about the behavior and phylogeny of extinct primate species. In particular, 3D dental topographic analysis has been extremely valuable in determining how tooth morphology can be a quantifiable method of estimating dietary type. The three metrics commonly applied are Relief index (RFI), Dricplet-Normal Energy (DNE), and 3D-Orientation Patch Counted Rotated (OPCR). These metrics can be applied to CT scans and surface scans of fossils or casts. We sought to verify the accuracy of these measures between scanning methods. To do this, we compared these metrics between surface scans of both high resolution resin casts and fossils, and CT scans of fossils. We used models created from CT-scans of the lower four cheek teeth (M3, M2, M3, and P4) of *Anapithecus henyaki* and surface scans of the same specimens created by an Enhanced Light Scanner. Each tooth was cropped and smoothed in Avizo and analyzed in Morphotester. The Morphotester analysis showed no significant difference in values obtained for all three metrics. This suggests that surface scans of casts and fossils provide similar values as CT scans made from the original specimens. We conclude that researchers can use high quality casts and surface scans for RFI, DNE, and OPCR measures when access to CT scans and fossils is limited.

Genomic and phenotypic diversity of antibiotic resistant *Escherichia coli* isolated from the gut microbiome of non-industrial populations

SHARMILY KHANAM¹, NISHA B. PATEL¹, LINDSEY O'NEIL¹, ALEXANDRA OBREGON-TITO^{2,3}, RAUL TITO^{2,3}, EMILIO GUIJA³, LUZMILA TRONCOSO³, LUIS

MARTIN⁴, CHRISTINA WARINNER^{2,5,6}, CECIL M. LEWIS² and KRITHIVASAN SANKARANARAYANAN¹

¹Department of Microbiology and Plant Biology, University of Oklahoma, ²Department of Anthropology, University of Oklahoma, ³Universidad Científica del Sur, Lima, Peru, ⁴Centro Nacional de Salud Pública, Instituto Nacional de Salud, Lima, Peru, ⁵Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Germany, ⁶Department of Periodontics, University of Oklahoma Health Sciences Center

We are now in an era of antibiotic resistance and in noticeable danger of a post-antibiotic age. Recent increases in incidence and severity of antibiotic resistant bacteria, especially in clinical contexts, has been attributed to the widespread use of antimicrobial chemicals in healthcare, agriculture, and our sanitized built environments. However, very little is known about the extent of antibiotic resistance in human-associated microbial ecologies prior to industrialization. Here, we report the recovery and characterization of antibiotic resistant *Escherichia coli* from the distal gut microbiome of a non-industrial antibiotic naïve population in South America. These *E. coli* strains belong to seven distinct genomic clades, and show acute resistance to the antibiotics Ampicillin, Chloramphenicol, Erythromycin, and Doxycycline. No resistance was observed against the synthetic antibiotics Ciprofloxacin and Ceftriaxone. Genomic analysis of these strains identified markers correlating with resistance to specific antibiotics including TEM-1 beta lactamase (Ampicillin), and the *tetC* efflux protein (Doxycycline). Among the strains resistant to Chloramphenicol and Erythromycin, no mechanisms known to confer acute resistance including antibiotic inactivation (chloramphenicol acetyltransferase) or target alteration (ribosomal methylation genes) were identified. While non-specific multi-drug efflux pumps such as *acrAB*, and *mdtEF*, are observed in these strains, they are ubiquitous in their occurrence in *E. coli*. Overall, these results suggest the presence of potential novel mechanisms underlying Chloramphenicol and Erythromycin resistance in these non-industrial *E. coli* isolates. Further, our study highlights the necessity for increased characterization of antibiotic resistance in non-industrial and non-clinical environments.

Evolution of pelvic list, hip adduction, and step width in hominins

MICHELLE KIKEL, RACHEL GECELER, RACHANA KELSHIKAR and NATHAN E. THOMPSON

Anatomy, NYIT College of Osteopathic Medicine

Human bipedal walking entails unique frontal plane balance strategies compared to other primates. Compared with bipedal chimpanzees, humans walk with step widths that are proportionally three times narrower, utilize stance-phase hip adduction rather than abduction, and use a

pattern of pelvic drop on the swing side rather than swing-side pelvic elevation. The degree to which step widths and pelvic motion are directly related remains unknown. We sought to determine if and how the human-like pattern of pelvic and hip motion is related to step width. Ten human subjects walked on a treadmill at narrow (~0 cm), normal, and wide (~3X normal) step widths. Full body kinematics were measured using the Plug-In Gait marker set with a 12-camera Vicon motion capture system.

Our results show there is a predictable change in hip adduction with step widths; narrow steps produced the highest adduction (~ +1°), while wide steps produced abduction (~ -8°). All step width conditions produced the same pattern of pelvic motion; swing-side pelvic drop. Wide steps resulted in an overall decreased range of pelvic motion compared with the normal and narrow condition (~3°). These results suggest that though hip adduction is highly correlated with step width, changes in step width alone are insufficient to explain the unique human-like pattern of stance-phase pelvic drop. The change to pelvic drop on the swing side in humans and perhaps some early hominins likely evolved independently, and not as a direct result of the emergence of valgus knees and narrow step widths.

This research is funded by the National Science Foundation Grants SMA 1719432

Shifting sleep ecologies among foragers: An intra-community comparison of village and forest sleep of BaYaka foragers from the Congo

ERICA KILIUS¹, DAVID SAMSON¹, SHEINA LEW-LEVY², MALLIKA SARMA³, LEE T. GETTLER³, ADAM BOYETTE⁴, VALCHY MIEGAKANDA⁵ and YANN RL. OUAMBA⁶

¹Department of Anthropology, University of Toronto Mississauga, ²Department of Psychology, Simon Fraser University, ³Department of Anthropology, University of Notre Dame, ⁴Department of Human Behaviour, Ecology, and Culture, Max Planck Institute for Evolutionary Anthropology, ⁵Institut National de Sante Publique, ⁶Ecole Nationale Supérieure d'Agronomie et de Foresterie (ENSAF), Université Marien Nguabi

Background: Sleep research has largely been conducted in Western, industrialized societies, where sleep disturbances are attributed to technological disruption and societal demands for work. Little is known, however, about sleep patterns in hunter-gatherer populations, who are less buffered from aspects of their natural ecology and whose cultural ecologies may differentially affect sleep. We conducted a naturalistic sleep study to investigate sleep patterns in the BaYaka, a semi-nomadic, non-industrial forager population in Republic of the Congo. Sleep patterns were characterized during two seasons of different subsistence activities within a community.

ABSTRACTS

Methods: Participants were recruited from a village (S1) and a forest camp during fall fishing and caterpillar season (S2). Non-invasive CamNTECH Motion8watch actigraphy devices were worn by individuals for ~7 days each season. Sleep data was scored on MotionWare software and analyzed to determine sleep characteristics.

Results: Sleep duration showed minimal variation but was low across seasons (S1 mean= 5.58 hrs, SE=0.1; S2 mean= 6.09 hrs, SE=0.09) as was sleep efficiency (mean= 64% vs 68%). Sleep onset and wake time differed markedly; in the village, participants fell asleep on average 41 minutes later and woke 49 minutes later compared to the forest. Sleep latency was higher in the village than the forest location (S1 mean= 0.34 hrs, SE=0.04; S2 mean= 0.18 hrs, SE=0.03).

Significance: Results demonstrate that the BaYaka overall exhibit short and fragmented sleep duration, and sleep timing differs by seasonal subsistence activities. Understanding the diversity of human sleep lends insight into the role of sleep in our evolution.

This research was supported by the Social Sciences and Humanities Research Council of Canada.

Late Miocene *Oreopithecus bambolii* Maxillary Molar Morphology Scores Compared to Extant African Apes

ALEXANDER KIM and FRANK L. WILLIAMS
Department of Anthropology, Georgia State University

Late Miocene *Oreopithecus bambolii* is characterized as exhibiting tall crested molars, which resemble cercopithecoid bilophodonty while remaining similar to the apes by exhibiting a larger paracone and protocone relative to the distal cusps. Based on convergent adaptations related to folivory, *Oreopithecus* should align more with *Gorilla gorilla*, compared to *Pan troglodytes*. Using Pilbrow's Great Ape Dental Scoring System, we examined the morphology of the first maxillary molars of *Oreopithecus bambolii* specimen IGF 11778, *Pan troglodytes* (n = 16) and *Gorilla gorilla* (n = 11). On the first canonical scores axis, all three taxa are largely separate with minor overlap between *Pan* and *Gorilla*. *Oreopithecus* is situated on the negative extreme of the first axis (86.1% of variance) based on the scores for the sulcus obliquus, and to a lesser extent, by the crista obliqua whereas *Gorilla* is polarized on the positive end by its mesial fovea and centroconule scores, followed by the anterior transverse crest, whereas *Pan* falls within these extremes. On the second axis (13.6% of variance), *Oreopithecus* overlaps with *Gorilla* based on the crista obliqua and anterior transverse crest, whereas *Pan*, and some *Gorilla*, are projected in a negative direction from their distal fovea, anterior transverse crest and hypocone essential crest scores. *Oreopithecus* is more distinctive from the African apes than *Pan*

and *Gorilla* are from each other. This taxon resembles *Gorilla* in such traits as the sulcus obliquus and crista obliqua, which contribute to the crest morphology of the molars, and presumably represents dietary adaptations for folivory.

Geumgwan Gaya (A.D. 43-532) Social Structure as Revealed from Funeral Practices at the Yean-ri Tombs, Gimhae, Republic of Korea

MIN-SU KIM¹, JAE-HYUN KIM¹, YEON-KYUNG PARK¹, KATHERINE I. HARRINGTON² and CHRISTOPHER J. BAE²

¹Department of Archaeology and Art History, Dong-A University, ²Department of Anthropology, University of Hawai'i at Mānoa

Excavations of ancient tombs in Yean-ri, Gimhae, located in the southern part of the Korean peninsula led to the discovery of 210 sets of human remains in variable condition. The Yean-ri tombs is an important site that has contributed to a deeper understanding of the funeral practices during the Geumgwan Gaya period (A.D. 43-532), which is a part of the broader Korean Three Kingdoms Period (57 B.C. – A.D. 668). The conventional norm in Korea is that all past Korean societies operated under a patriarchal system. However, through an analysis of the Yean-ri tombs we find this may not have always been the case. Using biological classifiers (sex and age) and grave goods (presence/absence of certain artifact types) from the Yean-ri tombs, we were able to reconstruct the social and hierarchical systems. These data were then compared over time (seven temporal divisions) to document changes in the social structure. Of the 210 individuals, 115 were in good enough condition for sex estimation (50 males, 65 females). The results indicate that over time the proportion of women and men in the cemetery remain constant, and that there is no clear difference in the types of grave goods between the sexes. An exception to this was that more women with grave goods are present in periods II and III, representing 64%-72% of the total number of graves with artifacts. We draw the conclusion that during the Geumgwan Gaya period, the society did not necessarily follow a clear patriarchal system.

Human health and adaptation along Silk Roads- a bioarchaeological investigation of Medieval Uzbek cemeteries

REBECCA L. KINASTON¹, LADISLAV DAMASEK², ROBYN KRAMER¹, JAN KYSELA², ANNA AUGUSTINOVÁ², MARKETA SMOLKOVA² and DANIEL PILAR²

¹Anatomy, University of Otago, Otago School of Medical Sciences, Dunedin, New Zealand, ²Institute for Classical Archaeology, Charles University, Prague, Czech Republic

Central Asia was a hub of economic and cultural interaction that flowed along the Silk Roads - vast overland trade networks that linked East Asia, the Middle East and Europe. During the Medieval period (ca. 2nd-16th c. CE) these networks famously facilitated the trade of material items, such as glazed pottery and lapis lazuli, which can be found in the archaeological record. However, little is directly known about the people who lived along the Silk Roads and how this vast interconnected network directly influenced diet, health and day-to-day living.

This paper presents the results of one of the first comprehensive bioarchaeological investigations focused on Medieval and other cemeteries in southwest Uzbekistan, including a possible double soldier burial that may be associated with the Hellenistic Period in the region (late 4th and 3rd c. BC). Individuals interred in two cemeteries (Bobolangar and Tell Garden) dating to the High Medieval Period (1000-1150 CE) and one later cemetery (Lungi Tepa) display a high prevalence of systemic disease, trauma and a large variation in body size. The aim of this research is to understand how people adapted to the harsh desert environment, procured their food, interacted with surrounding communities and cared for their sick and disabled in the context of the first globalised trade network. The research uses a biocultural approach that incorporates traditional osteological methods, ancient DNA and isotope analyses. These results are interpreted within current theoretical frameworks in Anthropology, including Niche Construction Theory and the Bioarchaeology of Care Model.

This research was funded by a University of Otago Out-of-Season Research Grant (UORG).

Bone strength and bone maintenance from femoral cross-sectional geometry in a Medieval Italian population (10th-12th centuries AD)

KATHERINE M. KINKOPF^{1,2}, SABRINA C. AGARWAL^{1,2}, VALENTINA GIUFFRÀ³ and GIULIA RICCIONI³

¹Anthropology, University of California Berkeley, ²Archaeological Research Facility, University of California Berkeley, ³Division of Paleopathology, University of Pisa

Bone loss has often been framed an inevitable aspect of aging and various studies have found sex- and age-based trends in bone maintenance and loss across modern, historic, and prehistoric populations. We present the results of femoral cross-sectional geometry in a rural Medieval Italian archaeological sample at the Pieve di Pava (n=92) in Southern Tuscany. The Pieve di Pava was a rural parish church located in the disputed area between the Diocese of Siena and Diocese of Arezzo during the Early Medieval Period and was continuously used from the 7th century BC through the medieval period. Both sexes show an

ABSTRACTS

age expected increase in medullary area; however, total area also increases with age and cortical area is therefore maintained, indicating that both males and females experienced endosteal bone loss and periosteal bone apposition in the femur. Our results show no significant sex difference in medullary area, total area, or cortical area; both sexes maintain both strength (Z_p and J) with increased age. These results suggest that bone loss in the rural medieval population of Pava may not accompany an overall decrease in bone strength, and that intensive physical activity associated with rural medieval lifestyle may help maintain bone strength in old age despite cortical bone loss. We discuss these results in the context of evidence for intraskeletal bone maintenance in this sample, and in other historic populations.

Stahl Graduate Research Grant, Archaeological Research Facility University of California Berkeley, Stahl Faculty Grant, Archaeological Research Facility University of California Berkeley

A comparison of axial rotation of the trunk during bipedal walking between human, white-handed gibbon and Japanese macaque

YUKI KINOSHITA¹, RYOSUKE GOTO², YOSHIHIKO NAKANO² and EISHI HIRASAKI¹

¹Primate Research Institute, Kyoto University,

²Graduate School of Human Sciences, Osaka University

In human walking, coordinated out-of-phase axial rotations of the thorax and pelvis is important for cancellations of angular momentum. It has long been thought that this rotational capability is a distinctive feature of humans because great apes, which have rigid and immobile trunk, seem to lack the ability of the thorax to counter axial pelvic rotations. However, Thompson et al. (2015) showed that chimpanzees also counter-rotate their thorax relative to the pelvis during bipedal walking, raising a question about the origins and development of this characteristics. In this study, we measured the axial rotation of the upper thoracic, lower thoracic, lumbar, and pelvic regions during bipedal walking in six humans, a white-handed gibbon and five Japanese macaques, to investigate if the axial rotations between thorax and pelvis are observed in non-hominid primate species. Our results showed that the thorax of the gibbon and Japanese macaques moves in phase with the pelvis, but there were as much counter rotations between the thorax and the pelvis as humans, suggesting that relative rotation is not unique to the hominid lineage, but a characteristics which is generated by mechanical requirements of bipedal walking such as the reduction of angular momentum. Given for the increased number of lumbar vertebrae in Japanese macaques and gibbons compared to chimpanzees, their lumbar region likely to have larger rotational capability.

However, the total range of motion between the thorax and pelvis is similar in these three species, indicating the existence of optimum trunk rotational amount during bipedal walking.

Reconstructing Vegetation Changes in Response to Holocene Climatic Variability in East Turkana, Kenya

RAHAB N. KINYANJUI¹, EMMANUEL K. NDIEMA¹, PURITY W. KIURA², DAVID BRAUN³, JACK W. HARRIS¹ and MARION K. BAMFORD⁴

¹Earth Sciences, National Museums of Kenya,

²Sites and Monument, National Museums of Kenya,

³Center for The Advance Study of Human Paleobiology (CASHP), George Washington University,

⁴Evolutionary Science Institute (ESI), The University of Witswatersrand

During Holocene East African region experienced rapid climatic events, driven principally by orbital forcing and the monsoon insolation. The most prominent event is the African Humid Period (AHP) (~10ka to 8ka). Mid-Holocene (~8ka to 5ka) was characterized by rapid shifts between wetter and drier climates. Dry climates have so far been consistent since late Holocene to present. Archaeological evidence from the Holocene Galana Boi deposits, indicate changes in subsistence activities from hunting, gathering and fishing during the early Holocene wetter period, to pastoralism in the mid-late Holocene period. Little is known about the vegetation structure and the response to changing climates. This paper presents phytolith data analysed from five Holocene sites occupied during different time periods: FxJj108 (~9.6ka~6ka), FxJj27 (~9.3ka to ~4.2ka), GaJj4 (~4.2ka), FwJj25 (~4.2ka to ~1.34ka) and FwJj5 (~0.93ka). Although phytolith counts were low, especially grass short silica cells (GSSCs), it was possible to identify changes in vegetation cover. Our data show that Holocene vegetation structure was generally dominated by woodlands/shrublands with some grasslands. Early- and mid-Holocene assemblages had significant proportions of aquatic indicators: palms, sedges, sponge spicules and diatoms indicating existence of riverine/riparian habitats with fresh/spring water resources and episodes of seasonally. Late Holocene assemblages indicate grasslands dominated by Chloridoideae grasses that have persisted to present. lph index shows high variation during the mid-Holocene period while the D:P indices have shown tree cover was moderately to highly dense, which resembles Sudanian vegetation structure (grassy woodlands). The results concur with previous studies, that Holocene climates were highly variable.

We would like to acknowledge the following grants NSF Archaeology Technological origins archaeology grant (#1624398) and supplemental REU #1930719 who have made this work possible

Variation in craniodental pathologies among cercopithecoid primates

CLAIRE A. KIRCHHOFF¹, SIOBHÁN B. COOKE^{2,3}, D. REX MITCHELL⁴ and CLAIRE E. TERHUNE⁴

¹Biomedical Sciences, Marquette University,

²Center for Functional Anatomy and Evolution,

Johns Hopkins School of Medicine, ³New

York Consortium in Evolutionary Primatology

Morphometrics Group, ⁴Anthropology, University of Arkansas

Testing how pathologic changes to the dentition covary with temporomandibular joint (TMJ) pathology will improve our understanding of masticatory function and dysfunction. Pathology rates are well documented for humans, but not for many other primate species. We compare the rates of craniodental lesions in six primate species: *Macaca fascicularis* (n=109), *Cercopithecus mitis* (n=65), *Theropithecus gelada* (n=13), *Nasalis larvatus* (n=54), *Colobus polykomos* (n=64), and *Papio anubis* (n=76). Each adult specimen was evaluated for TMJ osteoarthritis, antemortem tooth loss, periodontal disease, dental caries, pulp cavity exposure, dental abscesses, tooth crowding/malocclusion, and other craniofacial traumata and pathologies using standard criteria. Fisher's exact tests for sex and species differences as well as variation in pathology rates for animals with and without TMJ osteoarthritis were carried out in SPSS. Results identified sex differences only in the rate of antemortem tooth loss (p=0.004) and pulp cavity exposure (p=0.001) for *P. anubis*. There were several differences in pathology rates for monkeys with versus without TMJ osteoarthritis, including antemortem tooth loss (*Macaca*, p=0.011; *Cercopithecus* p=0.04), periodontal disease (*Macaca*, p=0.002; *Nasalis*, p=0.039), pulp cavity exposure (*Macaca*, p=0.002; *Cercopithecus*, p=0.004; *Nasalis*, p=0.001; *Papio* males, p=0.003; *Papio* females, p=0.025), dental abscesses (*Macaca*, p=0.002; *Papio* males, p=0.015; *Papio* females, p=0.019), and other craniofacial traumata (*Nasalis*, p=0.041). Also of note are differences in lesion rates between taxa, where baboon males generally sustain higher lesion rates relative to the other cercopithecoids included in this study. Future directions for this project include relating lesion rates to diet, social structures, mating strategies, and craniofacial/dental morphologies.

Funding provided by the National Science Foundation, award numbers: NSF BCS-1551722 (CAK), NSF BCS-1551669 (SBC), NSF BCS-15511766 (CET).

Anatomy of the nasal cavity and inter-orbital region of *Shoshonius cooperi* (Primates, Omomyoidea)

EDWARD C. KIRK and INGRID K. LUNDEEN

Anthropology, University of Texas

ABSTRACTS

The discovery in 1985-91 of multiple cranial specimens of the early Eocene omomyoid *Shoshonius cooperi* revealed several features shared with living tarsiers, including the presence of extremely large orbits and a "reduced" snout. Most subsequent phylogenetic analyses of large character-taxon matrices have favored the conclusion that *Shoshonius* and other omomyoids are stem tarsiiiforms. Here we provide a revised assessment of the anatomy of the nasal cavity and interorbital region of 4 crania of *Shoshonius* based on micro-computerized tomography. Although all of the examined crania are damaged to varying degrees, these scans reveal that *Shoshonius* exhibits key features of the nasal fossa that are probably plesiomorphic for Euarchonta. Such primitive features include the presence of 4 ethmoturbinals and 1 interturbinal, direct contact between the olfactory turbinals and cribriform plate, and the presence of an olfactory recess containing ethmoturbinal IV. These primitive features are noteworthy because extant haplorhines share the derived loss of all but 2 ethmoturbinals, loss of the interturbinal, loss of direct contact between the olfactory turbinals and cribriform plate, and loss of the olfactory recess. *Shoshonius* also differs from extant tarsiers in lacking the derived tubus olfactorius and posterior displacement of the olfactory fossa despite having very large orbits for its cranial size. These features provide additional support for the hypothesis that *Shoshonius* is not a crown haplorhine. Nevertheless, *Shoshonius* resembles small extant haplorhines in possessing an apical interorbital septum, which is consistent with the hypothesis that *Shoshonius* is a stem haplorhine.

Something to chew on: Comparing dentine exposure in ancient Egyptians and dental age estimation standards

CASEY L. KIRKPATRICK

Executive Director, Paleo-oncology Research Organization

Biological age estimation is central to every study of human remains, modern and ancient. Dental age estimates can be: influential in the identification and individuation of human remains and the reconstruction of osteobiographies, important to the differential diagnosis of paleopathology, necessary to the study of paleo-demography, and relevant to age determination in living individuals for legal purposes or sociocultural studies. Consequently, the accuracy and specificity with which we can produce age estimates is of supreme importance. Although Miles' (1962) site-specific method produces the most accurate age estimates based on dental wear, it is sometimes inapplicable due to the need for a sizeable population with numerous subadults for calibration. Consequently, dental age estimates for adult human remains are often determined through the use of Brothwell's (1963) standard,

which was based on prehistoric to early medieval British reference populations. This paper presents a comparison of dental wear relating to age in Brothwell's wear standard and relating to skeletal age in individuals from the Kellis 2 cemetery in Dakhleh Oasis, Egypt. Images from Brothwell's standard and photographs of dentition from Kellis 2 were analysed through the use of digital image analysis software (FIJI is Just ImageJ). This allowed for the quantification of dentine exposure relative to the occlusal area of selected teeth. Significant differences in dental wear progression were observed between Brothwell's standard and the ancient Egyptian dentition. Given these results, an argument is presented for the creation of region-specific macroscopic adult dental age estimation standards for cases where site-specific standards are inapplicable.

This research was supported by the Robert Hathaway Ontario Graduate Scholarship 2015 and the Ontario Graduate Scholarship 2013-2015.

Extending the reach of paleoanthropology with the Extended Evolutionary Synthesis

MARC KISSEL

Anthropology, Appalachian State University

Discerning the patterns and processes of the emergence of our species has been driven mostly by our ability to determine the origins of symbolic thought and the delineation of apomorphies in *Homo sapiens*. From these data, paleoanthropologists have relied on two major developments as identifying the emergence of contemporary humans: behavioral modernity and anatomical modernity. Using data collected from published sources I show that members of the genus *Homo* predating 300 ka were behaving in ways that are often assumed to only be possible by *Homo sapiens*. These results suggest that perhaps the links between behavior and modernity need to be reexamined. However, the majority of research on this question is based upon the evolutionary theories developed during the New Synthesis and tend to ignore or underplay the role of niche construction and symbolic inheritance. This paper shows how the Extended Evolutionary Synthesis (EES) can point a way forward in this debate by discussing how the use of the phrase "modernity" and "modern humans" complicates the data. I suggest the results here support the notion that the very concept of "modern" is problematic for both methodological and theoretical reasons. I also point to examples of how the framing of something as "modern" is often used to support colonialist and racist ideas. Following work from the EES, we should instead focus on the expansion of the human niche as a way to discuss the processes by which hominins became human

Geometric morphometrics in silver fox skulls: Implications for the domestication syndrome

TIMOTHY M. KISTNER and DANIEL E. LIEBERMAN
Human Evolutionary Biology, Harvard University

Domestication syndrome is a suite of behavioral, physiological and morphological traits that characterize many domesticated species, possibly including humans. One of the most famous experimental models of domestication involves an ongoing Russian experiment on silver foxes (*Vulpes vulpes*). Although there is a rich literature of behavioral and physiological alterations in these foxes, comparatively few studies have investigated skeletal changes associated with their domestication and none have used geometric morphometric methods to quantify differences in cranial size and shape among these foxes. Another previously unaddressed issue is the effect of several generations of fur farming in these foxes prior to the domestication experiment. Here, we performed a geometric morphometric analysis on the crania of three groups of silver foxes: those selected for reduced reactional aggression (tame), an unselected control group, and a wild population close to where the foxes were originally trapped. Analyses of 29 cranial landmarks show no significant difference in cranial shape or size between the tame and unselected groups. However, both groups differ significantly from the wild foxes in several features including increased cranial base flexion, a longer snout and wider zygomatic arches. The differences between farm raised animals and the wild population were driven by wild male foxes. These results suggest that initial selection on fox fur farms altered cranial morphology while later targeted selection for reduced aggression had marginal effects on cranial form. These findings challenge arguments about changes in cranial morphology attributed to selection on aggression in foxes, as well as in hominins.

The Crucial role of Asia in the Evolutionary History of Native American Populations

ANDREW KITCHEN

Anthropology, University of Iowa

Native American populations largely descend from a small group of indigenous peoples who lived in Beringia and entered the Americas roughly 15,000-years-ago after the retreat of the ice sheets that had inhibited the colonization of the American continents. Though much focus has been on the occupation of Beringia by the proto-Native American population for between 2,000 and 5,000 years, the role of Asia in the history of Native American populations is often overlooked. It was during this time in Asia, which extends from the Beringian occupation backwards toward emergence from Africa, that characteristics of proto-Native American

ABSTRACTS

populations emerged. I will discuss the role of the Beringian occupation in shaping the unique patterns of Native American genetic diversity, the Asian origin of pre-contact Native American dogs, and the possible inheritance of infectious agents reflecting the Asian origins of Native Americans. Each of these examples illustrate the fundamental influence of the Asian context on the evolution of Native American populations that extends to the present.

A multi-level cultural evolutionary framework for sustainability

MICHELLE A. KLINE

Psychology, Simon Fraser University

Humans are distinct from other animals in that we cooperate in large groups of unrelated kin in order to exploit natural resources, and we accumulate increasingly efficient resource exploitation techniques across. This mode of adaptability is a root cause of our climate crisis. Here, I apply cultural evolutionary theory to explain the evolution of both sustainable and unsustainable systems of resource use. I discuss how the uniquely human combination of human social learning, cooperation, and social dilemmas result in sustainability crises—but can also produce solutions. I draw on historical examples such as the collapse of global fisheries, multilateral agreements regarding ozone depletion, and the evolution of fisheries managements systems in subsistence societies in Fiji. I propose an explicitly evolutionary approach to study how crises and solutions may emerge, persist, or disappear. Building on this framework, I provide an a step-by-step process for designing a study of multi-level cultural systems of resource management, including: research design issues (e.g., tradeoffs between validity and control), time scale, and mixed methods (qualitative and quantitative) data collection and analysis. I propose synthetic roles for multiple types of evidence including historical accounts, new and existing data sets, case studies, and simulations. In addition, I present a tutorial and code in the R environment to lead users from theory to data to an illustration of an empirical test for group-level adaptive cultural systems in sustainability research. This framework as well as the R-based research tool are published and openly available for use.

Funded by National Socio-Environmental Synthesis Center, NSF DBI-1052875 and a John Templeton Foundation grant to ASU Institute of Human Origins. Opinions expressed here do not necessarily reflect JTF views.

Genetic structure of chimpanzees (*Pan troglodytes ellioti*) in Southern Taraba, Nigeria

LESLIE A. KNAPP¹, VOLKER SOMMER^{2,3} and KATHRYN AUCKLAND⁴

¹Anthropology, University of Utah, USA,

²Anthropology, University College London, UK,

³Gashaka Primate Project, Serti, Taraba, Nigeria,

⁴Wellcome Centre for Human Genetics, Nuffield Department of Medicine, University of Oxford, UK

The Nigeria-Cameroon chimpanzee (*Pan troglodytes ellioti*) is the most threatened, least distributed and least known subspecies of chimpanzees. Restricted to the border region of Cameroon and Nigeria and a few locations around the Niger delta, the largest population survives in Gashaka Gumti National Park (GGNP) in Nigeria's Taraba State. We conducted a two-year genetic survey of chimpanzees within GGNP and its buffer zone from November 2010-2012, collecting 236 samples of faeces and shed hairs from 30 nest groups, from which 174 samples from seven distinct locations were analyzed (N = 11 from the buffer zone; N = 19 from within GGNP, with most samples stemming from the Gashaka-Kwano community inside the park). We identified 76 unique individuals using mitochondrial DNA, sex determination, microsatellite genotyping and population admixture analyses. A high percentage of related individuals were observed in most nest groups; the average relatedness (r) of all dyads was 0.071, whereas the average r of all nest groups was 0.102. Genetic diversity was found to be relatively high, with an average heterozygosity of 0.8. Population structure analyses revealed high migration rates for these chimpanzees. Mismatch distributions and neutrality tests indicated that the Southern Taraba population of chimpanzees have remained stable for a long period of time. However, the survival of the Southern Taraba population is increasingly threatened by habitat destruction, even within the National Park.

Morphological integration of the masticatory apparatus in New World monkeys

RYAN P. KNIGGE

Pathology and Anatomical Sciences, University of Missouri

Understanding patterns of morphological integration and the covariation of traits is essential for deciphering the evolution of complex phenotypes and adaptations. Previous work suggests that functionally related traits tend to be highly correlated and evolve in a coordinated fashion. This is supported by findings that cranial phenotypic correlation and covariance structures of New World monkeys reflect dietary habits rather than phylogeny. However, the morphological patterns associated with changes in covariance structures across platyrrhines are not yet understood. This study examines patterns of morphological integration in the masticatory apparatus of five New

World monkey species (N=113): *Aotus trivirgatus*, *Cebus apella*, *Alouatta seniculus*, *Ateles geoffroyi*, and *Chiropotes satanas*, representing different clades and dietary habits. Three-dimensional landmarks and semi-landmarks were used to quantify skull morphology and divided into two functional components of the masticatory apparatus: masticatory muscle attachment sites and regions housing dentition (i.e., mandibular corpus and maxilla). Two-block partial least squares analysis, pooled by sex, was used to identify patterns of covariation between the two components for each species, with the RV coefficient providing a measure of integration. Differences in patterns of covariation were assessed by calculating angles between PLS vectors for each pair of species. Patterns of covariation between components were most similar in *Ateles* and *Cebus*, followed by *Aotus*. Unique patterns in *Alouatta* and *Chiropotes* may indicate distinct functional relationships for adapting to more specialized dietary preferences. Furthermore, reduced covariation between functional components in *Alouatta*, relative to other species, may result from changes in integration associated with vocalization adaptations.

This research was funded by the Graduate School and Department of Anthropology, University of Minnesota.

Confirming an old-husband's tale: The frequency of same-sex twinning increases across the generations, following a Fragile X-syndrome-like pattern

LAUREN KOERNER¹, KILIAN KELLY², HONG HUANG³, SONYA BHASKAR⁴ and LORENA MADRIGAL¹

¹Anthropology, University of South Florida,

²Department of Anthropology, Purdue University,

³College of Communication, University of South Florida,

⁴College of Medicine, University of South Florida

Work on the inheritance of twinning has focused on dizygotic (DZ) twinning because most researchers assume that monozygotic (MZ) is a teratogenic event whose frequency is equal across all populations. Early work has argued that fragile-X-syndrome-carrier [Frag(X)] families tend to have higher frequencies of twins¹⁻⁷. As Sherman³ said in 2000: "To date, data supporting increased twinning rates (among the carriers of the fragile X premutation) are conflicting and need to be resolved" (emphasis added). Using GWAS methods, we⁸ detected that MZ twins have a significantly different frequency of a SNP found in Xq27.2 from DZ twins. For this presentation we focus on families with a preponderance of same sex twinning (SST) who have a form of inheritance which mirrors that of the Frag(X). We propose that Frag(X), located at Xq27.3 may be linked to the MZ SNP, located at Xq27.2, in some families. We have assembled pedigrees with 5-10 generations with SST that follow our proposed pattern of inheritance. We tested for presence of an increase in

ABSTRACTS

the frequency of SST twinning by generation by using the Cochran-Armitage test for presence of a trend. Our results were significant ($X^2 = 239$, $df = 200$, $p = 0.02$), supporting the assertion that SST increases through the generations in these families, following a Frag(X) pattern. Our results raise issues about the life history of these families, who may increase their fertility via twinning, at the risk of reducing it via their higher propensity to Fragile-X-syndrome.

Funded by an EAGER NSF award.

Unmasking the primate face: DiceCT analysis of the mimetic muscles of *Eulemur flavifrons*

SHRUTI KOLLI¹, ANTONIO MEZA^{1,2}, ANNE BURROWS³, EDWIN DICKINSON¹ and ADAM HARTSTONE-ROSE¹

¹Biological Sciences, North Carolina State University, ²Biological Sciences, Sam Houston State University, ³Rangos School of Health Sciences, Duquesne University

The muscles of facial expression (the "mimetic muscles") are used in social interactions in visually orientated species. Although these muscles have been qualitatively studied in the past, traditional dissection techniques are largely limited to identifying the presence or absence of specific muscles. This is due to the fact that these muscles are extremely thin and highly integrated with other facial tissues. Using diffusible iodine-based contrast-enhanced computed tomography (DiceCT), we have reconstructed the three-dimensional anatomy of the mimetic muscles *Eulemur flavifrons* and have, for the first time, measured each of their volumes. These ranged from as small as 4-15 mm³ for the auricular muscles up to 459 and 339 mm³ for the orbicularis oris and oculi muscles respectively. The digital visualization of these muscles enabled several interesting observations, such as the extent of interdigitation between certain muscles. We conclude that DiceCT allows for the detailed study of the volumes and relationships between these muscles in ways that have not previously been possible based on traditional techniques. Further iterations of this method will be used to visualize these muscles *in situ* while the face is still associated with the underlying cranium. This will allow these muscles to be visualized, for the first time, from origin to insertion and to be able to study their *in situ* lines of action.

This work was funded, in part, by the National Science Foundation (IOS-15-57125 and BCS-14-40599).

Patterns of morphological integration in the primate midfoot and implications for the evolution of bipedalism

KLARA KOMZA¹, BENICE VIOLA^{1,2}, TEAGAN NETTEN¹ and LAUREN SCHROEDER^{3,4,5}

¹Department of Anthropology, University of Toronto, ²Institute for Archaeology and Ethnography, Siberian Branch, Russian Academy of Sciences, ³Department of Anthropology, University of Toronto Mississauga, ⁴Human Evolution Research Institute, University of Cape Town, ⁵Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo

Current fossil evidence suggests that the lateral aspect of the midfoot was the primary target of selection for bipedalism, as most fossil hominins have adaptations for a laterally stiff midfoot. Medially, more morphological variation can be seen, indicating variable suitability for both bipedal and arboreal locomotion. Here, we test this model by comparing patterns of morphological integration in the midfoot of modern primates (*Homo sapiens* [n=100], *Pan troglodytes* [n=65], *Pan paniscus* [n=24], *Gorilla sp.* [n=65], and *Pongo sp.* [n=45]). Integration was quantified based on interlandmark distances from the cuneiforms, navicular, cuboid, and metatarsals of all individuals, organized into sets of a priori defined functional modules. The pattern of integration across these functional modules was then compared against sets of random traits from the whole midfoot. Preliminary results show that modern humans have a significantly more integrated cuboid-metatarsal (Mt) 4 joint complex than chimpanzees, and that in both species, the medial cuneiform and Mt1 are less integrated than the midfoot as a whole. This integration pattern in humans may be associated with adaptations for midfoot stiffness, and may explain the relatively conserved nature of this joint complex throughout evolution. Furthermore, reduced integration in the medial elements corresponds with the morphological diversity we see in this anatomical region in fossil hominins. These results have implications for the evolvability of the tarsals and metatarsals, suggesting the cuboid and Mt4 may have experienced stabilizing selection, and that the medial cuneiform and Mt1 were more evolvable, leading to a wide range of locomotor adaptations.

This research was supported by the University of Toronto School of Graduate Studies (KK) and the Social Sciences and Humanities Research Council Insight Grant (435-2018-0943) (BV).

Prior probabilities and the age threshold problem

LYLE W. KONIGSBERG¹, SUSAN R. FRANKENBERG¹, VALERIE SGHEIZA¹ and HELEN M. LIVERSIDGE²

¹Anthropology, University of Illinois at Urbana-Champaign, ²Institute of Dentistry, Barts and the London School of Medicine and Dentistry, Queen Mary University of London

Konigsberg et al. (2019) considered the problem of dental developmental evidence presented in asylum seeker cases in which an age threshold of 18 years was in question. Because of this specific focus they considered development of only the third molar. In this presentation we consider the more general age threshold problem that may arise in cases concerning the minimum age of criminal responsibility, or admittance to institutions and organizations that rely on an age threshold lower than 18 years. Because of this younger age focus, we use Moorrees, Fanning and Hunt (1963) scores from the first, second, and third molars scored by the fourth author on radiographs of 1,326 girls and 1,351 boys from London. We fit multivariate cumulative probit models separately to data from the two sexes. This model allows for non-zero residual correlations between teeth after accounting for the effect of age.

Although prior probabilities are generally eschewed in forensic anthropology, a prior probability for age is necessary in order to calculate a Bayes factor from the dental evidence in age threshold cases. Age threshold cases generally have an implicit prior for age, as for example when one asks the question of whether an individual is over or under a certain age threshold. We make the prior explicit and always choose a prior that is symmetric around the age threshold. This makes the prior "evens" regarding whether the individual is over or under the age threshold. Our results show that Bayes factors are rarely much different than 1.0.

Vital records: The demography of an early twentieth century medical school anatomical cadaver collection

DERINNA V. KOPP and MEGHAN E. BANTON
Antiquities Section, Utah Division of State History

Construction on the George Thomas Building at the University of Utah in 2016 inadvertently unearthed human remains that were determined to be early twentieth century anatomical cadavers from the University of Utah School of Medicine (UUSM). Due to segmentation and postmortem fragmentation estimation of the biological profile was limited but provided insights into the collection. The minimum number of individuals was eleven based on the right proximal femur. In all 96% of the bones/fragments were determined to be adult, 2% subadult and 2% undetermined. There were no clearly identifiable female remains. Forty-four percent of the remains were identified as male, 17% probable male and 38% indeterminate. Only three of the cranial remains allowed for accurate ancestral affiliation: two were identified as European origin and one as probable mixed European and Native American origin (Hispanic). In 1907 Utah passed SB18, this allowed for unclaimed bodies to be used by the UUSM for instruction and resulted in

ABSTRACTS

the “place of disposition” on the death certificates of those individuals listed as the UUSM. This provided an opportunity to compare the remains with the individuals known to have been used by the UUSM. Chi-square tests examined how well the demography of the remains fit the known individuals. Results indicate that the remains fit the known individuals considerably well, with most tests showing little to no difference between the groups. The tests also narrowed the possible range of years from which the remains could have originated down to several distinct years or year groupings.

The analysis of the skeletal remains was funded by the University of Utah Campus Planning Department.

Sex- and age-related differences in bone density in African ape lumbar vertebrae

NIINA KORPINEN and JUHO-ANTTI JUNNO
Archaeology, University of Oulu

Osteoporosis related vertebral fractures are an increasing health problem in growing elderly population. Particularly women have been demonstrated to be even three-fold more susceptible for vertebral fractures than men mainly due to greater bone loss during aging as a part of normal aging processes. As these sex differences have such a large impact in worldwide human population, we wanted to examine if this feature is unique for humans or are there sex differences in bone density also in African apes. We used a sample of 47 Pan troglodytes (18 males and 29 females) and 37 Gorilla gorilla (17 males and 20 females) second last lumbar vertebrae to study potential sex and age differences. Peripheral quantitative computed tomography (pQCT) was used to examine the bone density. We could not detect any statistically significant sex- or age-related differences in Pan. In Gorillas, sex differences were present and in pooled-sex and female sample we could also detect some age-related changes. This partly indicates that sex differences exist in African apes and that apes too experience changes in bone density during aging. Differences between the species could suggest that these features are species-specific and could vary in primates even on subspecies and population level. The limited age-related changes that we found could also derive from wild apes not living old enough to experience significant decline in bone density.

This research was funded by Finnish Cultural Foundation

A three-dimensional morphometric comparison of cranium of females and males in Israel

TOM KOSENKOV¹, ELLA BEEN^{2,3} and ALON BARASH¹

¹Azrieli Faculty of Medicine, Bar Ilan University, ²Sports Therapy, Ono academic College, ³Anatomy

& Anthropology, Tel Aviv university, Faculty of Medicine

Determination of sex is a fundamental step in a biological anthropologist's work. Determining the gender of an unknown individual is essential, and may influence our understanding of age, stature, and health of the entire studied population. So much so, that there is a great body of work, in regard to discerning sexual dimorphism from skeletal elements. While this task is sometimes straightforward, especially when the entire skeleton is present, several factors highly influence our ability to accurately identify gender. This is further emphasized in Israel where the differences between and within populations is unknown.

In this study we used geometric morphometric techniques to quantify the shape of the skull. 450 landmarks and semi-landmarks were placed on 60 skulls of adult males and females, from contemporary medical CT scans. Using Procrustes analysis, we observed the shape differences between entire skull, and between discrete parts of the skull: forehead, midface, mandible, and calvaria.

When observing the entire skull, there is a clear and significant separation between males and females. Importantly, this was also true, when we observed areas, such as the calvaria, that are not usually associated with sexual dimorphism. Such differences are visible only when we examine them as a discrete part, in which they are not overshadowed by other more influential skull parts. To our best knowledge this is the first time such a study is done in Israel, where there is a great deal of integration between different populations.

The Temporal and Atmospheric Contexts of Howling Behavior Among Mantled Howler Monkeys (*Alouatta palliata*) at La Suerte Biological Field Station

EMILY L. KOSNIK¹ and LAURA M. BOLT²

¹Anthropology, Grand Valley State University, ²Anthropology, University of Toronto

Though howler monkeys (*Alouatta* spp.) are widely studied, the function of their loud calls remains the subject of much debate. It is clear that understanding the context of *Alouatta* loud calls may provide significant advantages to conservation efforts, serving as a tool for monitoring ecosystem health. To investigate this possibility, this study involved recording all occurrences of howling behavior throughout the observation periods, and monitoring and recording shifts in weather during sampling. Research was conducted on several groups of *A. palliata* living at La Suerte Biological Field Station in Costa Rica. Analysis focused on the relationship between howling behavior and precipitation, as well as between howling behavior and time of day. While howling did not occur more often in samples when it was raining, the most active samples

were taken in the early mornings and during visual contact between two groups. Given the distribution of active samples between various weather patterns and throughout the day, our findings support the theory that howling behavior is highly complex, but contextually relevant and therefore, intelligible. Additionally, recent research suggests that conservation-based educational initiatives have resulted in perceptions of *A. pigra*'s howls shifting from that of an ill omen, to predictors of changes in the weather among rural communities in southern Mexico. Further examination of local knowledge and beliefs about the significance of *Alouatta* loud calls, particularly as those opinions vary among communities, will provide insight that can be useful for conservation efforts.

Stature estimation in ancient Greek Antiquity

MARIANNA KOUKLI¹, FRANK SIEGMUND² and CHRISTINA PAPAGEORGIOPOULOU¹

¹Laboratory of Physical Anthropology, Department of History and Ethnology, Democritus University of Thrace, ²Abt. Ur- und Frühgeschichtliche Archäologie, Dep. of History, University of Münster, Germany

Stature is one of the key concepts when it comes to the study of human past. This paper applies for the first time the anatomical (Raxter et al. 2006-modified Fully) technique to ancient Greek populations and introduces new population-specific equations for this so far unexplored part of Europe. Additionally, it presents a new methodological tool, the Logarithmic Human Stature Index (LHSI), that simplifies inter-population comparisons in anthropometry. Our study was conducted on 129 ancient individuals (70 males, 59 females) sufficiently preserved for the anatomical method originating from two sites in Northern Greece, “Kitrini Limni” and “Thessaloniki”, dated from the Hellenistic (3rd c. B.C.) to early Byzantine times (6th c. A.D.). Anthropometric values between our populations were compared by the use of the LHSI index, proving that they were both similar enough to be considered as our “standard population” and as a reference sample for the creation of population-specific formulae. Mean anatomical stature values for these populations are 168.6 cm for males and 156.6 cm for females. The efficacy of the generated equations was evaluated through percent prediction error (%PE) and standard deviation values. We introduce ordinary least square (OLS) and reduced major axis (RMA) sets of equations for both “sex-specific” and “pooled-sexes” ancient Greek samples. Results show a slight superiority of the OLS equations, compared to their RMA counterparts, whereas

ABSTRACTS

"pooled-sexes" equations found to produce better estimations. The new formula could be applied on a broad set of Mediterranean and south-eastern European populations.

The State Scholarships Foundation, Operational Programme "Education and Life Long Learning" co-financed by the European Social Fund and national funds.

Reconciling Skeletal Indicators of Stress with Lived Experiences: A Case Study From the U.S.-Mexico Border

LAUREN G. KOUTLIAS¹, DIANA NEWBERRY², MICHELLE D. HAMILTON³ and KATE SPRADLEY³

¹Department of Anthropology, University of Tennessee, Knoxville, ²South Texas Human Rights Center, ³Department of Anthropology, Texas State University

In archaeological populations, it is impossible to observe specific events that resulted in the formation of the skeletal stress indicators. However, in modern populations, we have the opportunity to understand potential stressors. The purpose of this paper is to reconcile skeletal stress with the lived experiences which potentially caused them to form through a case study from the U.S.-Mexico border. Mandibular canines from 30 presumed-migrant individuals (15 males and 15 females) from the Operation Identification initiative at Texas State University were analyzed by co-author LGK under a DinoLite™ and in a SEM for incidences of linear enamel hypoplasia. For comparison, 29 white individuals (13 males and 16 females) from the Texas State Donated Skeletal Collection were also sampled. Ethnographic migrant narratives were recorded by co-author DN at a border shelter in Mexico. Interviews were conducted with no pre-established questions and the participants directing the flow. Instances in which the interviewee discussed their childhood experiences, their children, or childhood generally were extracted. Results of both dental and ethnographic studies showed a stark contrast between the stresses experienced by migrants compared to white American individuals. This is reflected in the narratives recounted from living migrants who discuss violent contexts in which they live, and in their higher frequencies of dental enamel defects. Cross-pollinating ethnographic approaches and skeletal stress data is uncommon in biological anthropology, but it could be of great interpretive value, since skeletal stress is poorly defined and often overly simplified.

Does Molar Shape Distinguish Robust Capuchin Hybrids (*Sapajus nigritus* x *libidinosus*) From Non-Hybrids? A 2D Geometric Morphometric Approach

EMMA A. KOZITZKY

Center for the Study of Human Origins, New York University, New York Consortium in Evolutionary Primatology

Genetic evidence shows that hominins hybridized multiple times during the Pleistocene. However, claims of hybrid ancestry based solely on hominin fossil morphology remain contentious. To generate hypotheses regarding the morphology of hominin hybrids, researchers have investigated the effect of hybridization on hard tissues in living primates. This study tests the hypothesis that there are significant differences in first molar (M1) shape among *Sapajus nigritus*, *S. libidinosus*, and museum specimens identified as *S. nigritus* x *libidinosus* hybrids. Landmarks were placed on digital photographs of minimally worn right upper M1s (n=112) and right lower M1s (n=95) at the four main cusp tips and 30 sliding semi-landmarks were placed around the crown perimeter. Upper and lower M1 landmarks were analyzed separately using generalized Procrustes analysis, Procrustes ANOVA, principal components analysis, and cross-validated discriminant function analysis (DFA). The Procrustes ANOVA showed significant differences in upper M1 shape among *S. nigritus*, *S. libidinosus*, and *S. nigritus* x *libidinosus* ($p = 0.001$), but no significant lower M1 shape differences. The cross-validated DFA correctly assigned 77% of hybrid upper M1s, and 58% of hybrid lower M1s. These results indicate that upper M1s discriminate among *S. nigritus*, *S. libidinosus*, and *S. nigritus* x *libidinosus* hybrids better than lower M1s and suggest that the phenotypic effects of hybridization may differ between maxillary and mandibular teeth. Because genetic studies indicate that *Sapajus* populations are highly admixed, the assumption made here that *S. nigritus* and *S. libidinosus* samples did not contain hybrids should be treated with caution.

Climbing and Canopy access in Human Foragers is not limited by Grip Strength or Endurance

ELAINE E. KOZMA^{1,2,3}, DAVID B. MORGAN⁴, CRICKETTE M. SANZ^{5,6} and HERMAN PONTZER^{3,7}

¹Anthropology, City University of New York, Graduate Center, ²New York Consortium in Evolutionary Primatology, NYCEP, ³Evolutionary Anthropology, Duke University, ⁴Lester E. Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo, ⁵Department of Anthropology, Washington University in St. Louis, ⁶Congo Program, Wildlife Conservation Society, ⁷Global Health Institute, Duke University

Arboreal behavior is thought to be constrained in humans and earlier hominins compared to living apes. Humans have proportionally shorter arms and less arm muscle mass than chimpanzees and gorillas, which could reduce strength and endurance and limit climbing. Here we set out to investigate the determinants of grip strength and endurance in a controlled sample of n=28 U.S. rock climbers, and test whether strength limits tree climbing in a sample of n=15 Mbandjele foragers from the Republic of Congo. Compared to non-climbers, rock climbers had greater

maximum grip strength and better endurance, measured as time to failure at 70% maximum voluntary grip force. Pre-climb maximum grip strength was positively correlated with body mass ($p < 0.05$). After 27 meters of ascent and 27 meters of descent on a vertical wall, mean strength and endurance decreased by $15 \pm 2\%$ and $43 \pm 7\%$ respectively. Both measures recovered to pre-climb values after 15 minutes of rest. In Mbandjele foragers, we found that men ascended an average of 52 ± 4 meters per day when collecting arboreal resources, significantly more than Western lowland gorillas (29 meters/day) inhabiting the same forests, but significantly less than chimpanzees (102 meters/day). Mbandjele men's grip strength exceeded that of U.S. rock climbers and was not significantly lower after tree climbing ($p = 0.39$). Together, these results show human foragers can accrue daily climbing rates comparable to other African apes without approaching the limits of arm strength or endurance. We discuss implications for understanding the ecology and evolution of living hominoids and fossil hominins.

This project was partially funded by the Leakey Foundation (general grant) and the National Science Foundation (grants 1732194 and 1646736).

A link between orbital convergence and locomotor behavior in leporids and its implications for the evolution of the primate visual system

BRIAN KRAATZ¹, LUISA FRANKENBERG², EMMA SHERRATT³ and LARS SCHMITZ²

¹Anatomy, Western University of Health Sciences, ²Keck Science Department, CMC/Pitzer/Scripps, ³Ecology and Evolutionary Biology, The University of Adelaide

Within primates, it has been proposed that orbital convergence (forward-facing eyes) relates to locomotor behaviors like nocturnal leaping as it increases the overlap of the monocular visual fields, improving image perception in an increasingly larger binocular visual field. Leporids (rabbits and hares) exhibit a surprising range of cranial shape and locomotor behavior, and skull transformations similar to those within primates; much of leporid cranial disparity is driven by pronounced cranial flexion (facial tilt). Furthermore, facial tilt angle is strongly correlated to locomotor mode and significantly predicts cranial shape variation on the major axis of cranial shape space. In short: the more leporids tilt their face downwards, the more likely they are to exhibit high-speed, cursorial locomotion. We previously hypothesized that leporid cranial transformations are driven to improve visual acuity. Here we measure orbital convergence angle in 184 leporid crania, representing 20 extant species, to test the relationships among cranial shape, locomotor behavior, and visual acuity. Our analysis shows significant correlation ($p < 0.001$) between

ABSTRACTS

orbital convergence and facial tilt: as leporids tilt their face downwards, they also increase orbital convergence and, therefore, the size of their binocular field. This relationship provides a functional link for the hypothesis that cranial shape variation within leporids is influenced by locomotor behavior: leporids may tilt their faces to improve visual acuity as they increase the speed of their locomotor habits. Though a relationship between orbital convergence and locomotor behavior has been proposed for primates, our study demonstrates strong quantitative links between these systems.

Healthy aging in non-WEIRD societies

THOMAS S. KRAFT¹, BENJAMIN TRUMBLE², HILLARD KAPLAN³, ANGELA GARCIA^{1,2}, JONATHAN STIEGLITZ⁴ and MICHAEL GURVEN¹

¹Anthropology, University of California, Santa Barbara, ²Center for Evolution and Medicine, Arizona State University, ³Economic Science Institute, Chapman University, ⁴Institute for Advanced Study in Toulouse

Physiological aging describes the somatic, cellular, endocrine, immune, and other physical changes that underlie age-related increases in mortality and declines in fertility. Understanding the dynamics of physiological aging is essential for elucidating how and why senescence occurs across species and human populations. However, much of what is known about physiological aging in humans is restricted to industrialized populations with high burdens of chronic "diseases of civilization." Little is known about physiological aging in varied environments, and local selective pressures have been under-appreciated as a source of variation. To better characterize human diversity in aging patterns, we examined physiological age trajectories among Tsimane horticulturalist-foragers from the Bolivian Amazon using longitudinal data ($n=21,543$) on 61 biomarkers that are combined into a statistical index (mahalanobis distance) of "biological age." Although few individual biomarkers showed a significant decline with age, a combined index revealed significant increases in "dysregulation" ($\beta = 0.15, p < 0.001$). Compared to relatively rapid increases in cardiovascular dysregulation with age ($p < 0.001$), dysregulation in the immune system remained constant ($p > 0.05$). Finally, we compared Tsimane aging profiles with those of Americans/Italians under the expectation that differences could arise due to higher lifetime exposure to pathogens, minimal sedentism, lean diet, and higher fertility, but found that rates of increase in standardized dysregulation were nearly identical ($\beta = 0.15$ vs. 0.14). Our results provide the first large-scale evidence of physiological aging in a subsistence context and highlight the diversity of physical aging profiles across different body systems and human populations.

Orangutan Canine Linear Enamel Hypoplasia Defects Assessed in Association with Flanging Status

ALEXANDRA E. KRALICK¹ and KATE MCGRATH^{2,3}

¹Department of Anthropology, University of Pennsylvania, ²Department of Anthropology, George Washington University, ³PACEA, Université de Bordeaux

Orangutans exhibit intrasex bimaturism, a trait rare among primates. Males exist in two morphs: flanged, with large bidiscoid cheek pads on their face and a laryngeal throat pouch, and unflanged, lacking secondary sexual characteristics and displaying "developmental arrest." Flanged males in captivity are shown to have higher levels of testosterone and cortisol than unflanged males. However, research on wild orangutans remains has a greater potential to inform differences in early life stress experiences, as zoo orangutans rarely remain developmentally arrested. Here, we use associated orangutan skins and skulls to assess flanging status, canine height ($n=37$), and measure an early life stress indicator, linear enamel hypoplasia (LEH) defect depth, using confocal profilometry ($n=7$). Of the 24 defects measured, flanged male defects were deeper (range 24.7-126.6, mean 73.4) than in unflanged adult males (range 12.1-63.5, mean 31.04) (t test $p=0.026$). While the majority of population-level variation in defect depth is related to how rapidly canines grow in height, when assessing intrasex variation, evidence from great apes suggests that deeper defects might reflect more severe stress events during development. Flanged and unflanged males likely have similar canine development given that canine projective crown heights are similar across all males regardless of morph ($p=0.47$) with no overlap between males and females ($p<0.001$) (means: flanged 23.15, unflanged 24.55, female 14.75). Therefore, our results may indicate an adaptive benefit to arresting development is avoiding chronic stress and its associated physiological impacts. Future directions include examining differences in micro-anatomical growth between morphs via histologic and surface analyses.

This project received funding from the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No798117, Penn Museum, and NSF Graduate Research Internship Program (GRIP).

Living with Environmental Uncertainty. Climate Change & Economic Decision Making among Maya Farmers

KAREN L. KRAMER and JOSEPH HACKMAN
Anthropology, University of Utah

Humans have been adapting to climate change, diversifying or replacing resources and strategies since they can be identified in the archaeological record. Working with traditional populations gives

anthropologists an opportunity to document the process by which small-scale societies adapt to climate change locally and in situ. Subsistence populations are well adapted to interannual variation. Until recently Yucatec Maya farmers planned for and made economic decisions based on crop failure due to hurricanes and flooding that predictably occurred every two out of ten years. More punctuated and erratic storms, however, have introduced novel uncertainty, and traditional means to buffer against interannual variation (surplus agriculture and storage) provide little solution. The central question we ask is how do we distinguish between strategies that mitigated interannual variation and those that are a response to climate change? We use a resilience theory approach to model when the rate of climate change renders ineffective mechanisms for coping with interannual variation, and traditional subsistence regimes are unable to bounce back to their original state and give way to a new way of making a living. Using 25 years of individual and community-level data, we find that Maya farmers have transitioned from making economic decisions under risk (known probability distribution of crop failure) to decision making under uncertainty (unknown probability due to increased amplitude in rainfall variation). One consequence of this uncertainty is diversification, and a community-level transition from economic homogeneity to heterogeneity.

The Maya research has been funded by the National Science Foundation (0349963, 0964031, 1632338) and NIH (AG 19044-01).

A comparative morphometric assessment of sexual dimorphism in the human sacrum

VIKTORIA A. KRENN^{1,2}, CINZIA FORNAI^{1,2}, NICOLE M. WEBB^{1,3} and MARTIN HAEUSLER¹

¹Institute of Evolutionary Medicine, University of Zurich, ²Department of Evolutionary Anthropology, University of Vienna, ³Senckenberg Research Institute, Natural History Museum Frankfurt

The human pelvis shape is remarkably sexually dimorphic owing to its central role during birth. Sexual dimorphism has also been described for the sacrum, but its pattern is unclear in non-European populations. Yet, published sex classification accuracy ranges greatly between 60% and 90%. Here, we investigated sacrum morphology within a sample of 150 individuals of known sex from Central Europe, South-East Asia, South America and Africa using both traditional and geometric morphometric (GM) approaches. Our 3D-GM analysis based on a dense configuration of 100 landmarks and semilandmarks demonstrated an extensive overlap between the sexes in shape space. The warps at the extremes of the distribution confirmed previous findings indicating a broader and shorter sacrum in females with respect to males, with a relatively smaller, more

ABSTRACTS

dorsally positioned superior articular surface. No differences in sagittal sacral curvature were found. The classification accuracies of the approach based on the corporo-basal index and of the qualitative visual classification ranged from 50% to 75%. However, the accuracy improved for all analyses by 10 to 15% when focusing on the Central European sample only ($n = 58$), implying that the pattern of sexual dimorphism is population specific.

Although the sacrum is part of the birth canal, its sexual dimorphism seems to be lower than anticipated, suggesting that sacrum shape is under weaker reproductive, or possibly locomotor-based, selective pressure than the other pelvic elements. This might be due to sacroiliac joint mobility during the birth process, but further investigation is warranted.

Swiss National Science Foundation grant No. 31003A_176319

Diet of the South Tombs Cemetery individuals at Amarna, Egypt

KRISTIN L. KRUEGER¹ and JESSICA R. SCOTT²

¹Anthropology, Loyola University Chicago,

²Anthropology, University of Arkansas at Little Rock

The city of Amarna has inspired archaeological, historical, and socio-political inquiry for centuries due to the unique circumstances of its founding and abandonment after about 15 years. However, the majority of research has focused on the lives of the elites and royals, which reduces balance in archaeological and historical interpretations of life in New Kingdom Egypt. For example, dietary abundance and variety is depicted at Amarna, including the consumption of meat; however, research of the South Tombs non-elite Cemetery (STC) individuals found evidence of nutritional deficiencies. The goal of this study was to assess the dietary regimes of a sample of individuals ($n=52$) from the STC using dental microwear texture analysis (DMTA).

Each molar occlusal surface was replicated using high-resolution molding and casting materials. Phase II facets, usually facet 9, were examined using a white-light confocal profiler at 100x. The total enamel area scanned was 204x276 μm , which was then uploaded into scale-sensitive fractal analysis software for texture characterization. The Amarna texture values were compared to a variety of comparative bioarchaeological samples of known diet and experimental microwear data.

Results show that the Amarna sample was similar in mean complexity to that of the Arikara, while the anisotropy mean was most congruent with that of the Tigara. The Amarna sample values also closely aligned with those obtained through

experimental chewing of dried meat with sand. Taken together, this suggests that the STC individuals may have been consuming tough, dried meat or foods similar in texture to meat, such as bread.

Funding for this project was provided to KLK by Loyola University Chicago Research Support Grant.

Food choice and nutritional analysis of frugivorous and insectivorous diets in captive Northern greater galagos (*Otolemur garnettii*)

MEAD A. KRÓWKA¹, B. KATHERINE SMITH², SYDNIE BIANCHI², JAMES E. LOUDON³, MICHAELA E. HOWELLS¹, ANDRES M. GOMEZ⁴, OLIVER C.C. PAINE⁵ and MATT SPONHEIMER⁵

¹Department of Anthropology, University of North Carolina Wilmington, ²Department of Anthropology and Sociology, University of Southern Mississippi, ³Department of Anthropology, East Carolina University, ⁴Department of Animal Science, University of Minnesota, ⁵Department of Anthropology, University of Colorado, Boulder

Understanding the food decisions of primates is fundamental for interpreting their feeding patterns and anatomical and physiological dietary traits. Primates may avoid foods high in structural fiber and secondary toxins, or positively select foods with elevated levels of protein, fat, or high energy yields. We examined the food choices of eleven captive Northern greater galagos (*Otolemur garnettii*). For a 14-day period, the galagos were given a frugivorous diet (blackberries, raspberries, and tamarind) and an insectivorous diet (crickets, mealworms, nightcrawlers, and redworms). Both diets included a pre-formulated primate chow (Lab Diet 5045) to ensure nutritional stability. We weighed each food prior to feeding and the amount leftover by each individual. We determined the preference for each food based on the weight consumed. All foods were analyzed for acid detergent fiber (ADF), neutral detergent fiber (NDF), crude non-structural carbohydrates (NSC), crude fat (CF), and crude protein (CP) to examine which nutritional properties may drive food selection. For the frugivorous diet, we found that the colony preferred tamarind to blackberries ($P<0.05$). Compared to both berries, tamarind was significantly higher in NSC ($P<0.0001$), and lower in ADF ($P<0.0001$), NDF, CP ($P<0.001$), and CF ($P<0.01$). For the insectivorous diet, the galagos preferred redworms and nightcrawlers ($P<0.0001$), both higher in NSC ($P<0.01$) and lower in NDF ($P<0.001$). We also found that mealworms were higher in CF ($P<0.0001$) while crickets and nightcrawlers were higher in CP ($P<0.0001$). For both diets we found that galagos select foods high in carbohydrates and low in fiber.

This project was supported by grants from the National Science Foundation (RAPID Award #1840977), and the University of North Carolina Honors College.

Trophic levels and taxonomic implications for Pleistocene hominids from Sangiran (Indonesia) revealed by histologically-controlled laser-based mass spectrometry (LA-ICPMS)

JÜLIDE KUBAT^{1,2}, LUCA BONDIOLI³, CHRISTOPHER DEAN⁴, DAVID EVANS^{1,5}, AXEL GERDES^{1,5}, ANGELA HELBLING^{1,5}, OTTMAR KULLMER^{6,7}, ALESSIA NAVA^{3,8}, BEATRICE PERIPOLI³, RICHARD A. ROPER^{1,5}, FRIEDEMANN SCHRENK^{6,7} and WOLFGANG MÜLLER^{1,5}

¹Frankfurt Isotope and Element Research Center (FIERCE), Goethe University Frankfurt, Frankfurt am Main, Germany, ²Institute of Anthropology, Johannes Gutenberg University Mainz, Mainz, Germany, ³Bioarchaeology Service, Museum of Civilization, Rome, Italy, ⁴Earth Sciences, Natural History Museum, London, UK, ⁵Institute of Geosciences, Goethe University Frankfurt, Frankfurt am Main, Germany, ⁶Department of Palaeoanthropology, Senckenberg Research Institute and Natural History Museum Frankfurt, Frankfurt am Main, Germany, ⁷Department of Paleobiology and Environment, Institute of Ecology, Evolution, and Diversity, Goethe University Frankfurt, Frankfurt am Main, Germany, ⁸DANTE Diet and ANcient TEchnology Laboratory - Department of Oral and Maxillo Facial Sciences, Sapienza University of Rome, Rome, Italy

Spatially-resolved mass spectrometry (LA-ICPMS) coupled with dental enamel histology is a promising technique to reconstruct the early life history and diet of mammals. In order to reconstruct hominin trophic levels and life histories of enigmatic specimens, we analyzed Sr/Ca and Ba/Ca ratios from isolated teeth of Pleistocene hominids (*Homo erectus* and fossil *Pongo*) and approximately contemporary faunal remains from Sangiran, Java (GHR v Koenigswald collection). Herbivorous (Hippopotamidae, Cervidae, Rhinocerotidae), omnivorous (Suidae) and carnivorous (Hyanidae, Felidae) faunal specimens were chosen for developing a trophic level framework to compare to the hominid specimens. Owing to biopurification processes in mammals, Sr and Ba concentrations decrease up trophic chains. A suite of diagenesis proxies such as U, Y, Ce, Pb, Mn, Al are used to evaluate the extent of post-mortem diagenetic overprint of Sr and Ba concentrations. Overall, Sr/Ca ratios allow reasonably clear trophic level reconstructions and hence reveal trends in dietary behavior, whereas Ba/Ca ratios show a high susceptibility to diagenetic alteration. *Homo erectus* clearly groups with omnivorous and carnivorous faunal specimens. Furthermore, geochemical compositions may support species allocations. Two *Pongo* teeth from Sangiran were recently re-classified as *Homo erectus* and *Meganthropus* by endostructural classification. These teeth show different Sr/Ca and Ba/Ca ratios: a non-cyclical pattern in

ABSTRACTS

the *Homo erectus* sample analyzed and a cyclic pattern with elevated ratios, respectively. Our pilot studies illustrate the potential of time-resolved, histologically-controlled geochemistry.

Laser-Induced Breakdown Spectroscopy for Categorization of Human Skeletal Remains

KELSI KUEHN¹ and MATTHIEU BAUDELET²

¹Anthropology, University of South Florida,

²National Center for Forensic Science, University of Central Florida

Bioarchaeology and forensic anthropology require the classification of unidentified fragmentary materials. In cases of mass disasters and commingling it is important to determine whether fragments are osseous or not to aid in the process of identifying individuals. Currently, most elemental analyses of bones are conducted using portable X-ray fluorescence (pXRF). However, there are limitations to the types of elements pXRF can detect without the need for additional equipment or analysis time, specifically elements with lower atomic weights. Handheld Laser-Induced Breakdown Spectroscopy (LIBS) offers a sophisticated alternative to pXRF by using rapid laser ablation to analyze elements. With this analysis occurring at the micro-scale, the technique is virtually non-destructive to the sample and cannot typically be seen by the naked eye. Human skeletal materials were utilized from the donated collection at the Institute of Forensic and Applied Science at the University of South Florida. The sample consists of nine donors: four males and five females ranging from 28-79 years old, including one set of cremains. A SciAps Z-300 LIBS Analyzer was used to collect 15 data shots at 206 locations across each skeleton. Preliminary results suggest LIBS can detect differences in the burial micro-environments, demonstrating an ability to categorize donors based on disposition. The LIBS spectral data revealed the presence of metals consistent with the cages placed over some donors to prevent scavenging, allowing the caged donors to be distinguished from the non-caged donors. Further analysis of the spectral data is necessary for greater discrimination of individuals in a commingled context.

Dental sexual dimorphism in two closely related monkey species is achieved through two distinct patterns of growth

CHRISANDRA KUFELDT

Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

Sexual dimorphism in the primate dentition develops through two processes: rate differences and bimaturation (males and females grow at the same rate, but males grow for longer periods). Previous studies have largely focused on canine development in hominoids and found that

dimorphism is primarily achieved through bimaturation. However, dental development is a complex process that has been linked to somatic development, habitat quality, phylogeny, and life history, and it remains unclear whether sexual dimorphism in enamel growth is present in non-canine teeth. Using incremental growth lines, enamel growth was measured in the mandibular medial incisors (I₁) and first molars (M₁) from mixed-sex samples of papionini monkeys, *Macaca mulatta* and *Papio hamadryas-anubis*. Results show that there are distinct sex-related differences in enamel growth in both species. In *Papio*, dimorphism in enamel growth is a product of bimaturation, while in *Macaca*, dimorphism is achieved through rate differences. In the latter, the rate of enamel secretion, extension, and crown formation are faster in males, while the duration of crown formation is longer in females. As the presence of sexual dimorphism is associated with inter-sex aggression and social organization, the finding that two closely related species with similar social structures differ in how sexual dimorphism is achieved has implications for interpreting development, socioecology, and phylogeny in the primate fossil record. To date, sexual dimorphism through rate differences in enamel growth has only been identified in the Eocene fossil *Cantius*, suggesting this process of dimorphism development has likely evolved numerous times across the primate lineage.

In vivo kinematics of the transverse tarsal joint complex in *Macaca mulatta* using XROMM

SHARON KUO^{1,2}, NICHOLAS J. GIDMARK^{3,4}, MICHAEL C. GRANATOSKY⁵, MYRA F. LAIRD^{4,6}, CALLUM F. ROSS⁴ and CAROL V. WARD¹

¹Pathology and Anatomical Sciences, University of Missouri, ²Anthropology, Pennsylvania State University, ³Biology, Knox College, ⁴Organismal Biology and Anatomy, University of Chicago, ⁵Anatomy, New York Institute of Technology, ⁶Integrative Anatomical Sciences, University of Southern California

The transverse tarsal joint consists of the talonavicular and calcaneocuboid joints. These joints are assumed to act as a single complex during locomotion in primates and have been used to make inferences about primate evolution, including the adoption of bipedality in hominins. However, the motions at the transverse tarsal joint are poorly understood due to the logistical difficulties of quantifying intertarsal rotation during locomotion. As a result, the degree to which the calcaneocuboid and talonavicular joints function together as a single transverse tarsal joint complex remains unknown. Accurate quantification of motion at the midfoot is important for interpreting the functional signal in fossils.

We used X-ray Reconstruction of Moving Morphology (XROMM) to quantify intertarsal rotations at the naviculocuboid, calcaneocuboid, and talonavicular joints in an adult male *Macaca mulatta* during locomotion. Data show 10-15° of rotation about the long axis of the foot between the cuboid and navicular. More inversion/eversion (11°-27°) than plantarflexion/dorsiflexion (8°-15°) occurred at the talonavicular joint whereas there were roughly equal amounts of inversion/eversion (9°-17°) and plantarflexion/dorsiflexion (6°-18°) at the calcaneocuboid joint. These results are consistent with previous observations that the talonavicular joint plays a larger role in midfoot inversion than the calcaneocuboid joint. Additionally, there was no significant correlation between the amount of inversion/eversion or plantarflexion/dorsiflexion between the two joints. The results of this study challenge the treatment of the talonavicular and calcaneocuboid joints as a single joint complex and have important implications for understanding how a stiff midfoot evolved in fossil hominins.

Funding statement: XROMM surgery, animal care, and scanning were funded by NSF MRI-DBI 1338066 and the University of Missouri Department of Pathology and Anatomical Sciences

Linear and cross-sectional asymmetry in the humerus during ontogeny

HELEN KURKI¹, LESLEY HARRINGTON², BENJAMIN OSIPOV³, LIBBY COWGILL⁴ and MARLA MACKINNON¹

¹Department of Anthropology, University of Victoria, ²Department of Anthropology, University of Alberta, ³Department of Orthopedic Surgery, University of California at Davis, ⁴Department of Anthropology, University of Missouri

In humans, the upper limb displays predominantly right-side dominant asymmetry, typically associated with asymmetrical mechanical loading. Arm asymmetries in linear dimensions and cross-sectional shape in adults are often used as measures of health and activity. While it is during ontogeny that the skeleton is most plastic, and adult asymmetries largely reflect activity levels adopted during this period, few studies have looked at asymmetry in sub-adults. Cross-section geometry (CSG) is used to assess habitual manipulative behaviors and activity levels, and may be expected to develop greater asymmetry than bone size alone (i.e., linear dimensions). Humerus asymmetry of linear dimensions (bone length, and proximal and distal breadths) and of maximum bending rigidity (I_{max}) at 30%, 50% and 70% bone length are examined to assess whether these aspects of biomechanical asymmetry develop in concert and in similar directions and magnitudes using archaeological hunter-gatherer sub-adult burials (n=82). Our analysis finds that I_{max} asymmetry magnitudes are consistently higher than for linear measures, and only directional asymmetry

ABSTRACTS

of articular breadths show moderate but significant correlations with those of I_{max} (distal with 30% and 50%, proximal with 50% and 70%). Humerus length displays the lowest and least variable directional and absolute asymmetries, I_{max} locations the highest and most variable. All directional asymmetries are positively correlated with age, but few absolute asymmetries are. There is high variability in the magnitude and direction of asymmetry of younger individuals (e.g., infants), suggesting that a baseline functional signal may be important for interpreting biomechanical properties of the humerus.

Funding for this research was provided by the Natural Sciences and Engineering Research Council of Canada (RGPGP-2014-00054), the University of Alberta, and the University of Victoria.

Human mothers' breast tissues role in neonate body temperature management

TIINA M. KUVAJA

Department of Archaeology, University of Oulu

Compared to other primates human females possess considerably large amount of fat tissue around their mammary gland throughout adulthood. In this study we wanted to test a potential hypothesis that suggests that externally ample female breasts developed to support the neonatal body's thermal balance through increased skin contact, thereby compensating for the loss of insulating fur and the relative developmental helplessness of the newborn. To conduct this study we wanted to determinate how female breast tissue itself reacts in varied temperatures. Test was conducted in climatic chamber and was documented via thermal imaging.

Climatic chamber introduced three different temperatures (+32, +27, +18 degrees of Celsius) where volunteers ($n=27$) were tested in three 20 minute periods with 30 minutes intervals between, allowing the tissue enough time to adjust to the new temperature. The subjects' temperature was documented with a thermal imaging camera (FLIR SYSTEMS ThermoCAM PM695 PAL) and the data analyzed with the Thermacell researcher program. Our study revealed clear differences between our study groups; breastfeeding women had clear resilience to the decrease in temperature and maintained a higher and more even temperature under all temperature conditions compared to the breast tissue of the other two groups. Men's breast tissue temperature decreased the fastest and lowest among the groups. The pilot study indicates that in addition to a larger surface area, a woman's breast, especially breastfeeding, is also a more effective source of heat for neonate by itself.

Correlation of genetic distance to morphological distance in dental metrics and non-metrics

RACHEL A. KUZMA

Anthropology, Washington University in St. Louis

Previous dental research has assumed that metric and non-metric characters have a genetic component and can be used to determine genetic affinity. This research tests the hypothesis that morphological distances based on dental metrics and non-metrics correlate to genetic distance across diverse human populations. Dental phenotypic matrices for both dental metrics and non-metrics were computed using the R-matrix method. Phenotypic matrices were calculated with a heritability estimate of $h^2=0.5$. This value is based on the approximate average of heritability estimates determined from family and twin studies assessing dental anatomy. Genetic R-matrices have been taken from published research that was conducted assessing the association between cranial morphological distance and genetic distance for the same sample populations. Off-diagonal R-matrix values from the genetic and phenotypic matrices were compared using Mantel tests, with the genetic matrices being compared against the metric and non-metric matrices independently. In addition, Dow-Cheverud tests were performed to determine whether dental metrics or non-metrics were significantly more correlated to genetic affinity. Results indicate that there is a correlation between dental phenotypic data and genetic affinity. Further, both metric and non-metric data can serve as proxies for genetic data. These results have important implications for assessing population level relationships among fossil hominins.

Reconstructing 10,000 years of human population history in western North and South America: Continuities and discontinuities with genomic and morphological data

SUSAN KUZMINSKY^{1,2} and LARS FEHREN-SCHMITZ²

¹Department of Anthropology & Applied Archaeology, Eastern New Mexico University,

²Anthropology Department, University of California, Santa Cruz

Conflicting genomic, archaeological and morphological studies have led to intense debates centered on the pattern and processes of ancient human dispersals into the Americas. Although there is a recent emphasis on genome-wide research to assess population history, previous biological studies focused largely on craniofacial data, many of which revealed differences between early and late Holocene populations and morphological variability among early American crania >8000 years BP. Given the purported discontinuity between cranial and genetic data,

we reexamine this assumption by comparing genomic and craniofacial 3D data for 250 individuals from 30 archaeological sites in the Americas (eight skeletons >8000 years BP). Using 3D geometric morphometrics, PCA and computed distance statistics, our results revealed the following continuities with genomic data: (1) similar to Anzick 1, Kennewick (N. America) and Baño Nuevo (Patagonia) early skeletons show biological affinities to ancient North and South American populations; (2) a shared ancestry between prehistoric California and coast/highland populations of Peru and Chile; and (3) patterns of shared ancestry and homogeneity between archaic North and South American populations, respectively. 3D morphological analyses support both a coastal and Clovis-interior migration route into the Americas, conflicting with some genetic and archaeological research that has favored a Pacific coastal model of dispersal into the New World. This study highlights the importance of combining datasets from prehistoric sites, but we still face limitations, namely a dearth of accessible human remains in key regions, including the North American plains, the Andean highlands and Amazon of South America.

Spina bifida occulta in a Basketmaker II sample from southeastern Utah: A case for nutritional deficiency in its etiology

GARNET A. KWADER and PATRICIA M. LAMBERT
Anthropology Program, Utah State University

In this paper we report on an unusually high frequency of spina bifida occulta (SBO) in a sample of 49 individuals with preserved sacra from Cave 7, a Basketmaker II site in SE Utah well known for its high rate of violent injury. Spina bifida (SB) is a congenital defect in which one or more vertebral arches fail to form properly, leaving a gap in the spinal column. SBO (closed SB) is a relatively mild and often asymptomatic form of the condition, usually affecting the sacrum. Although the causes of SB are not clear, both genetic predisposition and environmental factors—including maternal folate deficiency in particular—play a role in its expression. Here we bring together data on SBO, cribra orbitalia, and other health indicators with paleoclimatic data to examine possible causes and consequences of SB in this population.

In scoring SBO in the Cave 7 remains, we follow Molto et al. (2019) and exclude the sacral hiatus (S4-5). Observed defects include incomplete fusion or open arch defects of the S1, S1-S2, S2-S3, and S1-S5. In total, 39% of the sacra exhibit some form of SBO. This rate is about 2-3x the modern prevalence of SBO (12.4%-23%), evidence that environmental factors did play a causal role in SBO in the Cave 7 population. We suggest that genetic predisposition in combination with a folate-deficient maternal diet (emphasizing

ABSTRACTS

maize, pinyon nuts, seeds, and cottontail rabbits) may account for this high prevalence—especially as nutritional deficiency could have been exacerbated by drought and warfare.

This research was supported by a grant from the Mountain West Center, Utah State University

Ancient DNA reveals that few disease-associated loci have been strongly selected during recent human history

JOSEPH LACHANCE

School of Biological Sciences, Georgia Institute of Technology

Neutral and selective processes can alter the allele frequencies of disease-causing loci, and ancient samples allow us an unprecedented look at how our species has changed over time. Here, we analyzed a curated set of 2,709 GWAS loci in 143 ancient and 503 modern European genomes. We find that the majority of GWAS variants that impact health have negligible effects on fitness. Specifically, 895 of the 2,709 GWAS loci analyzed in our study show signatures of modest selection ($|s| > 0.001$), and 9 GWAS loci appear to be under strong selection ($|s| > 0.01$). Genetic variants that are located in the MHC region on chromosome 6 are enriched for signatures of selection. As expected, we found that protective alleles are more likely to be positively selected than alleles that increase the risk of complex diseases. This pattern was more pronounced for diseases that have an age of onset that occurs prior to reproduction. However, risk alleles at many disease-associated loci have increased in frequency over the last 10,000 years. This may be due to pleiotropy, recent relaxation of selection, and/or genetic hitchhiking of disease variants. Focusing on individual diseases, we find that alleles that protect against asthma are enriched for signatures of positive selection. Overall, these results demonstrate the potential of ancient DNA to improve our understanding of recent human evolution. Our results represent an important early step in using this new source of data to better understand how disease risk has changed over time.

This work was funded by startup funds from Georgia Institute of Technology and an NIH grant (R35GM133727) to Joseph Lachance.

Sweet tooth: Southwest Asian humans, their diet, and caries in the Middle and Upper Paleolithic

SARAH A. LACY

Anthropology, California State University Dominguez Hills

Evidence of oral pathology in Pleistocene humans has been more systemically documented now that non-paleopathologists recognize what it looks like. Dental caries or cavities, the disease

of dental tissue decay, is much more prevalent than initially assumed, but these cases in Late Pleistocene humans are not randomly distributed geographically: they cluster at lower latitudes, especially circum-Mediterranean. In Southwest Asia in the Middle Paleolithic, caries has been documented in six individuals from the site of Qafzeh and one from the site of Skhul (43.8% of total individuals examined). In the Upper Paleolithic to Epipaleolithic, Ohalo 1 and 2 both show carious lesions, and 15.4% of Natufian peoples sampled show caries. These values are relatively high for pre-agricultural populations elsewhere in the world, which begs the question: what about the Paleolithic Levantine diet or lifestyle is so (relatively) cariogenic? The bioavailability of dietary sugars is negatively correlated with latitude, and modern hunter-gathers at similar latitudes consume about a third of their calories from carbohydrates. More specific to the region, analysis of preserved dental calculus suggests consumption of dates and other sweet foods as well as many starchy foods. However, the explanation does not have to lay solely in diet. Multiple explanatory hypotheses beyond dietary sugar include dietary grit, ground water mineral content, and microbiome differences between hominins in Southwest Asia and elsewhere in Eurasia that could contribute to the carcinogenicity of their oral environments before the advent of wheat agriculture in the region.

This work was funded by the Leakey Foundation.

The Development and Application of Caribbean Isoscapes for Investigating Geographic Origins

JASON LAFFOON

Faculty of Archaeology, Leiden University

Isotopic analysis of bioarchaeological remains has become a powerful and widely employed method for addressing a wide range of research questions. The interpretation of stable and radiogenic isotope values for the purpose of inferring migration, mobility, movement, and geographic provenance requires comparisons with baseline isotopic variation and/or isoscapes. Over the last decade, strontium isotope ($^{87}\text{Sr}/^{86}\text{Sr}$) and oxygen isotope ($\delta^{18}\text{O}$) analyses have been extensively applied to the bioarchaeological record of the Caribbean region to address human paleomobility and the provenance of various biogenic raw materials and artefacts. This presentation focuses on the development and application of regional baseline oxygen and bioavailable strontium isotope data sets and associated isoscapes in the Caribbean. The effectiveness of integrating multiple isotope data and related isoscapes via a probabilistic approach has been recently validated with a modern individual of known geographic origin. This study illustrates the application of such an approach to bioarchaeological isotope data in

the Caribbean region. The results indicate that the use of these combined methods offers much potential for constraining the possible geographic origins of individuals but that the precision is highly variable and dependent on both the measured isotope values and the spatial distribution of baseline isotopic variation in the study area. This presentation will also highlight the potentials for further improving probabilistic assessments of geographic origin by: increasing the spatial extent and representativeness of baseline sampling, utilizing machine-learning methods for developing and refining regional isoscapes, and incorporating a wider range of isotopic and archaeological proxy data within Bayesian frameworks.

Sexual division of labor in a Celtic population from Northern Italy: patterns of enthesal changes and long bone shape and robusticity from Seminario Vescovile (Verona, 3rd-1st c BC)

ZITA LAFFRANCHI¹, DROSIA CHARISI¹, SYLVIA JIMÉNEZ BROBEIL¹ and MARCO MILELLA²

¹Department of Legal Medicine, Toxicology and Physical Anthropology, Medicine Faculty, University of Granada (Spain), ²Institute of Forensic Medicine, Department of Physical Anthropology, University of Bern (Switzerland)

The presence of a sexual division of labor has been the focus of bioarchaeological research in a broad range of prehistoric contexts. Nonetheless, few data are available about the presence and type of gendered activities among Celtic populations. This gap hampers the analysis of the social nuances characterizing these populations and a broader understanding of the socioeconomic patterns featuring Iron Age communities of Western Europe. Here, we address these issues by testing the presence of gendered activities in a Celtic population (Cenomani Gauls) from Seminario Vescovile (Verona, NE Italy, 3rd-1st c. BC).

Enthesal changes at 9 postcranial attachment sites, as well as humeral and femoral shape and robusticity indices calculated from external long bone measurements are compared between sexes in a sample of 56 adult individuals (N females=22; N males=34). The effect of sex, age, and side on the considered variables are tested by means of generalized linear models, generalized estimating equations, and Mann-Whitney tests.

Analyses show a lack of difference between sexes in long bone shape, a higher incidence of upper and, especially, lower limb enthesal changes in males, and higher long bone robusticity in females.

These results suggest the presence at SV of sex-specific activities mostly related to farming and differently influencing the considered variables. At the same time, this study underlines the

ABSTRACTS

need to consider non-functional factors (e.g. nutritional and developmental) when trying to infer patterns of physical activity from osteological variables.

Malagasy perspectives on pet lemurs outside of Madagascar

MARNI LAFLEUR¹, KIM E. REUTER² and SEHENO CORDUANT-ANDRIANTSARALAZA³

¹Anthropology, University of San Diego, ²N/A, Franklin Scholars, ³Plant Biology and Ecology, University of Antananarivo

In February 2019 "Malagasy ve ianao" (translates to 'I am Malagasy'), a popular Facebook page (~400K followers), shared a post of a Florida women's pet ring-tailed lemur (*Lemur catta*). We downloaded and categorized all 500 comments on this post to assess the responses. Our underlying hypothesis was that this post could negatively impact lemur conservation, since photos of pet lemurs could motivate people to acquire lemurs. The majority of comments (n=176) indicated that this lemur ownership is **permissible**, because the lemur has good welfare (n=79), or because conservation for lemurs is poor in Madagascar (n=97). The next largest collection of comments (n=144) indicated that it is ethically wrong to keep a lemur as a pet, because 'lemurs are not pets' (n=75), or because it is illegal to take lemurs from forests in Madagascar (n=52). 'Ethically wrong' rationales were more often cited for conservation reasons from English-language commenters (X²= 13.634, df 2, p = 0.0011, n = 145) and cultural reasons from Malagasy-language commenters (X²= 6.382, df 2, p = 0.0411, n = 145), although no other language specific differences were found. Only 2 comments indicated that people would like to have their own pet lemur. These results suggest that this post did not result in viewers wanting to acquire a lemur, and that people generally do not understand that pet lemurs globally come from stocks outside of Madagascar, while those in Madagascar come from the wild.

More than maize? New insights into dietary patterns at the early Fort Ancient site, Turpin (33Ha19), from microwear analysis.

EMMA M. LAGAN¹, CHRISTOPHER W. SCHMIDT² and ROBERT A. COOK¹

¹Department of Anthropology, The Ohio State University, ²Department of Anthropology, University of Indianapolis

Fort Ancient groups in the Middle Ohio River Valley are among the first farmers in the region, a claim that is supported by isotopic and paleobotanical evidence. These methods consider long-term paleodiet via carbon isotope values in human hard tissues. This study considers foods eaten by individuals (paleocuisine) at an early Fort Ancient site, Turpin (33Ha19), through dental microwear

texture analysis (DMTA). Occlusal texture complexity (Asfc) and anisotropy (epLsar) were calculated to assess dietary hardness in 39 individuals (M/M?=19, F/F?=11, U=9) and contextualized via comparisons to Mississippian and other late pre-contact groups. While anisotropy (epLsaravg = 0.00322) is consistent with Mississippian (and other) New World farmers, complexity (asfcavg = 1.73655) is higher than average (1.36). This suggests that while Fort Ancient people practiced maize agriculture, they also had either 1) a processing method unique to Fort Ancient farmers, or 2) supplementation of maize in the diet by hard-food objects, such as nuts. While nuts are present in the paleobotanical record, this possibility is not often explored. A subset of 15 individuals, including 3 strontium outliers (potentially migrants), are examined intra-individually with stable carbon isotopes ($\delta^{13}C_{\text{coll}}$ average = -9.8545, n= 11; $\delta^{13}C_{\text{apex}}$ average = -5.225, n = 4). This combination of methods explores ways of understanding food consumption over time (including nut and meat consumption), with the potential to reveal dietary shifts within individuals.

Proximal radial morphology of *Paranthropus* and early *Homo*

MICHAEL R. LAGUE

School of Natural Sciences & Mathematics, Stockton University

The discovery of a partial skeleton of *Paranthropus boisei* (OH 80) provided a much-needed comparative basis for the taxonomic identification of early Pleistocene hominin postcranial fossils. This study examines the morphology of the OH 80 radius to determine whether it differs significantly from early *Homo* morphology and to assess the taxonomy of four potential *P. boisei* specimens from eastern Africa (KNM-ER 1500e, 3956a, 3888; Omo 323-10003) and two potential *P. robustus* specimens from Swartkrans (SKX 3699, SK 2045). Multivariate ordination techniques were applied to landmark and linear shape data collected from 3D surface scans of the radii of fossil hominins (n = 17) and extant hominoids (n = 98). Mantel tests of matrix correlation were used to statistically test hypotheses about fossil morphometric relationships by comparing empirically-derived Procrustes distance matrices to hypothetical model matrices. Shape variation is consistent with a hypothesis of two morphotypes (*Homo* and *Paranthropus*) represented among early Pleistocene hominin radii. It is highly probable that all study specimens represent *Paranthropus* except for the radius from the KNM-ER 1500 partial skeleton, which bears a stronger resemblance to specimens belonging to *Homo*. Compared to *Homo*, purported *Paranthropus* specimens exhibit more chimpanzee-like radial head morphology (e.g., proximodistally shorter head) and (in *P. boisei*) a more pronounced degree of mediolateral neck constriction that is unusual

among hominoids. *Paranthropus* does not differ from early *Homo*, however, with respect to beveling of the medial aspect of the radial head, which is generally intermediate between *Pan* and modern *Homo* in both groups.

Supported by grants from the Leakey Foundation and the Wenner-Gren Foundation to J.M. Plavcan & C.V. Ward.

Gape drives temporalis muscle architecture dynamics in the tufted capuchin feeding system

MYRA F. LAIRD¹, MICHAEL C. GRANATOSKY², ANDREA B. TAYLOR³ and CALLUM F. ROSS⁴

¹Integrative Anatomical Sciences, University of Southern California, ²Anatomy, New York Institute of Technology, ³Basic Science, Touro University, ⁴Organismal Biology and Anatomy, University of Chicago

Bite force is key to understanding primate feeding-system form-function relationships. Maximum bite force capacity can be calculated from static estimates of a muscle's physiologic cross-sectional area (PCSA). However, for pinnate-fibered muscles, force output varies during contraction because pinnate fibers rotate as they shorten, altering the amount of force directed along the muscle's line of action. A lack of *in vivo* data on muscle architecture dynamics of the jaw adductors has limited our understanding of how gape impacts fiber length and pinnation angle during feeding. Here we present novel data on muscle architecture dynamics of the temporalis muscle in primates and examine the influence of gape on architectural measurements used to estimate PCSA.

We recorded fascicle-level architecture dynamics in the temporalis muscles of three adult female tufted capuchins (*Sapajus apella*) using biplanar video fluoroscopy and the X-Ray Reconstruction of Moving Morphology (XROMM) workflow. Subjects completed chewing trials on five foods of different material properties, resulting in 93 chewing cycles. Gape explained greater than 80% of the variation in fascicle length and 30-50% of variation in fascicle angulation; variation in fascicle angulation was two times greater in an anteroposterior compared to mediolateral plane. Fascicle rotation varied with gape such that the architectural gearing ratio was lowest during bite force production. Collectively, these data emphasize the importance of correcting for posture-dependent variation and the influence of velocity on bite force. Incorporating dynamic muscle architecture into models of the primate feeding system will improve bite force estimates in living primates and fossil taxa.

This research was supported through National Science Foundation (NSF-BCS-1440516, NSF-BCS-1440541, NSF-BCS-1440542, NSF-BCS-1440545, NSF-BCS-1627206) and the AAPA Cobb Award.

ABSTRACTS

Age Class and Species Differences in Agonistic and Affiliative Behaviors between *Alouatta palliata* and *Cebus capucinus*

CELESTE LAM¹, LAURA BOLT² and LYDIA LIGHT¹

¹Anthropology, UNC Charlotte, ²Primate Behavioral Ecology, Maderas Rainforest Conservancy Field School

Mantled howler monkeys (*Alouatta palliata*) and white-faced capuchins (*Cebus capucinus*) are excellent models to study social interactions, specifically the expression of agonism and affiliation, as these species vary from one another significantly. *A. palliata* is a species that is known to exhibit weak social relationships while *C. capucinus* is often used as a model of strong social bonds. In this study, I looked at the species and age class differences in agonistic and affiliative behaviors between wild populations of *A. palliata* and *C. capucinus* at the Maderas Rainforest Conservancy in La Suerte. Data was collected over a 21-hour period from June-July 2019 using 10-minute 1/0 sampling with 2-minute intervals. Overall, I found that *A. palliata* displayed lower levels of agonistic behaviors compared to *C. capucinus* (.002/minute -1.92 SD vs .019/minutes 1.924 SD) and this difference approached significance (Mann-Whitney $U = 1594$, $p = .0543$). In addition, *C. capucinus* exhibited higher levels of affiliative behaviors than *A. palliata* (.269/minute 2.798 SD vs .164/minutes -2.798 SD) and this difference approached significance (Mann-Whitney $U = 1250.5$, $p = .0051$). Age class did not differ significantly between groups ($p > 0.05$). Through understanding the differences in agonistic and affiliative behaviors between *A. palliata* and *C. capucinus* researchers can establish a behavioral baseline to better evaluate how the two species interact in their current ecosystem. This can help researchers determine how the two species might continue to coexist if resources diminish as their habitats shrink and the climate changes.

Examination of sex differences in condylar arthritis of the mandible using a documented osteological collection

KATHERINE M. LANE¹ and FRANK L. WILLIAMS²

¹Anthropology, University of Central Florida, ²Anthropology, Georgia State University

Condylar osteoarthritis is a well-documented pathology of the facial skeleton yet sex differences with respect to the aging process are poorly understood given the variability of masticatory stress. To address whether the sexes differed as a result of advancing age, an examination of right and left mandibular condyles was performed using 154 dry skeletal specimens—77 males and 77 females—of known age and sex curated at the William M. Bass Donated Skeletal Collection at the University of Tennessee, Knoxville. Each condylar

head was scored for osteoarthritic changes using a three-point scale to assess flattening, resorption, and osteophytosis. Age cohorts included young adults (25-49 years), older adults (50-65 years), and elderly adults (66-85 years). Right and left mandibular condylar heads were pooled as no significant asymmetry was identified using paired samples t-tests. For males, differences in osteoarthritis are not significant between young and older adults but are pronounced between older and elderly adults for flattening ($p=0.012$). For females, differences in osteoarthritic changes are not statistically significant between young and older adults but older and elderly adults are significantly different for resorption ($p=0.003$). Both sexes had marked differences between young adults and the elderly, with respect to flattening, resorption, and osteophytosis for males and resorption and osteophytosis for females. The results indicate an increase in the severity of osteoarthritic changes as a function of advancing age, with males exhibiting greater osteoarthritic changes, perhaps due to heavier masticatory loading or a more rapid aging of the skeleton.

Strontium analyses (⁸⁷Sr/⁸⁶Sr, [Sr]) reveals non-local origin of humans with intentionally modified crania in Mtskheta, Georgia in the 4th-7th centuries AD

NATALIE LANGOWSKI¹, ROLAND MAAS² and VARSHA PILBROW¹

¹Department of Anatomy and Neuroscience, The University of Melbourne, ²School of Earth Sciences, The University of Melbourne

The archaeology of Greater Mtskheta (Georgia) demonstrates interaction between local human populations and Greek, Roman, and Sassanid civilisations during the 4th century BC to the 7th century AD. Samtavro cemetery in Mtskheta records a cultural transition in the 4th-5th centuries AD, with declining tile-lined burials containing single interments, and proliferation of stone-cists containing multiple disarticulated skeletons and individuals with intentionally modified crania. The modified crania belong almost exclusively to adult females with no juveniles represented, suggesting a novel cultural influence was introduced to Mtskheta via an influx of migrants. Strontium concentrations [Sr] and isotope ratios (⁸⁷Sr/⁸⁶Sr) were measured from environmental samples in the area, and from tooth enamel of individuals with modified ($n = 14$) and unmodified ($n = 9$) skulls from 1st-7th century tombs in Mtskheta. Environmental ⁸⁷Sr/⁸⁶Sr in Mtskheta ranges between 0.70673-0.70861. ⁸⁷Sr/⁸⁶Sr of four head-modified individuals exceed the local Mtskheta range (0.70862-0.70894), suggesting a non-local origin. Further, head-modified humans show distinctly higher ⁸⁷Sr/⁸⁶Sr (0.70788-0.70894) and lower [Sr] ($= 177 \pm 65$ ppm) values than the unmodified group (⁸⁷Sr/⁸⁶Sr: 0.70722-0.70813; [Sr]: $= 246 \pm 76$ ppm), indicating different patterns of land-use and residence in

their early lives. These results confirm non-locals with modified skulls were present in Mtskheta in the 4th-7th centuries. The absence of both non-local burial goods and juveniles with modified heads suggests that the migrants were likely integrated into the local society and did not pass on the custom of cranial modification to the next generation.

This research was supported by the Leone Crawford Travel Grant [2016] from the Near Eastern Archaeology Foundation.

A re-evaluation of fossil hominin obstetric constraints

NATALIE M. LAUDICINA^{1,2} and MATT CARTMILL^{2,3}

¹Biomedical Sciences, Grand Valley State University, ²Anthropology, Boston University, ³Evolutionary Anthropology, Duke University

Compared to other primates, humans are claimed to have a more difficult childbirth involving extreme cephalopelvic disproportion and variable birth-canal cross-sections that necessitate fetal rotations. The antecedents of this "obstetric dilemma" in hominins are debated. Because traditional obstetric planes (inlet, midplane, outlet) may not accurately define points of constriction in non-human specimens, a re-evaluation of obstetric constraints in fossil hominins is called for.

Five fossil hominin pelves (A.L. 288-1, Sts-14, Sts-65, MH2, Tabun-1) were reconstructed and the minimum dimensions within each birth canal were determined, using appropriate pelvic elements from other fossil specimens to reconstruct fragmentary specimens. To assess the degree of cephalopelvic disproportion, estimated fetal head dimensions (length and breadth) and shoulder breadth were compared to the minimum AP and ML dimensions of the birth canal. Next, the pattern of shape change (AP/ML) throughout the birth canal was examined.

These analyses demonstrate that human-defined obstetric planes do not represent the true minimum dimensions in fossil hominin birth canals. The pelvic inlet represents the minimum AP dimension in modern humans and MH2, but in no other fossils. The fossil pelves exhibit shape changes throughout the birth canal that differ in each specimen. Inferred birth mechanisms in these fossil hominins differ correspondingly, and do not present a clear, anagenetic trajectory from easy to difficult childbirth. Interspecific differences in birth canal morphology and fetal dimensions suggest that birth was accommodated in different species by differing mechanisms, including altered pelvic morphology, cranial molding, and different fetal rotation patterns.

Wenner-Gren Foundation Dissertation Fieldwork Grant and Boston University Summer Graduate Research Abroad Fellowship

ABSTRACTS

The influence of foot orientation on side foot forces during walking in a straight line

STEVEN G. LAUTZENHEISER^{1,2}, ADAM D. SYLVESTER³ and PATRICIA A. KRAMER^{1,2}

¹Department of Anthropology, University of Washington, ²Department of Orthopaedics and Sports Medicine, University of Washington, ³Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine

Ground reaction forces (GRFs) are typically measured in terms of a world coordinate system (WCS) that is also used to describe the physical surroundings and aligns well with anatomical directions. In straight-line walking, side GRFs are much smaller than forward or vertical GRFs, leading to the assumption that side forces are of negligible importance in understanding foot morphology. The orientation of the foot, however, is not necessarily aligned with the WCS. We hypothesized that side forces in the foot coordinate system (FCS) are larger than the presumed negligible ones in WCS.

Using an eight-camera Qualisys system with four Kistler force plates, kinetic and kinematic data were collected for 20 unshod participants walking at their self-selected normal pace. The FCS, which tracks the orientation of foot as it moves through space, was calculated from the position of the heel and first and fifth metatarsal heads. GRFs were translated and rotated from WCS to FCS using custom software. Forward, side, and vertical forces were compared between WCS and FCS.

In FCS, side forces developed during the propulsive phase are 150-200N larger than in WCS ($p < 0.001$), and the maximum side force is directed toward the centerline of the body in WCS, while in FCS it is directed laterally. Given that the foot and its individual elements are asymmetrical, it suggests that side forces in the foot are greater than previously assumed because of limitations of using the WCS. Consequences for the foot are unclear and warrant further investigation.

The Yale Peabody Museum Sifaka Database: A resource for teaching and research

RICHARD R. LAWLER¹, DIANE K. BROCKMAN², JEANNIN RANAIVONASY³, JOELISOA RATSIRARSON³, ERIC J. SARGIS^{4,6}, RUSSELL D. WHITE⁵ and ALISON F. RICHARD⁶

¹Department of Sociology and Anthropology, James Madison University, ²Department of Anthropology, University of North Carolina Charlotte, ³School of Agronomy, University of Antananarivo, ⁴Division of Vertebrate Zoology, Yale Peabody Museum of Natural History, ⁵Collections and Research, Yale Peabody Museum of Natural History, ⁶Department of Anthropology, Yale University

When compared to most other mammals, primates are distinguished by their relatively late age at sexual maturity and long lifespans. To this end, long-term data on wild primates are important for characterizing demographic and reproductive patterns that influence both the microevolutionary dynamics and the conservation status of primate populations. The Sifaka Database is a publicly accessible database that contains information on over 750 individual Verreaux's Sifaka (*Propithecus verreauxi*). Between 1984 and 2011 individual sifaka have been captured, measured, marked, released, and subsequently censused at Bezà Mahafaly Special Reserve, southwest Madagascar. The database includes the following information on individuals: age, body mass, social group membership (including transfers between groups), reproductive history of marked females, location of individuals, and qualitative and quantitative data on body condition and body segments. The database was accessioned to the Yale Peabody Museum (YPM), Division of Vertebrate Zoology under a collaborative agreement between the YPM and the Ecole Supérieure des Sciences Agronomiques (ESSA), University of Antananarivo, Madagascar. A joint YPM/ESSA Steering Committee oversees the safeguard and facilitation of use of the database by researchers and teachers. Examples of how the database has been used include a quantitative genetic study of tooth dimensions and a comparative study of sexual dimorphism in mammals. We discuss several additional ways to use the database including as a teaching resource for biostatistics and vertebrate demography, as well as to address myriad theoretical and applied research questions that require information on the life history events of individuals in an evolving primate population.

Funding provided by the Liz Claiborne and Art Ortenberg Foundation.

Morphological differences in the mandibular dental arch and symphysis of great ape subspecies and their significance for the hominin fossil record

JULIE LAWRENCE¹ and CHRIS ROBINSON^{2,3,4}

¹School of Human Evolution and Social Change, Arizona State University, ²Department of Biological Sciences, Bronx Community College, ³Doctoral Program in Anthropology, The Graduate Center, CUNY, ⁴NYCEP, New York Consortium in Evolutionary Primatology

Other than teeth, mandibular remains are the predominate elements recovered in the hominin fossil record. However, debate remains over their efficacy in differentiating among taxa, which is critical given the importance of alpha taxonomy in our ever-growing bushy family tree. Our great ape relatives, gorillas, chimpanzees, and orangutans, are a vital source of information on how subtle differences in diet, geography, and morphology may coalesce with phylogeny. We

examined 3D landmark data from two commonly preserved anatomical regions of the mandible, the dental arcade and symphysis, in recognized subspecies of Gorilla (*G. beringei graueri* (n=29) and *G. b. beringei* (n=15)), and Pan (*P. troglodytes verus* (n= 28), *P. t. troglodytes* (n=48), and *P. t. schweinfurthi* (n=30)). Both the dental arch and symphysis morphology were able to significantly differentiate between subspecies of Gorilla *beringei*. Chimpanzee subspecies differed in their dental arch morphology but *P. t. schweinfurthi* and *P. t. troglodytes* overlapped in their symphyseal morphology. We compared our results with species-level analyses by including Gorilla gorilla (*Gorilla gorilla* (n=44), *Pan paniscus* (n=25), and *Pongo* (*P. abelii* (n=36) and *P. pygmaeus* (n=34)). These data to some extent mirror those of previous linear analyses of the dental arcade and mandibular symphysis. Further, more extensive morphological differences between taxa may echo known differences in diet among these taxa.

Allometry used for the osteometric sorting of multiple long bones simultaneously

AMANDA B. LEE^{1,2} and LYLE W. KONIGSBERG²

¹Anthropology, University of Illinois at Chicago, ²Anthropology, University of Illinois at Urbana-Champaign

The resolution of commingling requires the re-association of all skeletal elements. Typically, osteometric techniques of skeletal re-association involve linear regression analyses. These analyses are limited to two-bone comparisons at a time, lengthening and complicating the assessment of assemblages. This study describes and tests an algorithmic approach to osteometric sorting based on shape variables and multivariate distance in long bones that sorts multiple long bones simultaneously.

The algorithm produces Mosimann shape variables for every possible combination of bones and compares these variables to the reference sample centroid using Mahalanobis distances (D^2)—a multivariate measure of distance. This method is evaluated in trials using a reference data set (N=2,271) of postcranial remains to test a separate sample data set (N=25). This new approach is compared to published sorting methods using the same reference data set. Receiver operating characteristic curves and Youden's J statistic demonstrate the method's diagnostic ability. For the paired models, the humerus-femur sorting models outperformed other combinations of the two-bone models (e.g., humerus-radius). For the three-bone matching model, the humerus-radius-femur model outperformed other combinations of the three-bone models. The four-bone model outperformed all two-bone and three-bone models.

ABSTRACTS

This research is novel in that there are currently no automated tools for re-associating more than two bones at a time. The automation of simultaneous matching of multiple bones reduces the need for multiple paired comparisons and the amount of processing power and manpower needed for these analyses. These results have implications for greatly expediting the osteometric sorting process, especially with large assemblages.

Where are the women warriors? Evidence for Gender Equality on the Mongolian Steppe (209 BC-840 AD)

CHRISTINE LEE and YAHAIRA GONZALEZ

Anthropology, California State University, Los Angeles

This study looked for evidence of women warriors among the nomadic pastoralists of ancient Mongolia. Twenty-nine elite burials (16 males, 10 females, 3 indeterminate) were analyzed. These were divided into three time periods, Xiongnu (209 BC-93 AD), Xianbei (147-552 AD), and Turkic (552-840 AD). Potential warriors were defined through evidence of prolonged horseback riding, archery, and trauma patterns. Skeletal elements were observed for arthritis, musculoskeletal markers (scapula, clavicle, humerus, ulna, pelvis, femur, tibia), Schmorl's nodes, and trauma. Males (83-100%), females (33-100%), and adolescents (100%) exhibit evidence for horseback riding through all time periods. Males appear to be practicing archery through all time periods (80-100%). Women's participation in archery is more varied (50-100%). Trauma percentages for males and females increase from the Xiongnu to Xianbei Periods. Male trauma percentages (60-83%) were consistently higher than females (0-33%). All of the trauma appears to be accidental and related to horseback riding. Half of the women in the Xiongnu Period participated in horseback riding and archery. Xianbei Period women appear to be the most martial and mobile. Turkic Period women were the most sedentary and secluded. So, the Xianbei Period has the best evidence for potential warrior women. This time period is associated with the Ballad of Mulan and was characterized by political fragmentation and unrest. It may have been that women were needed to defend home and country alongside the men.

Household food production shows little effect on body size and composition in two samples of young adult women

KATHARINE MN. LEE¹, MARY P. ROGERS², ANDRZEJ GALBARCZYK³, GRAZYNA JASIENSKA³ and KATHRYN CLANCY^{1,4}

¹Department of Anthropology, University of Illinois Urbana-Champaign, ²Carl R Woese Institute of Genomic Biology, University of Illinois Urbana-Champaign, ³Department of Environmental Health, Faculty of Health Sciences, Jagiellonian University

Medical College, ⁴Beckman Institute of Advanced Science & Technology, University of Illinois Urbana-Champaign

Gardening and household food production are associated not only with increased access to nutritious foods, but also with increased physical activity. Together, these factors can have marked effects on health. We compare two samples of young (age 18-25) healthy white women, urban and suburban Polish-American women from Illinois (n=34) and rural Polish women at the Mogielica Human Ecology Study Site (n=31), to examine whether gardening and household food production contribute to differences in measures of body size and composition.

The two populations were not significantly different for any measures of body size (height, weight, BMI, percent body fat, lean mass, biacromial breadth, wrist breadth, elbow breadth, waist-to-hip ratio). The Polish sample was significantly (Fisher's exact test, p=0.005) more likely to report working in a garden than the Polish-American population (Polish: 66%, 19/29; Polish-American: 28%, 9/32) and to report that a portion of their summer diet consists of plant-based foods they grow themselves (Fisher's exact test, p=0.002; Polish 80%, 25/31; Polish-American 41%, 14/34) and animal-based foods they raise themselves (Fisher's exact test, p <0.001; Polish 45%, 14/31; Polish-American 3%, 1/34). Working in a garden was associated with lower percent body fat (p=0.035, post-hoc Tukey HSD: 3.97), but it was not associated with any of the other measures of body size.

Our results show that the rural Polish sample does more labor to produce their food than the Polish-American sample, but that this does not result in marked changes in body size in these young adult women.

This material is based upon work supported by the NSF (BCS-1317140, BCS-1732117, BCS-1650839, DGE-1144245), Wenner-Gren (#084918, #089812), APS Lewis and Clark Fund, Beckman Institute CS/Al Award, Sigma Xi, & more.

Virtual Reconstruction of Hungsu Child No. 1: The Case of Paleolithic Child Burial in Korea?

SANG-HEE LEE¹, GARY RICHARDS² and MARCELLA MORA¹

¹Anthropology, University of California at Riverside, ²Biomedical Sciences, University of the Pacific

Hungsu No. 1 is a child skeleton discovered in 1982 in Turubong, Korea. Its date has been unsettled despite several attempts at radiometric dating of the specimen, ranging from the often-cited date as the oldest Paleolithic burial in Korea, possibly as old as 40,000 years, to the controversial date of

17-19th century. In this paper, we present a virtual reconstruction of the Hungsu No. 1 and results of preliminary comparative analysis with other juvenile specimens.

The original Hungsu skeleton was CT scanned on a hospital scanner and reconstructed as isosurfaces in Amira. A similarly aged juvenile allowed replacement of missing bones or portions of bones; elements were reconstructed as meshes, rescaled, and refit. We also used MeshLab for merging meshes. Significant portions of the face and long bones had been reconstructed in plaster and this was removed and any errors corrected during reconstruction. An endocranial reconstruction was prepared from the cleaned cranium and compared to those of modern juveniles (6-8 years, n=7).

Endocast reconstruction and comparisons with recent humans confirms the extremely large cranial capacity (cf. Park and Lee 1990). The cranial vault is typical of recent humans. However, it differs from recent juveniles by having unusually strong temporoparietal expansion and accentuated bilateral waisting of the parieto-occipital region. The postcranial skeletal age lags behind the dental age. Dental caries are present and this is extremely unusual in Paleolithic specimens, suggesting a late date. Further research may shed light on the circumstances of the burial and taphonomy.

This research was supported by University of California, Riverside.

Immature female social preferences in wild populations of bonobos and chimpanzees

SEAN M. LEE¹, GOTTFRIED HOHMANN², BARBARA FRUTH^{3,4}, ELIZABETH V. LONSDORF⁵, KAITLIN R. WELLENS⁶, MARGARET A. STANTON⁵ and CARSON M. MURRAY¹

¹Center for the Advanced Study of Human Paleobiology, George Washington University, ²Department of Primatology, Max Planck Institute for Evolutionary Anthropology, ³School of Natural Sciences and Psychology, Liverpool John Moores University, ⁴Centre for Research and Conservation, Royal Zoological Society of Antwerp, ⁵Department of Psychology, Franklin and Marshall College, ⁶Department of Biology, Trinity Washington University

Primate socioecological theory predicts that in female-dispersing species, immigrant and resident females form weak social bonds due to being unrelated. In chimpanzees, one of humans' closest living relatives, dispersing females generally adhere to this prediction. However, in our other closest living relative, bonobos, dispersing females form cooperative social bonds with resident females outside of kinship. It is unclear whether female bonobos develop distinct social skills prior to dispersal when compared to female chimpanzees, which may facilitate

ABSTRACTS

their ability to form such bonds with nonkin, or whether females of the two species develop similar social skills that are expressed differently upon immigration. We compared behavioral data on immature females prior to dispersal in wild populations (n=14 bonobos, ~500 focal hours, LuiKotale, DRC; n=16 chimpanzees, ~5,000 focal hours, Gombe, TZ) in order to evaluate the extent to which social development differs between females of the two species. Using linear mixed modeling, we found that female bonobos socialized significantly more with unrelated adults than did female chimpanzees, even after controlling for social opportunities ($F_{1,40,114} = 17.930, P < 0.001$). We also found that, of these unrelated adult social partners, female bonobos interacted significantly more than expected with males as opposed to females during late infancy (age 2-4: $X^2_1 = 77.759, P < 0.001$; age 4-6: $X^2_1 = 86.119, P < 0.001$). We discuss our findings as they relate to female strategies in *Pan* and the potential role that species-differences in adult male social tolerance may play in immature female social development.

GWU; Explorers Club; SigmaXi; Leakey; Wenner-Gren; Max-Planck-Society; Federal Ministry of Education and Research (Germany); Royal Zoological Society of Antwerp; Jane Goodall Institute; NIH (R00HD057992); Leo S. Guthman Foundation; National Geographic Society.

Measuring nitrogen isotopes in tooth enamel: A novel method for characterizing trophic position in fossil ecosystems

JENNIFER N. LEICHLITER¹, TINA LÜDECKE², NICOLAS DUPREY⁴, DANIELA WINKLER¹, THOMAS TÜTKEN¹, MARCUS CLAUSS³ and ALFREDO MARTÁNEZ-GARCÍA⁴

¹Institute of Geosciences, Johannes Gutenberg University Mainz, ²Senckenberg Biodiversity and Climate Research Centre, Senckenberg Research Institute and Natural History Museum Frankfurt, ³Clinic for Zoo Animals, Exotic Pets and Wildlife, University of Zurich, ⁴Climate Geochemistry, Max Planck Institute for Chemistry

Carbon and oxygen isotope analyses of tooth enamel have greatly enhanced our understanding of the dietary ecology of fossil taxa including our hominin ancestors, but they reveal little about trophic position. $\delta^{15}\text{N}$ is widely used as a trophic indicator in modern ecosystems, however, $\delta^{15}\text{N}$ measurement in the fossil record is limited to relatively young (<100 ka), well-preserved collagen extracted from bone or dentine. While tooth enamel is far less susceptible to diagenetic alteration, nitrogen isotope analysis of tooth enamel has long been hindered by enamel's low nitrogen content.

Here, we present a novel oxidation-denitrification method for measuring the isotopic composition of inter-crystalline-bound nitrogen ($\delta^{15}\text{N}_{\text{enamel}}$) in

modern and fossil tooth enamel. This method requires 200-fold less nitrogen than traditional approaches and represents a promising dietary proxy applicable to deep time.

As proof of concept, we first analyzed modern tooth enamel samples from a controlled trophic feeding experiment and wild modern African fauna. $\delta^{15}\text{N}_{\text{enamel}}$ values were cross-validated against $\delta^{15}\text{N}$ values of tissues (e.g. collagen, muscle, etc.) from the same individuals. We then analyzed fossil tooth enamel of fauna from different fossil sites of varying ages and depositional settings, including two early hominin localities (Sterkfontein M4, South Africa and Chiwondo Beds, Malawi). In all modern and fossil datasets, we observe the same pattern of $\delta^{15}\text{N}_{\text{enamel}}$ enrichment (+ 2-3 ‰) between trophic levels.

These initial datasets give us a framework for interpreting $\delta^{15}\text{N}_{\text{enamel}}$ values in the fossil record and the potential to directly assess the consumption of meat and/or faunal resources by early hominins.

The project was funded in part by the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme (ERC CoG grant agreement No 681450) to T.T.

Allometric correlates of infant mass growth rate variation

STEVEN R. LEIGH¹, DANIEL J. NAUMENKO^{1,2}, NABEEL AFFARA³, DAVID B. DUNGER⁴, KEN K. ONG^{4,5}, ANDREW M. PRENTICE⁶, SOPHIE E. MOORE⁷ and ROBIN M. BERNSTEIN^{1,2}

¹Department of Anthropology, University of Colorado, ²Institute of Behavioral Science, University of Colorado Boulder, University of Colorado, ³Department of Pathology, University of Cambridge, ⁴Department of Paediatrics, University of Cambridge School of Clinical Medicine, ⁵MRC Epidemiology Unit, University of Cambridge School of Clinical Medicine, ⁶MRC Unit, The Gambia at LSHTM, Banjul, The Gambia, ⁷Department of Women and Children's Health, King's College London

Perturbations of growth and development may have serious, persistent consequences. We investigate weight growth irregularities to determine the consequences of possible perturbations on morphological integration and allometric relations during infancy. A primary hypothesis is that irregular weight growth (weight vs. age curve) is associated with decreased morphological integration and allometric shifts in other dimensions.

Repeated somatometric measures from a mixed-sex sample of 50 individual Gambian children from the HERO-G study (Hormonal and Epigenetic Regulators Of Growth), are analyzed to explore allometric correlates of weight growth irregularity. We calibrate irregularities qualitatively. Specifically, we distinguish individuals showing relatively smooth weight-for-age trajectories ("regular") from those showing clear and

repeated weight growth reductions and rebounds ("irregular"). Allometries are described by bivariate analyses of all variable pairs (weight, length, head circumference, and knee-heel length) measuring correlations and allometric coefficients. We test for mean differences in correlations and coefficients between groups.

Individuals categorically described as experiencing irregular growth generally show statistically significantly lower correlations for all 6 variable pairs, with the possible exception of length and weight vs. head circumference (both approach significance at $p=.05$). Allometric coefficients are consistent, with no major group differences in coefficients.

These preliminary results suggest that irregularities in weight growth are associated with reduced morphological integration during ontogeny. This may pose challenges for individuals with respect to catch-up growth, and could have biomechanical implications. However, allometric slopes appear to be robust to such irregularities, suggesting that general allometric relations between dimensions are preserved through disruptions.

Funded by the Bill and Melinda Gates Foundation (OPP1066932).

Paleoenvironments of Gona, Ethiopia, between 3-1 Mya: Evidence from faunal analysis

AMANDA C. LEISS¹, MICHAEL J. ROGERS² and SILESHI SEMAW³

¹Department of Anthropology, Yale University, ²Department of Anthropology, Southern Connecticut State University, ³Department of Prehistory, Centro Nacional de Investigación sobre la Evolución Humana

Gona, Ethiopia has arguably the longest continuous record of Early Stone Age (ESA) archaeology in the world, including the earliest confirmed evidence of carcass processing in the archaeological record (~2.6 million years ago [Ma]; Semaw et al., 2003; Domínguez-Rodrigo et al., 2005) and among the earliest Oldowan and Acheulian stone tool assemblages. The origin of the Oldowan and subsequent appearance of the Acheulian industrial complexes were instrumental in the ecological adaptations of early hominins. Due to the scarcity of deposits in the archaeological record, especially during the 2.8-2.3 Ma time range, little is known about the paleoenvironment(s) mediating the origin of the Oldowan or the emergence of the Acheulian; Gona provides a unique window for examining the context in which these changes occurred. More than 2000 fossil specimens were analyzed from collections at the National Museum of Ethiopia, including recently-collected finds, to reconstruct paleoenvironments between 3-1 million years ago at Gona. Community assemblage data including bovid tribal abundances and correspondence analysis provide evidence for

ABSTRACTS

heterogeneous landscapes through time. These data depict periods indicative of a mosaic landscape with seasonally flooded grasslands and a nearby wooded component, interspersed with seasonally arid grasslands. These paleoenvironmental reconstructions provide unparalleled context for the Early Stone Age assemblages at Gona and insights into hominin-environment interactions of early stone tool use.

This project was funded by The Leakey Foundation, The Wenner-Gren Foundation, Yale Institute for Biospheric Studies, Yale MacMillan Center, Sigma Xi, and the Council for Archaeological Studies, Yale University.

Improving juvenile stature estimation by incorporating maturational data

MAKENNA B. LENOVER^{1,2} and MAJA ŠEŠELJ¹

¹Anthropology, Bryn Mawr College, ²Anthropology, Pennsylvania State University

Juvenile stature estimation is very important in forensic and bioarchaeological contexts, as knowing the stature of an individual helps with identification and reconstructing population demographics. Unfortunately, juvenile stature prediction has been under-researched, and many current predictive models require known age, or have been modeled on samples of single geographic origin. Skeletal maturity could be a helpful variable to improve stature modeling, especially in samples of varied geographic ancestry, and thus body proportions.

To examine the relationship between skeletal growth and maturation, we first used logistic regression to quantify the relationship between long bone lengths and cumulative skeletal maturity scores for each bone while controlling for age (known age, N=269, and dental age, N=526). A strong correlation between growth and maturation given age exists, suggesting the integration of maturational variables could improve juvenile stature estimates. We then produced a series of regressions estimating stature with and without the skeletal maturation score in addition to long bone length and dental age. We found the inclusion of maturational data significantly improves the fit of stature prediction models independently of variables denoting population affinity or geographic ancestry (representing nine populations from four geographic groups).

Juvenile stature modeling could be improved by the addition of skeletal maturity information for each bone, thus not requiring any additional sources of information. Future research conducted on larger samples of diverse geographic origin, or data that

are longitudinal in nature, will allow for the formulation of more accurate predictive models of juvenile stature encompassing both growth and developmental data.

National Science Foundation DDIG #0925861; Wenner-Gren Foundation; NYU Graduate School of Arts and Science; New York Consortium in Evolutionary Primatology

A New Approach Toward Discovering and Characterizing Orphan Genes in the Human and Neanderthal Genomes

NATHAN H. LENTS¹, HUNTER R. JOHNSON², BEATRIZ MERCADO¹, JOSÉ GALVÁN¹, SAMANTHA VEE¹ and WILLIAM HIGGINS¹

¹Sciences, John Jay College, The City University of New York, ²Mathematics and Computer Science, John Jay College, The City University of New York

Although the genome sequence of >250 extant species is available, methods to model the evolution of these genomes are still developing. Among the most surprising results from the genomics era is the abundance of taxonomically-restricted genes (TRGs), casually called orphan genes, that appear to have no orthologs in closely related taxa. TRGs can be restricted to any taxonomic level, including species and genera, and a variety of mechanisms underpin their origin, from gene duplication and rapid divergence to creation of *de novo* genes through elaborate genomic rearrangements. In this project, we have endeavored to adapt genomic alignment tools, principally MUMmer 4.0, to the task of identifying genes that do not have orthologs in other extant African apes. Initial analysis of chromosomes 21, 22, X, and Y have revealed several genes on each chromosome that, upon detailed scrutiny, appear to be TRGs. Surprisingly, many TRGs we have identified to date encode micro-RNA molecules (miRNA) with no known orthologs in other species, arguing that regulation of gene expression by miRNAs may play an underappreciated role in recent human evolution. In further scrutinizing a subset of these, we have discovered a possible mechanism for the genesis of new miRNA genes through the duplication and rearrangement of tRNA and rRNA genes and pseudogenes. Moreover, we have found that the Neanderthal genome includes most, but not all, of these new miRNA genes. Herein, we present these results and our hypothesis for the origin of new miRNA genes in the human, Neanderthal, and Denisovan genomes.

The PRISM program at John Jay College supports the students, faculty, and research supplies for student-faculty research collaboration. This project is not supported by any specific funding at this time.

A preliminary study on the relationship between age-at-death, BMI and age-at-death estimations using pelvic indicators

NAOMI S. LEVIN

Anthropology, Texas State University

Obesity in America affects 34 million people. It is important to understand how BMI affects the skeleton and how it may alter age-at-death estimations in a medico-legal setting. Related biomechanical and load-bearing changes in the hips may lead to unreliable age-at-death estimations. Three questions were addressed: 1. How does BMI affect the inaccuracy of age-at-death estimations of the pelvis? 2. Is the inaccuracy of ADBOU 2.1 similarly affected by age-at-death and BMI? And 3. Are age-at-death estimations using the pubic symphysis and auricular surface similarly affected by BMI?

33 individuals were randomly sampled from the Texas State Donated Skeletal Collection including 2 underweight, 13 normal, 9 overweight and 9 obese individuals. Using ADBOU 2.1, age-at-death estimations were compared to recorded ages.

A Pearson's correlation test was run to test the associations between estimation inaccuracy from the pubic symphysis and auricular surface separately with BMI and age-at-death. The results show the auricular surface to be more affected by BMI than the pubic symphysis. The ages of younger individuals in this study were overestimated and underestimated for the older ones. Due to the small sample size, younger ages were underrepresented. Lastly, the ages for underweight and obese samples were overestimated on average. This effect should be taken into account when estimating the biological profile of an individual in a medico-legal setting.

Health implications of diet at Tell el-Amarna

CHEYENNE J. LEWIS

Anthropology, University of Arkansas

The health and living conditions from the rapidly urbanized environment of Akhetaten (the modern site of Amarna) are thought to be severe compared to the conditions of the prior capital city of Thebes. Childhood growth and development is a sensitive indicator of health and diet, and previous research revealed the Amarna children had poor nutrition, stunted growth, and accelerated rates of carious lesions and antemortem tooth loss. This research explores whether this poor nutrition and likely diminished diverseness of foodstuffs was also present prior to Amarna through dietary toughness and the plasticity of the maxillomandibular complex. Skulls from the South Tomb Cemetery (STC) consisting of young adults (n=15) and older adults (n=15) were used to test the conditions of growing up at Amarna versus Thebes and a sample of adults (n=15) from Lisht, a 12th

ABSTRACTS

Dynasty capital, is utilized to establish a 'normal' standard. Differences in the shape and size of the maxillomandibular complex were evaluated using inter-landmark distances and angles measured from 3D models. Discriminant function analysis revealed a distinct separation of the STC younger adults from the STC older adults, and both STC samples distinct from the Lisht sample. Principle component analysis reveals variation in the forward projection of the maxillae and mandible and the size of the maxillomandibular complex. These results indicate that both the period prior to Amarna and during Amarna had a softer diet of foods such as bread and gathered soft fruits compared to a more diverse diet that was eaten at Lisht.

A new extinct large predator in Madagascar: predation pressure on large-bodied Malagasy lemurs through time

MARGARET E. LEWIS¹, LAURIE R. GODFREY², JEAN CLAUDE RAKOTONDRAVAO³, ZACHARY S. KLUKKERT^{4,5}, NICK SCROXTON⁶, STEPHEN J. BURNS⁷, BROOKE E. CROWLEY⁸, DAVID MCGEE⁹, KATHLEEN M. MULDOON¹⁰, LINDSAY R. MEADOR¹¹, PHILLIP LEHMAN⁴, NOROMAMY J. RAHANTAHARIVAO³ and LOVASOA RANIVOHARIMANANA³

¹Biology Program, Stockton University, Galloway, NJ, ²Department of Anthropology, University of Massachusetts Amherst, MA USA, ³Bassins sédimentaires Evolution Conservation, Université d'Antananarivo, Madagascar, ⁴Madagascar Cave Diving Association (MCDA), Antananarivo, Madagascar, ⁵Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, Baltimore, MD USA, ⁶School of Earth Sciences, University College Dublin, Ireland, ⁷Department of Geosciences, University of Massachusetts Amherst, MA USA, ⁸Departments of Geology and Anthropology, University of Cincinnati, OH USA, ⁹Department of Earth, Atmospheric and Planetary Sciences, Massachusetts Institute of Technology, Cambridge, MA USA, ¹⁰Department of Anatomy, Midwestern University, Glendale, AZ USA, ¹¹University College, Washington University, St. Louis, MO USA

The largest mammalian predator specializing on primates in Madagascar today is the fosa (*Cryptoprocta ferox*), a member of the endemic family Eupleridae. Its larger congener, *C. spelea*, became extinct sometime during the past 2000 years. Here we report the recovery of a new fossil *Cryptoprocta* humerus that is much larger than that of co-occurring *C. spelea* from Mitoho Cave at Tsimanampesotse National Park, southwest Madagascar. We analyzed metric differences between this new *Cryptoprocta* humerus and humeri of 17 *C. spelea*, 9 subfossil and 11 modern *C. ferox*, and 160 specimens belonging to 32 additional extant carnivorous species (including euplerids). We employed multivariate and bivariate analyses of 11 linear humeral measurements to reconstruct the locomotor behavior and body

mass of extinct *Cryptoprocta* and to test for geographic structure in *C. spelea*. We made a 3D model of the new humerus using photogrammetry. Analyses of shape data indicate that, in comparison to other *Cryptoprocta*, the new species had increased strength in flexion and greater supinator abilities. It may have been more arboreal than its scansorial congeners. Our conservative body mass estimate for the new species is 27-32 kg (considerably larger than other *Cryptoprocta*). Stable isotopic data indicate that *C. ferox* and *C. spelea* in the southwest targeted different lemur prey. Furthermore, the new species of *Cryptoprocta* changes our understanding of the Malagasy carnivore paleoguild and may explain carnivorous damage to *Megaladapis*. All *Cryptoprocta* species likely preyed on lemurs, with the new species and *C. spelea* targeting some of the largest-bodied extinct lemurs.

Funding from the National Science Foundation [BCS-1750598 to LRG, AGS-1702891 to SJB, EAR-1439559 to DM, BCS-1749676 to BEC, BCS-1749211 to KMM] and Stockton DFF, CDA, and SS grants to MEL.

Group composition is influenced by climate in Verreaux's sifaka (*Propithecus verreauxi*)

REBECCA J. LEWIS¹, ANNE C. AXEL² and CELESTE WILLIAMS³

¹Anthropology, University of Texas at Austin, ²Biology, Marshall University, ³Social Sciences, Oxford Brookes University

Little is known about species-specific responses to local consequences of climate change. We examined the effect of temporal variation in green vegetation on lemur demography in Kirindy Mitea National Park in Madagascar. Monthly censuses of 5 social groups of Verreaux's sifaka inhabiting the 1 km² Ankoatsifaka study area were conducted from 2007 to 2015. We created a monthly time series of an index of green vegetation, the Enhanced Vegetation Index (EVI), over the time period for the 1 km² forest block. Maximum value composite images were computed by recording the highest EVI value for each of 36 pixels for each month. We assessed the temporal variability within each year using the coefficient of variation (CV) of mean monthly EVIs for the 12 months. Median group size was 6 individuals and not influenced by the CV of EVI. However, CV of EVI predicted the range in group size: groups were more stable when green vegetation was more variable across the year. The CV of EVI also predicted the median number of subadult males and subadult females in groups. In more variable years, subadult females stayed in their natal groups and fewer subadult males joined/ remained in social groups, skewing sex ratios towards more females relative to males. By contrast, in drier years when vegetation was more stable across the year, subadult females left their natal groups resulting in delayed reproduction,

and more subadult males joined/ remained in social groups. Thus, young sifaka respond to droughts by changing where they seek reproductive opportunities.

Relationships among three-dimensional os coxae shape, locomotor behavior, phylogeny, and size in haplorhine and strepsirrhine primates

KRISTIL L. LEWTON

Integrative Anatomical Sciences, University of Southern California

Aspects of three-dimensional (3D) pelvic shape have been associated with adaptations to locomotor behaviors in primates, including the shape of the iliac blade, length and orientation of the ischium, and shape and size of the pubis. Similar 3D pelvic shapes among primates have been primarily attributed to locomotion and body size, while the empirical effect of phylogeny has been less well understood. This study examines 3D pelvic shape in primates using an integrated, phylomorphospace approach to investigate the interrelationships among shape, phylogeny, locomotor function, and size. 3D landmarks (N=24) were collected on a large sample of primate pelvises (711 individuals from 39 species), and standard geometric morphometric methods (Generalized Procrustes Analysis followed by Principal Component Analysis) were used to examine shape variation. Statistical analysis of shape coordinates (principal components, PCs) incorporated a phylogeny to adjust for shared evolutionary history; the degree of phylogenetic signal in PCs was statistically significant (p=0.001). Phylogenetic generalized least squares models were constructed with PCs as dependent variables and locomotor behavior and size as independent variables; analyses were conducted on the whole sample and on taxonomic subsamples. Among both non-human and non-hominoid primates, shape along PC1 was significantly related to locomotion and size, but not the interaction of the two. Along PC2, only size significantly affected pelvic shape. Although it is common for taxa within clades to share locomotor behavior, there are significant size and locomotor differences in pelvic shape that cannot be solely accounted for by phylogeny alone.

Molecular Archaeological Research on Horse Remains from Shatangbeyuan Archaeological Site in Longde County, Ningxia Province

CHANG LI and NING KANG

School of Archaeology, Jilin University

In order to explore the origin, domestication and diffusion of Chinese horses, ancient DNA analysis was carried out on 5 horse specimens excavated in the Neolithic Shatangbeyuan site in Longde

ABSTRACTS

county, Ningxia Province. Each sample was taken 200 mg of bone powder for ancient DNA extraction; a 300 bp mitochondrial DNA control region fragment (nucleotide position 15473-15772) was amplified using two pairs of nested primers. And mitochondrial DNA sequences were successfully retrieved from 3 out of 5 samples. Two samples share the same haplotype and could be attributed to the subhaplogroup C1 originated in Europe. The results further support that the Gan-Qing area is an important part for horses in the route from the West to China, reflecting complex origins of Chinese domestic horses. We notice that the sequence of another sample is highly similar to an extinct horse *Equus ovodovi* discovered in the late Pleistocene Proskuriakova cave in the Khakassia region of southwestern Siberia, Russia. This discovery has changed our previous understanding that the wild horses inhabiting China mainly are *Przewalski's* horses, which provides new insights into the evolutionary history of horses in China, including the species composition, distribution and adaptability of Chinese wild horses.

Ancient DNA reveals two paternal Hg C2 lineages in the old nomadic people distributed on the Mongolian Plateau

JIAWEI LI¹, DAWEI CAI¹, YE ZHANG², HONG ZHU¹ and HUI ZHOU^{1,2}

¹College of Archaeology, Jilin University, ²College of Life Science, Jilin University

Since Xiongnu, a series of nomadic tribes have been active in the eastern part of the Mongolian Plateau. Genetic research on these nomadic people has always attracted considerable attention. The development of next-generation sequencing (NGS) technology has provided us with a new technology for use in our research and helped us uncover more genetic information about ancient humans.

In our research, whole-genome shotgun sequencing and capture sequencing of the non-recombining region of the Y chromosome (NRY) were performed on six ancient Hg C2 individuals from six sites distributed on the Mongolian Plateau during different periods. After NRY capture sequencing, three of the six ancient samples were attributed to C2c1b/F845, and the other three ancient samples belonged to C2b1a1b1a/F3830. Combined with the results of genome-wide sequencing, we conclude that there were two important paternal lineages, C2b1a1b1a/F3830 and C2c1b/F845, downstream of Hg C2/M217 in the ancient nomadic people distributed on the Mongolian Plateau. The C2b1a1b1a/F3830 lineage, mainly located in the north Mongolian Plateau, made important genetic contributions to modern Mongolic- and Manchu-speaking populations in the Mongolian Plateau. The C2c1b/F845 lineage, which has a relatively southern geographical location, probably originated from the farming

population in southern East Asia, made certain genetic contributions to the gene pool of both the north nomadic people and the south farming people in East Asia.

Skeletal Demography in Neolithic and Bronze-Iron Age Northern China

JIAXIN LI¹, QUANCHAO ZHANG¹ and QIAN WANG²

¹School of Archaeology, Jilin University,

²Department of Biomedical Sciences, Texas A&M University College of Dentistry

Sex and age distribution are important factors in bioarchaeological analysis to rebuild demographic structure and population history as well as sex-based differences in health and life expectancy. In this study, sex and age distribution patterns were investigated in 85 cemeteries of Northern China in a comparison between the Neolithic Age (8,000 -1,800 BCE) and the Bronze-Iron Age (2,100 BCE - 8 CE). In total, there were 22,393 individuals. Sex could be determined in 17,671 individuals among these groups. The overall ratio of female vs. male was 0.814: 1, indicating a general burial bias towards males. The Female vs. Male ratio was significantly lower during the Neolithic Age (0.596: 1) than the Bronze-Iron Age (0.995: 1), indicating a reduction of sex-based bias in burials over time. Females had a higher burial percentage between 15-23 years (19.9% Female vs. 12.6% Male), which might denote higher female mortality during adolescent and young adult periods. Compared to Neolithic Age cemeteries, the Bronze-Iron Age cemeteries had higher percentages of representatives in youth (0-14 years), and mid-adult (36-55 years) categories. This discrepancy suggests increased fertility and life expectancy along with population growth during the Bronze-Iron Age. Consequently, these differences further indicate a shift of the demographic system from "low pressure" to "high pressure" in Northern China from the Neolithic Age to the Bronze-Iron Age. The richness of the skeletal remains in Northern China provide a solid basis for the Global History of Health Project Asia Module.

Respiratory disease in ancient China: a bioarchaeological analysis of maxillary sinusitis and inflammatory rib lesions in people from Shaanxi (2800 BC to 220 AD)

MOCEN LI¹, CHARLOTTE A. ROBERTS¹, LIANG CHEN², QINGGANG GENG³, DONGYUE ZHAO² and HANQING ZHAO³

¹Department of Archaeology, Durham University,

²School of Cultural Heritage, Northwest University,

³Shaanxi Provincial Institute of Archaeology

As one of the leading causes of death, chronic respiratory disease claimed more than 3.55 million deaths globally in 2015. It affects the upper and lower respiratory tracts, causing inflammatory bone changes in the maxillary sinuses

and/or the visceral surface of ribs, respectively. Bioarchaeological studies have identified these lesions as reflecting poor air quality. However, research in this field has not yet been published in China or the rest of East Asia. To address this gap in knowledge, 249 skeletons excavated from Shaanxi, China (2800 BC to 220 AD) were macroscopically examined for maxillary sinusitis and inflammatory rib lesions (46 subadults; 84 females; 95 males; 18 unsexed adults; six individuals of an unknown sex and age category). The results showed that the highest rates for both lesions (41.67% for maxillary sinusitis; 15.56% for rib inflammation) were found among urban citizens (n=56) in the Western Zhou Dynasty (976 to 771 BC), while the lowest rates (16.67% for maxillary sinusitis; 0% for rib inflammation) were found among inhabitants (n=45) of a small-scale agricultural society in the Longshan Period (2800 to 2000 BC). The majority of people affected were adults, while more males were affected than females. Urbanism, handicraft production, and the indoor and outdoor environment were considered possible causes for the respiratory disease seen in Shaanxi during this time period. This study contributes to a lack of knowledge about the history of respiratory disease in East Asia, revealing possible risk factors for a serious health problem worldwide today.

Handprints on Bricks from Xiheidai Cemetery during the Jin and Yuan Period in Inner Mongolia, China

PENGZHEN LI¹, TING GAO¹, YE FEI¹, LINGYU AN¹, QIAN WANG², QUANCHAO ZHANG¹

¹School of Archaeology, Jilin University,

²Department of Biomedical Sciences, Texas A&M University College of Dentistry

Bricks used for building or decoration have a long history since the Neolithic Age. Fingerprints are often found on ancient bricks left by people who made or transferred the bricks before they hardened. Rarely, near or full handprints are also found on bricks at archeological sites, possibly formed by artistic experiments or as intentional funeral objects. In this study, we report handprints on bricks excavated from the Xiheidai cemetery, located in Jungar Banner, Inner Mongolia, China. Handprints were found on six bricks which came from the fillings of the tomb, Ö-M5. The burial style and funeral goods indicated that II-M5 belonged to the Jin and Yuan Period (1,115-1,368 CE). Based on the morphology and measurements of handprints, especially that of the digits, sex, age, and height of people who left them were analyzed, in addition to hand preference. Results demonstrated that these handprints were left by adult males as well as a female and a non-adult with medium posture, all right-handed. Identities of people who left these handprints were unknown. They might include brick-making laborers and their family members as helping

ABSTRACTS

hands who had a leisurely moment of artistic experiments and experiences. These discoveries bring out not only the first-hand hand morphology beyond bones, but also vivid working scenarios of ancient laborers, adding to our understanding of the daily life of a working class living in northern China nearly a millennium ago.

A Palaeopathological Study of Dental Health from the Yinzhou Site (ca. 4000-3500 BP), Guangdong Province, China

ZIYI LI¹, TINA JACOB¹, REBECCA GOWLAND¹ and KEJIA HUANG²

¹Archaeology, Durham University, ²Archaeology, Beijing Union University

This poster discusses the dental health of 52 individuals from the Yinzhou shell mound site, a prehistoric settlement located in the Pearl River Delta, South China. The site dates from the late Neolithic period to the early Bronze Age. Separated into adults (n=25) and non-adults (n=27), dental condition, including caries, periodontal disease, periapical lesions, calculus, ante-mortem tooth loss and tooth avulsion were macroscopically recorded, and the results were compared to other prehistoric Chinese populations. Approximately 54% of the individuals (28/52) had dental disease. Twelve out of 25 adults (48%; 44 out of 286 teeth) had caries, which demonstrates a similar prevalence to contemporaneous sites in central China. Periodontal disease and ante-mortem tooth loss rates were high, especially in a population where most adults did not reach the age of 45 years. Possible reasons may include a high-carbohydrate diet. The diet of the Yinzhou population has not been studied yet, but research at nearby Neolithic sites indicates that people ate rice, nuts and shellfish. Five adults showed tooth ablation of the upper second incisors or canines, which was also frequently found in contemporaneous sites of Guangdong province. Common rituals may exist at these sites. As for the non-adult group, 11 individuals (41%) had caries of the permanent dentition (11/ 295 teeth), while 7 of them (26%; 23/144 teeth) exhibited carious deciduous teeth, which was rare in central and northern China in the late Neolithic period. The rate of deciduous caries may indicate a high-carbohydrate diet for non-adults at the Yinzhou site.

The Skeletal Remains of Members of the Royal Orchestra of the Marquis Yi of Zeng During the Zhou Dynasty, China

XUEZHU LIAO¹, TING GAO¹, YE FEI¹, LINGYU AN¹, QUANCHAO ZHANG¹ and QIAN WANG²

¹School of Archaeology, JILIN UNIVERSITY,

²Department of Biomedical Sciences, Texas A&M University College of Dentistry

The tomb of the Marquis Yi of Zeng (Zeng-Hou-Yi), located at the Central China and dated to be around 443 BCE during the Zhou Dynasty, was an unusual discovery with a large set of musical instruments including now world famous Bianzhong (the great set of bells). In addition to the remains of the Marquis himself (a male with an estimate of age at death around 40 years), there were twenty-one skeletons belonging to young females, estimates of age of death ranging from 13 to 25 years, who were believed to be members of the royal orchestra and were sacrificed after the Marquis's death. Among them, eight individuals with an average age at death of 22 years were buried with the Marquis in the East Chamber, while thirteen individual with an average age at 18.6 years were buried in the adjacent West Chamber. Morphological analysis demonstrated that all females had relatively a gracile skull, a narrow face, and a short stature, which might reflect the physical criteria for the selection of royal orchestra. Dental micro-wear analyses indicated that East Chamber females had a better quality of the diet, suggesting their higher court status than West Chamber females; they might be the concubines of the Marquis and players of the innermost circle of the court orchestra, while West Chamber females might belong to the general court orchestra. These findings provide a rare glimpse of the lifestyle of a particular group of people in a royal court of an ancient kingdom of China.

The effect of habitat type on vocalizations of white-handed gibbons (*Hylobates lar*) living in a mosaic landscape in western Thailand

LYDIA E O. LIGHT and SARAH DAMERON
Anthropology, UNC Charlotte

Primate vocalizations are commonly used by conservationists to locate groups and estimate population sizes. However, differences in vocalization patterns between habitat types may reflect important environmental contexts. White-handed gibbons (*Hylobates lar*) living in Huai Kha Khaeng Wildlife Sanctuary are an ideal population for studying the effects of habitat type as some groups live in evergreen forest and nearby groups in savannah habitat. Previous studies have identified lower resource availability, lower gibbon group density, and larger gibbon home range areas in the savannah habitat compared to the evergreen forest. Thus, we hypothesized that evergreen groups will spend more time vocalizing than savannah groups as they will come into contact with neighbors more often. We also hypothesized that evergreen groups would vocalize at shorter distances away from the home range spatial mean. As expected, evergreen groups spent significantly more time vocalizing than savannah groups based on monthly average activity budgets (E: 13.6% ± 2.5% SE; S: 4.8% ± 0.8% SE;

Mann-Whitney $U = 118, p = 0.0005$). Evergreen groups also vocalized closer to the spatial mean (E: 137.4 ± 7.7 SE m vs. S: 237.7 ± 14.1 SE m; $U = 2173, p \leq 0.0001$). The relationship was reversed when controlling for different home range areas (E: 6.9 ± 4.1 SE m/ha vs. S: 4.3 ± 3.0 SE m/ha; $U = 2947, p = 0.0002$). We suggest that measures of distance may relate more to distance from the territory border.

Research in Thailand was supported by the IIE Fulbright, National Science Foundation #1154603, American Society of Primatologists, and University of Texas at San Antonio.

The Red Colobus Conservation Action Plan: Coordinating and Mobilizing Conservation Efforts to Protect Africa's Most Endangered Group of Primates

JOSHUA M. LINDER¹, DREW T. CRONIN², NELSON TING³ and SCOTT MCGRAW⁴

¹Department of Sociology and Anthropology, James Madison University, ²Conservation, Education and Science Department, North Carolina Zoo, ³Department of Anthropology, University of Oregon, ⁴Department of Anthropology, The Ohio State University

The 1996 Status Survey and Conservation Action Plan for African Primates called for a red colobus action plan to be prepared and implemented given the large number of highly localized and threatened populations of red colobus monkeys. Nearly 10 years later, Thomas Struhsaker published a review of the status of and threats to red colobus monkeys and presented a conceptual framework for their conservation. Despite these calls to action, the conservation status of most red colobus species has continued to worsen. All 17 species of red colobus are now threatened with extinction, making red colobus the most threatened group of primates in Africa. A range-wide and taxon-based five-year (2020-2025) conservation action plan, the first for any African monkey group, has been developed that recommends actions to prevent red colobus extinctions and protect the most viable populations of each taxon. Range-wide conservation priorities include actions that aim to improve government investment in wildlife conservation, expand and improve protected areas, determine taxon-specific distribution and abundance, engage with local human populations and integrate them into conservation activities, remove barriers that prevent local access to human healthcare and family planning, and raise awareness of the plight of red colobus monkeys. A red colobus action plan Coordinator has been recruited and a working group has been

ABSTRACTS

formed under the authority of the IUCN Primate Specialist Group to oversee the implementation of the action plan. Challenges to developing a conservation action plan are also discussed.

Funding for the development of the action plan provided by Mohamed bin Zayed Species Conservation Fund, Margot Marsh Biodiversity Foundation, and Global Wildlife Conservation

On the margins of the western chimpanzee (*Pan troglodytes verus*) range in Senegal

STACY LINDSHIELD¹, PAPA IBNOU NDIAYE², JILL D. PRUETZ³, GRAY TAPPAN⁴, ERIN WESSLING⁵, ASSANE GOUDIABY⁶ and KELLY BOYER ONTL⁷

¹Anthropology, Purdue University, ²Biologie animale, Université Cheikh Anta Diop, ³Anthropology, Texas State University, ⁴Earth Resources Observation Systems Data Center, United States Geological Survey, ⁵Human Evolutionary Biology, Harvard University, ⁶Institut des Sciences de l'environnement, Université Cheikh Anta Diop, ⁷Anthropology, Ball State University

Environmental predictors of chimpanzee (*Pan troglodytes*) biogeography are often reductionist but nonetheless, they inform conservation and management programming. High-resolution landscape analyses strengthen reductionist approaches by contextualizing local ecological processes. We analyzed the vegetation composition and physiognomy of landscapes in a semi-arid environment on the margins of the chimpanzee geographic distribution in south-eastern Senegal. We identified a total of 12 sites for landscape analyses, including N=7 landscapes inside and N=5 landscapes outside of the species' range, by supplementing published surveys with reconnaissance walks in previously neglected areas. Trees, shrubs, and grasses within these areas were identified from high-resolution multispectral satellite images. We used t-tests to compare woody vegetation cover (%) and physiognomy (patch aggregation, largest woody patch, patch perimeter-area fractal dimension) between landscapes. In addition, we considered river and road densities as potential explanatory variables. Unexpectedly, percent woody vegetation cover ($t = 3.096$, d.f. = 25.066, $P < 0.01$) and largest patch index ($t = 3.269$, d.f. = 28.454, $P < 0.01$) were significantly higher in landscapes outside of the species' range. In landscapes with chimpanzees, river density was higher ($t = 5.627$, d.f. = 43, $P < 0.0001$) and there were fewer roads ($t = 5.627$, d.f. = 43, $P < 0.0001$). This analysis shows that there is a complex relationship between chimpanzees and woody vegetation cover, and for relevant potential interactions between woody vegetation

physiognomy and surface water availability. Moreover, our analysis indicates that the northern border of the species range is limited, in part, by human activities.

Funding for this study was provided by National Science Foundation, Leakey Foundation, Purdue University, Rufford Foundation, Primate Conservation, Inc., and Iowa State University.

New insights into Metabolic Syndrome among ancient populations in mainland Asia

NELLISSA LING¹, SIÂN HALCROW¹, MARC OXENHAM², KATE DOMETT³, STACEY WARD¹, CHARLES HIGHAM⁴, DOUGALD O'REILLY², LOUISE SHEWAN⁵, THI MAI HUONG NGUYEN⁶, TRAN THI MINH⁶, TRUONG HUU NGHIA⁶, HOANG TRINH HIEP⁶ and HALLIE BUCKLEY¹

¹Department of Anatomy, University of Otago, ²School of Archaeology and Anthropology, Australian National University, ³College of Medicine and Dentistry, James Cook University, ⁴Department of Anthropology and Archaeology, University of Otago, ⁵School of Earth Sciences, University of Melbourne, ⁶Institute of Archaeology, Hanoi, Vietnam

Metabolic syndrome (MetS) is a well-known noncommunicable disease and notable health problem. The condition is closely linked to having a detrimental lifestyle as a consequence of an unhealthy diet and being physical inactive. MetS prevalence may also be tied to a predisposition towards the condition that is present in some population groups, such as in the Pacific Islands. Despite MetS being recognized as a global health issue today, there is little known about its evolutionary history, particularly in mainland Asia. This study builds on our current understanding of MetS by investigating the existence of the condition in Asian prehistory and learning how local conditions may have influenced its development in these ancient population groups.

For this study, we examined four skeletal assemblages from Thailand (Non Ban Jak, Khok Phanom Di) and Vietnam (Con Co Ngua, Man Bac), representing different settlement types, and with an overall occupation period stretching between 6000 -1500 BP. The presence of MetS was investigated through the skeletal evidence of two joint diseases, diffuse idiopathic skeletal hyperostosis and gout, both of which are associated with the condition. These data are compared to measurements of selected body parameters used as markers for non-specific stress to identify possible correlations. Through this investigation, we contribute to a more holistic knowledge of MetS in human history. We also highlight the

importance of understanding how this disease has progressed through time, particularly among Asian populations, and prior to its lead up to becoming a global health epidemic today.

University of Otago Doctoral Scholarship, Skinner Fund, The Andrew Sherratt Fund

Bisulphite sequencing of ancient genomes

BASTIEN LLAMAS

School of Biological Sciences, The University of Adelaide

Epigenetic mechanisms such as DNA methylation modulate gene expression without changing the underlying genetic sequence. They can respond to environmental cues and may lead to transgenerational changes in some physiological and psychological phenotypes.

Statistical methods have recently been developed to infer DNA methylation in ancient genome sequencing data. On the other hand, experimental studies of ancient DNA methylation have been restricted to a limited number of target loci and a small sample size, due to DNA degradation and low levels of endogenous DNA in sub-fossil remains.

Here, we present a method to perform whole-genome bisulphite sequencing of ancient DNA extracts. To demonstrate the power of this method, we characterised methylomes in 10 extinct and 14 contemporary bison samples from North America that span a time range of more than 50,000 years. Amongst all identified differentially methylated regions, two genes (GSTT4 and TNFRSF10D) show consistent differential methylation that correlate with climate variations.

Our method provides a unique opportunity to study the methylomes of past mammals at an unprecedented level of resolution and could easily be applied to humans to study the long-term impact of cultural transitions and disruptive socio-cultural or natural events.

Morphometric analysis of Eocene primate astragali from India

CATHERINE J. LLERA, KENNETH D. ROSE and ADAM D. SYLVESTER

Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Early Eocene postcrania from the Vastan lignite mine of Gujarat, India, provide a window into the time soon after the haplorhine and strepsirrhine divergence. Previous metric analyses of Asiadapidae indicate they were generalized arboreal quadrupeds, while *Vastanomys* was more engaged in leaping. Analyses of long bone cross-sectional properties, however, do not clearly distinguish the fossils. The purpose of this study

ABSTRACTS

is to examine astragalar morphology of the Vastan material in order to refine the taxonomic assessment and locomotor reconstructions of these fossils.

A comparative sample was obtained by down-loading surface models representing 31 extant primate species (n=122) from MorphoSource. Surface models of fossil specimens, *Marcgodinotius indicus* (n=3) and *Vastanomys major* (n=1), were segmented from scans. A morphological analysis was carried out using weighted spherical harmonics (SPHARM). This is a Fourier-based method which represents genus zero surfaces using coefficients associated with a common set of spherical harmonic functions. The coefficients describing each astragalar were then used as variables in a principal components (PC) analysis, and bivariate plots were created to visualize morphological differences.

The first three PCs explain 53.4% of shape variation. The *Marcgodinotius* fossils fall well within the range of extant Lorisiformes in the first two PCs which is consistent with original fossil descriptions and indicates it was an arboreal quadruped. The fossil specimen assigned to *Vastanomys* falls outside the range of variation of extant primate morphology along the first three PCs. Consequently, it is unlike extant primates and may represent a more primitive euprimate morphology.

Supported by NSF DGE-1746891, National Geographic Society, Leakey Foundation

Changes in molar topography and 3D shear crest lengths with tooth wear in two cercopithecoid primates from Malaysia

ELLIS M. LOCKE

Institute of Human Origins & School of Human Evolution and Social Change, Arizona State University

As herbivorous, diphyodont mammals with relatively low-crowned molars, primates experience changes in dental function during their lifetimes as teeth become progressively worn. Maintaining tooth function with wear is thought to pose a particular challenge for folivorous primates whose diets emphasize molar shearing actions. Recent studies using dental topographic methods suggest that certain primate folivores have molar morphology that maintains or increases functional shearing surfaces with tooth wear ('dental sculpting'). Evidence for this phenomenon has been found in folivorous but not frugivorous New World monkeys, supporting the hypothesis that dental sculpting is an adaptive trait linked to diet. This analysis extends these methods to two sympatric Old World monkeys from Sabah, Malaysia, possessing distinct diets

and dental morphologies: the folivorous colobine *Trachypithecus cristatus* (n=25) and the more frugivorous cercopithecine *Macaca fascicularis* (n=22).

For each species, 3D shear crest lengths and four dental topographic variables (relief index, slope, angularity, and Dirichlet Normal Energy [DNE]) were measured from variably worn lower second molars. Preliminary results indicate that for any given degree of wear, *Trachypithecus* has longer shear crest lengths and higher relief, slope, angularity, and DNE than *Macaca*. The two species exhibit different patterns and degrees of change in topography and shearing crest lengths across the wear series. However, these changes do not always match expectations based on their respective diets. Correlations between 3D shear crest lengths and other dental topographic measurements suggests that the type of metric used to assess shearing potential may affect whether or not dental sculpting is detected.

This research was supported by the National Science Foundation (BCS-1846153) and the Graduate & Professional Student Association Grant Program (Arizona State University).

Support size and thumb position preferences in humans during suspension and vertical climbing: Implications for hominin hand evolution

VICTORIA A. LOCKWOOD^{1,2}, SZU-CHING LU^{2,3}, SAMANTHA WINTER⁴ and TRACY L. KIVELL^{2,5}

¹Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, Washington, DC, USA, ²Animal Postcranial Evolution (APE) Lab, Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, Marlowe Building, Canterbury, Kent, CT2 7NR, UK, ³Laboratory for Innovation in Autism, School of Education, University of Strathclyde, Glasgow, G1 1XQ, UK, ⁴School of Sport and Exercise Sciences, The Medway Building, University of Kent, Chatham Maritime, Kent, ME4 3AU, UK, ⁵Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig, 04103, Germany

Exploring how the human hand interacts with the support substrate during arboreal-like activities can provide insight into whether, and how, early hominins exploited arboreal habitats. Previous ergonomic work suggests that supports 30-40mm in diameter provide the greatest grip force and comfort and are optimal for the human hand. In this study, participants (n=28) completed static postural and dynamic vertical climbing and suspensory activities on three diameters (45mm, 80mm, and 105mm), on a custom-built apparatus. Hand posture (thumb adducted and abducted) and diameter preference data were collected for each activity. Data was analyzed using exact binomial tests with Bonferroni corrected alpha values. Reported significance are alpha values below the

Bonferroni corrected alpha value. In suspension the 45mm diameter, closest to the human hand optimal grasping diameter, was significantly preferred, despite hand size variation. In both suspension and vertical climbing the largest diameter was significantly the least preferred. Thumb posture preference was analyzed separately for the static condition and dynamic locomotion on each diameter for suspension and vertical climbing. No preference was found for thumb position across all suspension activities. In climbing, there was a significant preference for an abducted thumb during static and dynamic activities on the 45mm diameter, despite hand size differences. These results suggest a support size preference during arboreal-like locomotion, but it varies by locomotion type. Participants generally had no strong thumb position preference during these arboreal-like activities, which suggests arboreal locomotion had minimal influence on thumb evolution within the hominin clade.

Funded by ERC Starting Grant 336301 (TLK, S-CL). Lewis N. Cotlow Fund and Sigma Xi, The Scientific Research Society, Grant-In-Aid of Research, Grant G201903158539371 (VL).

An archaeothanatological approach to commingled and fragmentary remains

TISA N. LOEWEN¹ and KENNETH C. NYSTROM²

¹School of Human Evolution and Social Change, Arizona State University, ²Department of Anthropology, The State University of New York at New Paltz

Commingled and fragmentary human skeletal remains pose numerous difficulties for analyses due to missing information from secondary disturbances. Feature based methods have mediated these issues by providing ways to determine the minimum number of individuals (MNI) and account for variations in pathological conditions, markers of trauma, and preservation.

This study analyzed remains from a necropolis in Nadin, Croatia and observed a pattern of sidedness that was confirmed by a bilateral comparison of percentage of completeness (%C) of long bones. Additional data was simulated in RStudio to account for varied sample sizes based on the standard deviation between each element's percentages of completeness for different contexts and using its site wide %C as the mean. A two sample t-test between the right and left sides for humeri, ulnae, and femora produced statistically significant differences (p<0.05), with left sides indicating higher percentages of completeness. Repeated simulations of other long bones varied in significance. Nevertheless, the overall results suggest that preservation by side may have discernable patterns.

Bone density based taphonomy was considered, providing an explanation for only some of the representation of elements. Additional

ABSTRACTS

contributors to variations in bilateral fragmentation can include soil acidity and environmental effects. Accounting for the differential preservation is challenging, but may be related to mortuary patterns caused by substantial reuse and disruption of the site's crouched inhumations and related cultural factors. This study proposes that similar archaeoanthropological approaches may prove insightful when burial practices are complicated by the preservation of remains.

Fieldwork was funded in part by the Lambda Alpha National Anthropology Honor Society and the New York University Center for Ancient Studies.

Trade-off between resting metabolic rate and growth quality in men but not women

DANIEL P. LONGMAN¹, SAKURA OYAMA^{2,3}, JAMES CRACKNELL⁴, NATHAN THOMPSON⁵, DAN GORDON⁶, JAY T. STOCK^{4,6,7} and JONATHAN CK. WELLS⁸

¹School of Sport, Exercise and Health Sciences, Loughborough University, ²Department of Anthropology, Yale University, ³Yale School of Medicine, Yale University, ⁴Department of Archaeology, University of Cambridge, ⁵Department of Life Sciences, Anglia Ruskin University, ⁶Department of Anthropology, University of Western Ontario, ⁷Department of Archaeology, Max Planck Institute for the Science of Human History, ⁸Childhood Nutrition Research Centre, UCL Institute of Child Health

Life history theory predicts the existence of trade-offs between competing physiological functions. In the absence of increased energy availability, a greater allocation of energy toward one trait necessitates reduced investment in others. The core metabolic cost of self-maintenance (measured by resting metabolic rate, RMR), varies significantly between individuals. However, the fitness consequences are unclear.

This study tests whether there is a trade-off between a measure of maintenance (RMR) and fitness (fluctuating asymmetry, FA). FA reflects growth quality and is linked to success in both intra and intersexual selection. Two theories predict contrasting relationships between RMR and FA. The 'increased intake' hypothesis contends that RMR reflects metabolic capacity, with high RMRs allowing greater energy allocation to growth, reducing FA. Conversely, the 'compensation' hypothesis predicts that high RMRs consume energy, reducing energy for growth, increasing FA.

Measurement of RMR and FA in university rowers revealed a significant positive correlation amongst men ($n=57$, $r=0.344$, $p=0.009$, 1-tailed), and a weak non-significant positive relationship amongst women ($n=48$, $r=0.142$, $p=0.169$, 1-tailed). The results provide support for the 'compensation' hypothesis in males, but not females. Intersexual selection favours low FA in both sexes, while intrasexual selection favours larger body size in

males only. Male selection for both growth quality and quantity may therefore impose a greater energy stress, resulting in the positive relationship observed here.

Food availability is thought to modulate the fitness consequences of RMR variability. As rowing imposes high energy demands, further work is required to investigate the effect of energy balance on this trade-off.

This study was funded by the European Research Council under the European Union's Seventh Framework Programme, Grant/Award Number: (FP/2007-2013)/ERC Grant Agreement n.617627 to Jay Stock.

Vertebral neural canal growth and developmental stress: a case study from the American Southwest

SAMUEL M. LOPRESTO¹, DANIEL H. TEMPLE¹ and DAVID R. HUNT²

¹Department of Sociology and Anthropology, George Mason University, ²Department of Anthropology, National Museum of Natural History, Smithsonian Institution

This study aims to understand the risk of mortality in relation to vertebral canal growth disruptions at the Pueblo Bonito (AD 800-1200, $n=60$) and Hawikku (AD 1400-1680, $n=110$) sites in the pre- and protohistoric American Southwest. The vertebral neural canal encodes information from the intrauterine period until the age of 5 years for midsagittal diameter and adolescence for interpedicular diameter. Maximum midsagittal and interpedicular measurements of the neural canal were collected for all vertebrae. Age was estimated using transition analysis. An ANOVA with a Games-Howell post-hoc test found that reduced neural canal diameter was significantly associated with early adult mortality at Hawikku for two types of cervical vertebrae and one lumbar vertebra ($P \leq 0.05$). Significant associations with early adult mortality were also found at Pueblo Bonito for two types of cervical vertebrae, eight types of thoracic vertebrae, and all of the lumbar vertebrae ($P \leq 0.05$). Additionally, survival analysis revealed decreased survivorship for Pueblo Benito individuals with smaller mean interpedicular diameter of the L1 and L2-L4 vertebrae ($n = 34$, $X^2 = 4.441$; $P \leq 0.035$) ($n = 103$, $X^2 = 16.35$; $P \leq 0.0001$), and for midsagittal diameter of the L2-L4 vertebra ($n = 99$, $X^2 = 13.773.009$; $P \leq 0.0001$). These results are interpreted within the Developmental Origins of Health and Disease framework by demonstrating that individuals in ecologically similar, but contextually different pre- and post-contact environments who survive growth stunting early in life have an increased risk of mortality at later stages of life.

Human exposure to heavy metals 5000 years ago: Human health in the context of metalwork, pigments and cosmetics

KIRSI O. LORENTZ¹, MESSAOUD HARFOUCHE², IOSIF HAFEZ¹, YUKO MIYAUCHI¹, GRIGORIA IOANNOU¹, MOHAMMAD R. ZARURI³, FARZAD FORUZANFAR⁴ and MANSOOR SM. SAJJAD⁵

¹Science and Technology in Archaeology and Culture Research Center (STARC), The Cyprus Institute, ²XAFS/XRF beamline, SESAME (Synchrotron-light for Experimental Science and Applications in the Middle East), ³Golestan Branch, RICCHT, ⁴Emeritus, ICAR (Iranian Center of Archaeological Research), ⁵Archaeology, ICAR (Iranian Center of Archaeological Research), Iran

Heavy metals such as copper (Cu), arsenic (As) and lead (Pb) were mined, manufactured, and used at ancient archaeological sites, enabling technological advances. Cultural aesthetics led to the use of heavy metals in pigments decorating artefacts, and cosmetics for enhancing personal appearance. Archaeological remains from the 5000-year-old urban long-distance-trading site of Shah-i Sokhta (Iran) show use of Cu, Pb and As in artefacts, pigments and cosmetics. What impact, if any, might this processing and use of heavy metals have had on human health? Our hypothesis was that (some of) the heavy metals in use were integrated to human tissues. We analysed ancient human tissues using the newly opened SESAME Synchrotron in the Middle East. In specific, we analysed 45 samples of bone and teeth from 28 individuals, together with soil and salt samples, first with conventional X-ray fluorescence (XRF) and then with synchrotron radiation XRF (SR-XRF) in order to explore presence of Pb, Cu, and As. Samples from two selected individuals of interest with elevated levels of Pb and Cu (IUR3214 and MDX5806) were then analysed further with EXAFS and XANES, in order to explore the structural environment and speciation of specific heavy metals at atomic level. We discovered evidence for a Pb compound bound with calcium (Ca), consistent with lead-based cosmetics use, and different Cu(II) species. In addition to population level analysis, we focus in detail within this paper on a perinate infant with evidence of lead, and a young woman with evidence of copper in her tissues.

Travel funds to SESAME synchrotron were provided by EU H2020 CALIPSOplus (INFRAIA-01-2016-730872). Funding in kind (beamtime) was provided by the SESAME Synchrotron. Research travel was funded by the Cyprus Institute.

Fecal nutritional values of captive *Otlemur garnettii* reflect dietary shifts from frugivorous to insectivorous diets

JAMES E. LOUDON¹, B. KATHERINE SMITH², SYDNIE BIANCHI², MEAD A. KROWKA³, ANDRES

ABSTRACTS

M. GOMEZ¹, OLIVER C.C. PAINE⁵ and MATT SPONHEIMER⁵

¹Anthropology, East Carolina University, ²Anthropology and Sociology, University of Southern Mississippi, ³Anthropology, University of North Carolina-Wilmington, ⁴Animal Science, University of Minnesota, ⁵Anthropology, University of Colorado, Boulder

Despite decades of behavioral observations of galagids, the dietary patterns of many species remain largely unknown. This gap in our knowledge is principally linked to the difficulties of observing a taxa that includes several small, fast-moving, nocturnal species. To improve our understanding of nutritional needs of galagos and provide potential insights into understanding their dietary shifts in the wild, we conducted a six-week feeding study on a colony of Northern greater galagos (*Otolemur garnettii*). We attempted to mimic naturally occurring "frugivorous" and "insectivorous" diets by feeding the galagos specific fruits and invertebrates. For each food provided to the galagos, we measured crude protein (CP), crude fat (CF), acid detergent fiber (ADF), neutral detergent fiber (NDF), and crude non-structural carbohydrates (NSC). The same nutritional properties were analyzed for each galago's fecal sample, collected the following day. When the nutritional properties of each food were pooled into the two diets, differences in CF and CP were found ($P < 0.01$). In contrast, differences in CP, ADF, and NDF were detected in feces ($P < 0.01$). Using nutritional geometric frameworks, we plotted the plant and fecal nutritional data onto bi-plots with three axes to represent nutrient space. Taken together, these data emphasized nutritional differences between each major diet type and showed that fecal nutritional values accurately tracked dietary shifts in a captive galago model. Although this approach requires field testing, it demonstrated the promise of using nutritional studies in captive settings to provide insights into the feeding ecology of cryptic, nocturnal wild primates through time and space.

This project was supported by a grant from the National Science Foundation (RAPID Award #1840977).

More than twenty years of geometric morphometrics and the species conservation. A tribute to Dennis E. Slice

ANNA LOY¹, PAOLO CIUCCI², PAOLO COLANGELO³, GIULIA GUIDARELLI¹ and CARLO MELORO⁴

¹Biosciences and Territory, University of Molise, ²Department of Biology and Biotechnologies 'Charles Darwin', University of Rome 'La Sapienza', ³Institute for Ecosystem Study, CNR, ⁴Research Centre in Evolutionary Anthropology and Palaeoecology, School of Natural Sciences and Psychology, Liverpool John Moores University

Management and conservation strategies of endangered species with a wide geographical range are strictly dependent on the identification

of the most critical populations in need of specific and urgent conservation actions. While genetic data provide the general framework for the identification of Evolutionary Significant Unit (ESU), morphological information can still depict both divergent taxonomic units and their unique adaptive traits. Digital imaging combined within the geometric morphometrics (GMM) framework permit an holistic approach to the analysis of complex anatomical structures whose intra and interspecific variation might inform species taxonomy and conservation. We provide examples based on the study of mammalian skulls to demonstrate that GMM data can be quite relevant to fill the gap between taxonomic research and conservation practice. We evidenced a strong phenotypic divergence in the Apennine brown bear (*Ursus arctos marsicanus*) that was contrasting with conclusions drawn from molecular data. This will inform potential re-inforcement also in the light of results obtained on fluctuating asymmetry in European brown bear populations. The analyses of shape and allometric trajectories in three dolphins equally demonstrated significant differences between Mediterranean and the extra-Mediterranean populations, supporting the institution of unique Management Units. Divergent cryptic populations of the genetically homogenous Eurasian otter (*Lutra lutra*) were equally identified for the skull shape of the European populations. These studies greatly own their achievements to the pioneer works of Dennis E. Slice on the vertebrate skull morphometrics, and will hopefully contribute to establish a pragmatic link between morphological research and conservation biology.

The gut microbiome and reproductive state in two Old World primates

AMY LU^{1,2}, KATHERINE R. AMATO³, ALICE M. BANIEL¹, JACINTA C. BEEHNER^{4,5}, THORE J. BERGMAN^{4,6}, CAROLA BORRIES^{1,2}, ANDREAS KOENIG^{1,2}, ELIZABETH K. MALLOTT⁷ and NOAH SNYDER-MACKLER^{8,9}

¹Department of Anthropology, Stony Brook University, ²Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, ³Department of Anthropology, Northwestern University, ⁴Department of Psychology, University of Michigan, ⁵Department of Anthropology, University of Michigan, ⁶Department of Ecology and Evolution, University of Michigan, ⁷Department of Anthropology, Dartmouth College, ⁸Department of Psychology, University of Washington, ⁹Center for Studies of Demography and Aging, University of Washington

Recent research suggests that the composition of the gut microbiome in female primates shifts to support the unique physiological demands of pregnancy and lactation; however empirical data supporting this hypothesis remain limited, particularly from wild populations. Here, we examine how female reproductive state influences gut microbial composition in two species of

wild Old World monkeys - geladas (*Theropithecus gelada*) (N=504 samples; 60 females) and Phayre's leaf monkeys (*Trachypithecus phayrei crepusculus*) (N=93; 14 females). In both species, reproductive state significantly predicted aspects of microbial composition and diversity (geladas: weighted Unifrac, $p=0.006$; leaf monkeys: richness, Shannon's Diversity, unweighted Unifrac, all $p < 0.05$); however, it explained a significantly smaller proportion of variance compared to environmental factors such as rainfall. Although small sample size prohibited more fine-grained analyses in the leaf monkey dataset, among geladas we found that lactating and gestating females had reduced Euryarchaeota compared to cycling females, and lactating females contained more microbes involved in bacterial lipopolysaccharide and folate synthesis—processes linked to inflammation and nutritional support of infant development. The unique opportunity to model reproductive hormones in conjunction with microbial composition in leaf monkeys allowed us to demonstrate that fecal progesterone concentrations were better predictors of microbial composition (all $p < 0.01$ for alpha and beta diversity measures) than coarse categories of reproductive state. These results support the hypothesis that female gut microbiomes shift, potentially in response to reproductive demands, and suggest that future studies should investigate how hormones might drive these relationships.

Research was funded by the National Science Foundation, Leakey Foundation, National Geographic Society, Fulbright, Wenner-Gren Foundation, University of Michigan, Northwestern University, Stony Brook University, and University of Washington

From bad to worse. Diachronic changes in oral pathology in Iron Age Italy

MICHAELA LUCCI^{1,2}, EMANUELA CRISTIANI^{1,3}, ANDREA CUCINA⁴, VINCENZO D'ERCOLE⁵, FRANCESCO LAPASTINA⁶, ALESSANDRA SPERDUTI^{7,8} and ALFREDO COPPA⁹

¹DANTE, Diet and Ancient Technology laboratory, Rome, Italy, ²PIN Polo Prato, Università di Firenze, Firenze, Italy, ³Department of Oral and Maxillo Facial Sciences, "Sapienza" Università di Roma, Rome Italy, ⁴Facultad Ciencias Antropológicas, Universidad Autónoma de Yucatán, Mérida, Mexico, ⁵Dipartimento di Lettere, Arti e Scienze Sociali, Università degli Studi di Chieti "G. D'Annunzio", Chieti, Italy, ⁶Archmat, University of Évora, Évora, Portugal, ⁷Servizio di Bioarcheologia, Museo delle Civiltà, Rome, Italy, ⁸Dipartimento Asia Africa e Mediterraneo, Università degli Studi di Napoli "L'Orientale", Naples, Italy, ⁹Dipartimento di Biologia Ambientale, "Sapienza" Università di Roma, Rome, Italy

Italian Iron Age populations have been generally described as suffering from a high prevalence of dental diseases. However, previous studies have focused on single skeletal samples with few individuals and limited comparisons at regional and diachronic level. This study provides

ABSTRACTS

a more extensive picture of the phenomenon by presenting the data from 37 necropolises from central and southern Italy (most of them previously unpublished). Three pathological affections were considered: dental caries was observed for presence, severity and position in 774 individuals (14,255 teeth). Ante-mortem tooth loss (AMTL) was recorded in 610 individuals (13,326 alveoli); periapical lesions in 576 individuals (9,797 alveoli). Only individuals with at least 5 teeth (caries) or alveoli (AMTL and periapical lesions) were included in the analysis.

Overall, the results indicate a high prevalence of oral pathologies: 71,83% of the adult individuals (18+ years) show at least one carious tooth; 54,26% of the sample has at least one case of AMTL; periapical lesions affect 37,15% of the individuals. No differences are recorded between sexes, while a significant age-related increase was observed for caries and AMTL, but not so for periapical lesions. Early Iron age communities (IX-VIII century BCE) show significant lower affection than the following time periods (Orientalizing/ Archaic Phase, VII-V century BCE and Hellenistic Phase, IV-III century BCE), with some differences across sites and ethnic groups. These results may be the reflection of sociopolitical and subsistence strategies shifts among the different periods, regions and ethnicities of the Italian Iron Age.

European Research Council (ERC Starting Grant Project HIDDEN FOODS, G.A. no. 639286 to E.C.).
H2020 Programme ARIADNEplus project, contract no. H2020-INFRAIA-2018-1-823914.

Rough-and-Tumble Play in Immature Monkeys at Kibale National Park, Uganda

SARA G. LUCCI¹ and JESSICA M. ROTHMAN^{2,3}

¹Anthropology, University of Texas at San Antonio, ²Anthropology, Hunter College, City University of New York, ³Anthropology, New York Consortium in Evolutionary Primatology

Rough-and-tumble play includes grabbing and tumbling between one (dyadic) or multiple (polyadic) partners. The "Training for the Unexpected" theory predicts differences in play between age and sex classes, and recent research predicts greater frequency of polyadic play than dyadic play in more gregarious species. These predictions were tested in four species in Kibale National Park, Uganda over 100 days in 2018. Behavioral data were collected for immature red colobus (*Procolobus rufomitratus*), black-and-white colobus (*Colobus guereza*), grey-cheeked mangabeys (*Lophocebus albigena*), and redtail monkeys (*Cercopithecus ascanius*). We predicted that frequency of rough-and-tumble play will differ between males and females in red colobus and grey-cheeked mangabeys because males engage in more aggressive interactions. We also predicted greater rough-and-tumble play frequency in juveniles than infants in all species, and greater frequency of polyadic play than dyadic play in the

more gregarious redtail monkeys and black-and-white colobus. Observations included 20-minute focal observations, and frequency of rough-and-tumble play and the number of play partners were recorded. Red colobus, black-and-white-colobus, and grey-cheeked mangabeys did not show differences in frequency of rough-and-tumble play between age or sex classes. Frequency was different between male and female redtail monkeys (Wilcoxon, $p=0.0418$), but not when infants and juveniles were examined separately. Red colobus, redtail monkeys, and grey-cheeked mangabeys showed no difference in frequency of polyadic and dyadic play, but black-and-white colobus immatures had a greater frequency of dyadic play (Wilcoxon, $p=0.0001769$). These results suggest that aspects of rough-and-tumble play in these species are not necessarily affected by species, age, or sex.

This project was supported by the Hunter College Department of Anthropology Research and Training Program Grant.

Hominin Behavioural Ecology through the use of Organic Tools: Primate modelling and percussive tool use

LYDIA V. LUNCZ¹, DAVID R. BRAUN², JOAO MARREIROS^{3,4}, MARION BAMFORD^{1,5} and SUSANA CARVALHO^{1,6}

¹Primate Models for Behavioural Evolution Lab, University of Oxford, ²Department of Anthropology, George Washington University, ³TraCEr, Laboratory for Traceology and Controlled Experiments, Archaeological Research Centre and Museum for Human Behavioural Evolution, ⁴Institute for Prehistoric and Protohistoric Archaeology, Johannes Gutenberg University, ⁵Bernard Price Institute for Paleontological Research, University of Witwatersrand, ⁶Gorongosa National Park, Sofala, Mozambique

Organic tools are absent from the archaeological record until ca. 400 000 years ago, as the potential for preservation of plant material is low. However, based on the universal use of vegetation tools seen in modern non-industrialized human societies and in the tool-kits of extant chimpanzees, we expect that tools made of plants played a key role in the technological evolution of early hominins. Here, we describe the use of robust wooden tools by wild chimpanzees (*Pan troglodytes verus*) and report on percussive wear on tools used at the Tai National Park (Côte d'Ivoire). Chimpanzees use branches as hammers and roots as anvils to crack open nuts. The inflicted damage leaves a diagnostic pattern that may endure the fossilisation process. We describe the shape morpho-types corresponding to external fibre damage, as well as patterns of internal damage of wooden cells at the centre of the percussive impact area. Experiments replicating continued percussive activities, using tropical wooden species, provide the first data on damage development across different species of wood. These include species

currently used by chimpanzees as well as wood with similar properties to the Plio-Pleistocene fossil vegetation of the Koobi Fora Formation (KFF), Kenya. The resulting use wear catalogue is compared with fossil wood specimens recovered from the KFF. Preliminary results show similarities between fossil specimens and damage patterns of chimpanzee wooden tools. This first examination of fossil wood opens the way to identify early hominin behaviour that would, otherwise, remain undetected.

Funding: Leverhulme Trust, NSF Archaeology grant (#1624398) and supplemental REU #1930719

Deliberation methods as community engagement

JUSTIN LUND

Anthropology, University of Oklahoma

A legacy of harmful research has shaped attitudes toward genomics in tribal communities. To advance community discussions on these issues, we have recently worked to cultivate a dialogue about the potential benefits and risks of genomics research for American Indian/Alaska Native (AI/AN) people through successive deliberations in three distinct tribal communities from Oklahoma, Alaska, and South Dakota. The three events were designed to adhere to key tenets of public deliberation. This methodological approach often convenes people from varied backgrounds to learn, discuss, and carefully weigh their perspectives on a set of complex issues that concerns them while offering reasons for their positions and priorities. Over the course of the three events we convened 50 participants, ranging in age from 22-74, with education levels between some high school to post-baccalaureate. This paper explores the implementation of hypothetical scenarios as a strategy to encourage participation and supplement group discussion. The scenarios were carefully written in attempt to be respectful to an understanding of cultural nuance and locality. While many of the cultural considerations written into the scenarios were well received and encouraged rich discussion, the introduction of hypothetical scenarios also produced unforeseen concerns that speak to the importance of developing engagement strategies and discursive exercises in culturally appropriate and community-specific ways. Notably, we found that the scenarios allowed participants from any background to demonstrate their ability to speak to a range of complex topics and to express their deeply held values.

Variation in intake rates between two sympatric folivores in Kibale National Park, Uganda

RISA LUTHER¹ and JESSICA M. ROTHMAN^{2,3}

¹Department of Anthropology, University of Minnesota, ²Department of Anthropology, Hunter

ABSTRACTS

College of the City University of New York, ³New York Consortium in Evolutionary Primatology, New York, New York, USA

It has long been thought that leaves are ubiquitous in rainforest habitats and leaf-eating primates have ample resources; however, recent studies have demonstrated that leaves vary in availability and nutritional quality. Two sympatric colobines in Kibale National Park, Uganda, the black-and-white colobus (*Colobus guereza*) and red colobus (*Piliocolobus tephrosceles*), overlap considerably in their leafy diets and both species preferentially select young leaves over mature leaves. Though red colobus are smaller in size than black-and-white colobus, red colobus live in larger groups, travel further, and experience more food competition. Therefore, red colobus monkeys are expected to consume foods at a higher rate (g/min) compared to black-and-white colobus monkeys. We estimated intake rates for 31 leaf species consumed by red colobus and 21 consumed by black-and-white colobus during two months. We found significantly higher intake rates of all foods on a dry weight basis (Poisson GLMM: coef = 0.29 ± 0.06, p < 0.05) consumed by red colobus (1.80 g/min, SD = 6.34) compared to black-and-white colobus (1.00 g/min, SD = 5.13). In both species, we found significantly higher intake rates in males than females. Additionally, juveniles exhibit significantly higher intake rates than subadults who exhibit significantly higher intake rates than adults. These data support the idea that folivores experience food competition, and there are significant differences among intake rates of different age-sex classes of individual monkeys.

Inferring geographic origins and migration among Middle Formative individuals from the Central Highlands of Mesoamerica using strontium isotopes

PAIGE A. LYNCH¹, HEATHER J. H. EDGAR¹, VICTOR J. POLYAK², GISELLE CANTO AGUILAR³, ALEJANDRO ARGÜELLES⁴, COREY S. RAGSDALE⁵, YEMANE ASMEROM² and KEITH M. PRUFER¹

¹Anthropology, University of New Mexico, ²Earth and Planetary Sciences, University of New Mexico, ³Centro Regional de Morelos, Instituto Nacional de Antropología e Historia, Morelos, ⁴Instituto de Investigaciones Antropológicas, Universidad Nacional Autónoma de México, ⁵Anthropology, Southern Illinois University, Edwardsville

Strontium isotopes from enamel can provide geochemical evidence for mobility in humans between infancy/childhood and adulthood. Studies in Mesoamerica have investigated mobility in large complex states, but few data exist for the Middle Formative (900-400 BCE). Zazacalca, located in Morelos, Mexico, has a long history of occupation, dating from 800 BCE to 1150 CE. Fifty-six individuals were assigned to the Middle Formative by association with ceramics and carved sculptures. This project seeks to

understand the degree of mobility of individuals buried at Zazacatla, a site proposed to be key in linking Olmec centers to sites in the south and south-central coast. The timing and frequency of individual migration will be informative of interactions among Olmec-period sites across Mesoamerica.

Previously published data shows strontium isotopes from the central highlands/Basin of Mexico range from 0.7046–0.7055. We assume individuals buried in Zazacatla would have ⁸⁷Sr/⁸⁶Sr values within or close to that range. Enamel from individual teeth were sampled for Sr analysis (N_{total} = 9). Results range from 0.7048–0.7069. Compared to previously published strontium data, only two individuals are within the range for Central highlands/Basin of Mexico, suggesting the other seven individuals were nonlocal. Ratios for these individuals fall within the ranges for the Mexican volcanic belt and Altiplano. Further study will include $\delta^{18}\text{O}_{\text{enamel}}$ to understand if these individuals were from coastal or highland regions, creating a more precise estimate of geographic origin.

Diachronic and Regional Analysis of Congenital Defects in the Ancient Peru: 3,000 Years of Skeletal Developmental Anomalies in the Lambayeque Valley Complex

OLHA LYSA and HAAGEN D. KLAUS

Department of Sociology and Anthropology, George Mason University

Congenital defects and developmental anomalies of the human skeleton are perhaps the least studied and most poorly understood series types of conditions in the Central Andean skeletal record. In this work, we examine the patterning of congenital defects in human skeletal samples from the northern coast of Peru in the Lambayeque Valley Complex. The sample spans more than 2,600 individuals from 27 archeological sites occupied between 2800 BCE to 1750 CE. We hypothesize that as population size, mating networks, and gene pools expanded over time, congenital errors decreased in frequency until the demographic contraction associated with Spanish conquest. A range of congenital errors were observed in the samples ranging from cleft (butterfly) vertebrae to cleft palate, Klippel-Fiel syndrome, spina bifida occulta, congenital dislocation of the femoral head, and deciduous mandibular incisor twinning in the dentition. In general and across this 3,000 year period, congenital anomalies are very rare involving less than one percent of these individuals. Despite major social and demographic changes no perceptible changes in frequency are observed through time. However, cleft vertebrae

are by far the most common anomaly, echoing regional findings by other researchers pointing to a possibility of founder effect underlying its patterning.

This work was funded by grants to HDK from the National Science Foundation, Wenner-Gren Foundation, National Geographic, and George Mason University since 2004.

Bioarchaeological analysis of Late Neolithic inhumations from a dolmen in Switzerland

SANDRA LÄSCH¹, INGA SIEBKE¹, ANJA FURTWÄGLER², NOAH STEURI³, ALBERT HAFNER³, MARIANNE RAMSTEIN⁴ and JOHANNES KRAUSE^{2,5}

¹Dept. of Physical Anthropology, Inst. of Forensic Medicine, University of Bern, Switzerland, ²Dept. of Archaeo- and Palaeogenetics, Inst. of Archaeological Sciences, University of Tübingen, Germany, ³Dept. of Prehistoric Archaeology, Inst. of Archaeological Sciences, University of Bern, Switzerland, ⁴Archaeological Service, Canton of Bern, Switzerland, ⁵MPI, Max Planck Institute for the Science of Human History, Jena, Germany

We investigated inhumations from the Neolithic dolmen of Oberbipp in the context of contemporaneous remains from Switzerland in the framework of an interdisciplinary project. Apart from answering archaeological and physical-anthropological questions, the aim was to shed light on their diet, social stratification, migration, kinship, population genetics and phenotype.

The analysis of the commingled remains, which date to the Late and Final Neolithic, revealed a MNI of 42 with both sexes and all age classes represented. We analyzed the stable isotopes $\delta^{13}\text{C}$, $\delta^{15}\text{N}$, $\delta^{34}\text{S}$ as well as ancient DNA. Nitrogen isotope ratios were homogenous for males and females within the dolmen but differed significantly from other contemporaneous sites. Therefore, we hypothesize similar diets and thus an equal social status of both sexes. In general, their diet was rich in carbohydrates compared to other sites, which is also reflected by caries intensities. Animal products seem to have been less important than food derived from agriculture, and additionally, all investigated individuals were lactose-intolerant. The results from population genetics show that the Oberbipp individuals possessed ancestry components from two sources: Western Hunter-Gatherers and Neolithic Anatolian Farmers. However, the sulphur isotope ratios, which were compared to regional animal data, suggest some local mobility.

ABSTRACTS

We detected first-degree kinships only between males while none of the females within the dolmen were related. This, most probably indicates a patrilocal society. Investigations of the phenotype show that they had light skin pigmentation and variable eye colors.

This research has been funded by the Swiss National Science Foundation (CR313L_157024) and by the German Research Foundation (KR4015/4-1)

Accelerated mutation rate of genes controlling for cognitive brain functions in humans

FABIO MACCIARDI¹, GUIA GUFFANTI², GENNADI V. GLINSKY³ and GABRIELE SCORRANO⁴

¹Psychiatry and Human Behavior, University of California, Irvine, ²Psychiatry, Harvard University, ³Institute of Engineering In Medicine, University of California, San Diego, ⁴Evogenomics Section, GLOBE Institute, University of Copenhagen

Expanding the original formulation of a neutral mutation rate across the human genome, several reports identified genomic regions with variable mutation rates. This variability is possibly due to either positive (adaptive) or negative (balancing/purifying) selection mechanisms. Bustamante et al (2005) have shown that ~ 9% of 3,377 informative loci across the human genome displayed signs of rapid molecular evolution in their coding sequences, an indication of positively selected genes. Conversely, 13.5% of about 6,000 other loci presented signs of weak negative or balancing selection. Most of the following reports kept analyzing the mutation rate across coding exons, while we are missing details for the non-coding, regulatory genome and for genes that are relevant in specific tissues.

With our own work, we have initially looked at the genomic regulatory regions that are active in the brain tissue. We found that ~94.5 % of expressed elements derived by Transposable Elements and putatively *cis*-controlling brain-expressed genes are shared with non-human primates, suggesting a remarkable conservation across at least 8 Mya of evolution. However, we also identified about 4.5% of expressed regulatory elements that are present only in the human genome. Comparing sequences of brain-relevant genes and regulatory regions across modern humans, ancient hominins and non-human primates, our current findings suggest that genes and regulatory elements related to high-cognitive functions and/or related disorders show a marked acceleration of their mutation rate. If confirmed, our findings point to an accelerated positive selection of genes that putatively control for human-specific traits in *H. sapiens*.

The work presented here is partially funded by an NIH grant NIMH R21-MH115327-01 (to FM and GG).

The role of dispersal and school attendance on reproductive dynamics in small populations

SHANE J. MACFARLAN¹, RYAN SCHACHT², ERIC SCHNITER³ and DIEGO GUEVARA BELTRAN⁴

¹Anthropology, University of Utah, ²Anthropology, Eastern Carolina University, ³Economic Science Institute, Chapman University, ⁴Psychology, Arizona State University

Individuals from small populations face challenges to initiating reproduction because stochastic demographic processes create local mate scarcity. In response, flexible dispersal patterns facilitating the movement of individuals across groups are argued to reduce mate search costs and inbreeding depression. Furthermore, factors that aggregate dispersed populations, such as rural schools, could lower mate search costs through expansion of mating markets. However, research typically suggests that dispersal and school attendance are costly, causing individuals to delay marriage and reproduction. Here, we investigate the role of dispersal and school attendance on marriage and reproductive outcomes in four small, dispersed ranching populations in Baja California Sur, Mexico. Our analyses yield the following results. First, we find no evidence that dispersal increases the age at marriage or first reproduction for women. For men, dispersal results in younger ages of marriage than those who remain natal. Second, we find that dispersal increases genetic relatedness among marriage partners. This is likely a mechanism to establish social support for raising offspring in novel communities. Third, counter to typical results for the role of education on reproductive timing, attending school serves to lower age at marriage for both sexes and to lower age at first birth for women. Factors like dispersal and school attendance, that are typically associated with delayed reproduction in large populations, actually lower mate search costs in small, dispersed populations with minimal access to labor markets. We highlight the relevance of population size for understanding the generalizability of reproductive dynamics.

The effects of anteroposterior limb bone curvature on muscle and joint moments in humans: An applied musculoskeletal modelling approach

MARLA MACKINNON¹, JOSH GILES², HOOMAN SHIRZADI² and ALISON MURRAY¹

¹Department of Anthropology, University of Victoria, ²Department of Mechanical Engineering, University of Victoria

Greater limb bone curvature is characteristic of more active human populations in the past, yet it is not immediately clear why, as increasing the curvature of a bone *increases* strain in the tissue. One suggestion is that curvature makes strain more predictable when loading is highly variable.

Here we investigate the comparative effects of variation in femoral and tibial anterior curvature on the muscle and joint forces within a subject when walking on flat versus steep terrain. To do so, we use an innovative approach applying engineering-based musculoskeletal biomechanical modelling techniques to three-dimensional digital models of matched prehistoric human femora and tibiae. Our pilot work includes building two custom lower limb models from individuals of similar estimated body size using the musculoskeletal modelling software OpenSim: one model consists of a curved femur and relatively straight tibia, the other a curved tibia and relatively straight femur. These custom models have been run through simulations of both normal walking and stair-climbing (a proxy for mobility in steep, uneven terrain), with the resulting forces and torques exerted in the ankles, knees, and hips and all key muscles of the lower limb quantified across the full activity cycle. Datasets from the two models are compared at select stages of the activity cycle to explore the effect that limb bone anterior curvature has on muscle and joint forces during walking in variable terrain. Preliminary results of these comparisons will be discussed, contributing to a better understanding of the biomechanics of curvature in the archaeological record.

This research was supported by a University of Victoria Internal Research/Creative Project Grant (2019-2020).

Theory in paleoanthropology, a historical outlook

PAIGE MADISON

Center for Biology and Society, Arizona State University

The problem of accepting, adapting, and applying large theoretical frameworks to the fossil record is not new to paleoanthropology. This presentation examines the history of evolutionary theory in anthropology—from Charles Darwin to the evolutionary synthesis and EES—while examining the relationship between theory and fossil interpretation, asking: what can conversations about the extended evolutionary synthesis (EES) and human origins learn from the past? Drawing on the work of historians and philosophers of science, this historical analysis finds that understanding the patterns and processes of human origins requires extended conversation and collaboration. While some scholars have suggested that integrated theoretical frameworks such as EES can allow scientists to stop talking past each other, I use historical examples to show that these theoretical frameworks are only successfully applied when basic definitions and core assumptions are explicitly discussed across different disciplines. Through historical examples in which core assumptions were not explicit, leading to disjunctions between theory and interpretation of

ABSTRACTS

evidence, I illustrate the potential hazards in order to look ahead at how paleoanthropology could potentially adapt to new ways of thinking about the evolutionary past.

Funded provided by the Center for Biology and Society at Arizona State University and The Fulbright Program.

Deciduous enamel growth rates in modern and ancient children

PATRICK MAHONEY¹, ROSIE PITFIELD¹, GINA MCFARLANE¹, CAROLINA LOCH², SOPHIE WHITE², NINA SABEL³, MARK SKINNER⁴, PRISCILLA BAYLE⁵, MONA LE LUYER^{1,5}, BRUCE FLOYD⁶, CHRIS ARIS¹, CHRIS DETER¹ and DEBBIE GUATELLI-STEINBERG⁷

¹Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, ²Department of Oral Sciences, University of Otago, ³Institute of Odontology, University of Gothenburg, ⁴Department of Archaeology, Simon Fraser University, ⁵De la Préhistoire à l'Actuel: Culture, Environnement et Anthropologie, Université de Bordeaux, ⁶School of Social Sciences, University of Auckland, ⁷Department of Anthropology, The Ohio State University

Most of what is known about the cell mechanisms that generate human tooth enamel comes from studies of permanent teeth. Much less is known about these mechanisms for deciduous teeth and there are almost no data for incremental enamel growth rates of living children. Here, we investigated the rate enamel increased in thickness and in height for clinical samples of deciduous molars ($n=140$) from England, France, Sweden, and Canada. Cuspal and lateral daily secretion rates (DSRs) were calculated for all children. Initial extension rates were calculated for English children. Data were compared to rates for medieval England.

Mean DSRs varied only slightly when equivalent molar regions were compared between groups of modern-day children and enamel increased in thickness with a trajectory that remained generally constant. In contrast, DSRs from mid and outer molar regions of the English children, or any of the modern-day children, were significantly slower when compared to DSRs from medieval England. The initial rate that molars increased in height was significantly slower in modern-day English children compared to those of medieval England.

Our findings reveal two enamel growth trajectories. Enamel formed slowly and with a trajectory of DSRs that changed only slightly for modern-day children. Medieval molars formed at a faster rate and with a trajectory that accelerated from inner to outer molar surfaces. Results suggest that while

incremental enamel growth rates were generally similar among modern-day children from Europe and North American, rates have slowed down from medieval to modern day England.

Study undertaken as part of The Biorhythm of Childhood Growth project funded by The Leverhulme Trust (grant number RPG-2018-226). The Royal Society provided an equipment grant (grant number RG110435).

Genome-wide ancient DNA investigation of Eneolithic individuals from southwestern Russia reveals a genetic contact point between the forest-steppe and steppe populations

KERTTU MAJANDER^{1,2,4}, KERKKO NORDQVIST⁵, ARKADII KOROLEV⁶, ALEXANDER KHOKHLOV⁶, ROMAN SMOLYANINOV⁷, HENNY PIEZONKA⁸, PÄIVI ONKAMO⁹, JOHANNES KRAUSE^{2,4} and WOLFGANG HAAK²

¹Institute of Evolutionary Medicine, University of Zurich, ²Department for Archaeogenetics, Max Planck Institute for the Science of Human History, ³Department of Biology, University of Turku, ⁴Institute for Archaeological Sciences, Archaeo- and Palaeogenetics, University of Tübingen, ⁵Faculty of Arts, University of Helsinki, ⁶Department of History, Samara State University of Social Sciences and Education, Samara, Russian Federation, ⁷Department of Anthropology, Lipetsk State Pedagogical University, Lipetsk, Russian Federation, ⁸Institute of Pre- and Protohistoric Archaeology, Kiel University

Recent ancient-DNA studies have described substantial gene flow from Bronze-Age populations of the Eurasian steppe, with likely connections to the spread of Indo-European languages. The origins of these people and their later dispersals to the northwestern end of Eurasian steppe zone remain less understood. In northeastern Europe, the Neolithic and Eneolithic (Chalcolithic) periods witnessed the transition of subsistence strategies from the foraging lifestyle into pastoralism. These changes both caused and encouraged large-scale environmental modifications and substantiated divisions between boreal forests, temperate grasslands, and the intermediate belt of forest-steppe. Whether the genetics and evolution of local languages of human populations reflect these environmental zones, is yet largely to be explored.

Here we target the population-genetic transition processes through genome-wide next-generation sequencing data of 25 Eneolithic to Bronze-Age individuals from seven archaeological sites in southwestern Russia. We observe a consistent signal of the hunter-gatherer-like ancestries, followed by the earliest occurrences of individuals with Iranian Neolithic-related ancestry (previously described as 'steppe ancestry') mixed with these. In addition, remnants of the genetic ancestry from early Siberian populations, today mainly prevalent in the Native Americans, are present in the region. These results provide novel insight to an integral

contact zone between major cultural movements, illuminating the role of the forest-steppe populations in Eurasian prehistory and their early contacts with the Eurasian agro-pastoralists. Furthermore, the waves of cultural and genetic input may have heralded language exchange between the early forms or predecessors of Uralic languages, with the Indo-European effects still observed in their modern equivalents.

Understanding the Potential of Chemical Anthropology in Human Burned Remains

CALIL MAKHOUL^{1,2}, LUÁS BATISTA DE CARVALHO², DAVID GONÇALVES^{1,3,4} and EUGÉNIA CUNHA^{1,5}

¹Department of Life Science, Laboratory of Forensic Anthropology, Centre of Functional Ecology, University of Coimbra, Portugal, ²Department of Chemistry, "Molecular Physical-Chemistry" R&D Unit, University of Coimbra, Portugal, ³Department of Life Science, Research Centre for Anthropology and Health (CIAS), University of Coimbra, Portugal, ⁴, Archaeosciences Laboratory, Directorate General Cultural Heritage and LARC/CIBIO/InBIO, Portugal., ⁵, National Institute of Legal Medicine and Forensic Science, Lisbon, Portugal

Burned human skeletal remains pose challenging analytical problems to forensic anthropologists due to heat-induced changes. This research explores the potential of vibrational spectroscopy in determining the structural and chemical degradation based on spectra from the organic and inorganic composition of burned human skeletons. To explore this issue, an assemblage of 560 samples from 40 skeletons of the 21st Century Identified Skeletal Collection (University of Coimbra) experimentally burned at different maximum temperatures (from 500 °C to 1050 °C) and durations (from 45 to 240 minutes) were analyzed through vibrational spectroscopy, namely FTIR and MicroRaman. The variation of the intensity of the bands assigned to either organic or inorganic components such as amide I and II vibrational modes of proteins, CH₂ bending and stretching vibrational modes of lipids, carbonate, hydroxyapatite, phosphate, hydroxylation patterns were investigated. The correlation of the spectra of the organic and inorganic components with the maximum temperature of exposure is clear. Transition from polymorphic hexagonal to monoclinic hydroxyapatite occurs at a temperature higher than 800 °C. The band (Ca-OH) (ca. 345 cm⁻¹) is detected only for burning temperatures equal or above 700 °C, being absent for lower temperatures. It has also been observed that the chemical degradation of the burning experiment could reveal discriminatory "fingerprinting" in cases of commingled or scattered contexts thus allowing reconciling bones belonging to the same

ABSTRACTS

individuals. This study obtained promising results regarding the potential of analyzing vibrational spectra from such remains to assess maximum temperature at which they have been exposed to.

A comparison of specific gravity and creatinine for determining urine concentrations in captive orangutans for monitoring health status and physiology

BRYANNA B. MALBOUF^{1,2}, ERIN E. KANE¹, LARA S. DURGAVICH¹ and CHERYL D. KNOTT^{1,2}

¹Anthropology, Boston University, ²Biology, Boston University

Biomarkers including reproductive hormones and indicators of energy balance can be used to analyze health status and physiology in wild animals. Non-invasive collection of urine or feces enables biomarker monitoring, important for critically endangered species like orangutans. Hormonal measurements must control for urine concentration, typically done using creatinine or specific gravity. Specific gravity measurement compares the density of urine with the density of water. Creatinine is a breakdown product of muscle metabolism that is excreted from the body at a relatively stable rate, and it is an indicator of relative muscle mass in many species. Here, we measure specific gravity in urine samples from captive female orangutans using a digital hand-held urine specific gravity refractometer. We compare specific gravity to previously measured creatinine values and assess the influence of time of collection and refractometer temperature on specific gravity. We found a significant positive correlation between specific gravity and creatinine concentrations (N=1021, Pearson's R=0.578, p<0.001). While we found no significant correlation between the time that samples were collected and specific gravity readings (N= 314, Pearson's R=0.079, p=0.17), readings from morning samples were slightly but significantly lower (N=255, mean=1.008) than afternoon samples (N=60, mean=1.009) (independent samples t-test, $t_{312}=-1.969$, p=0.05). We found a significant negative correlation between specific gravity and refractometer temperature (Pearson's R=-0.23, p<0.001), highlighting the need to control for urine temperature when using thawed samples.

This research was funded by Boston University's Undergraduate Research Opportunities Program, the National Science Foundation (BCS-1638823, BCS-0936199); National Geographic Society; US Fish and Wildlife (F15AP00812, F12AP00369, 98210-8-G661).

Palaeoenvironmental Reconstruction of the Okote, KBS and Upper Burgi Members in East Turkana Using Ecomorphology of Bovid Distal Metapodials

MEGAN MALHERBE¹ and FRANCES L. FORREST²

¹Archaeology, University of Cape Town, ²Education, American Museum of Natural History

The Okote, KBS and Upper Burgi members of East Turkana cover an important time in hominin evolution ranging between 1.4 and 2 million years ago. The Omo-Turkana basin has seen various environmental shifts during this time (Bobe 2011, Cerling et al. 2015) and environmental variation has been suggested to correlate with behavioural and anatomical changes within the hominin lineage. Palaeoenvironmental reconstruction in this area is imperative to provide a framework for understanding how climate and environmental change has influenced hominin evolution. The current study uses three-dimensional geometric morphometrics (3D GM) to quantify morphological shape variations in bovid metapodials (n=29). Fossils were compared with data previously published on extant African bovids with known habitat preferences and locomotor patterns (n=370). Ecomorphological analysis was conducted to determine fossil bovid locomotor behaviour, and by extension habitat preference and the palaeo-vegetation of three subregions in the Koobi Fora Formation. Twenty landmarks were collected from the distal metapodial epiphyses. Landmark data were subjected to generalized Procrustes, principal components and discriminant function analyses (DFA). DFA jackknife (cross-validation) analysis resulted in classification success rates of 81% and 78% for metacarpals and metatarsals respectively. The majority of Upper Burgi fossils (66.7%) classified with modern open-habitat dwelling species. All KBS samples were classified into either heavy cover or closed habitats. The Okote samples were classified across categories, but with the majority (65%) in closed or heavy cover habitats. Results are mostly consistent with previous habitat reconstructions at East Turkana, suggesting a particular mix of habitats across the Omo-Turkana basin.

PAST, National Science Foundation (BCS-1624398, REU supplement1930719) and the National Museums of Kenya.

Beyond Distance Alone: Testing the Efficacy of Skeletal Biological Methods in Capturing Population Gene Flow

ANGELA M. MALLARD and BENJAMIN M. AUERBACH

Anthropology, University of Tennessee

Multiple studies demonstrate that human migration leaves different signatures in genes, morphology, and material culture, often resulting from inherent distinctions in the way past population movements affected these indicators.

Researchers need to assess how analytical tools used for one or more of the measures reflects these signatures. Comparing two modeling methods on the same data may be one such approach. We examine skeletal morphology with models based on a comparison of trait means (Mahalanobis D^2 biodistance) and trait variance (Relethford-Blangero analysis) to assess signals of ancient gene flow in an archaeological context (east-central Arizona, A.D. 1200-1400) where migration, and potentially gene flow, has been supported by material culture. We assess these models using a combination of cranial and post-cranial traits among four of the largest pueblos (n=267). Biodistance analysis suggests the closest relationship in the region is between two contemporaneous pueblos, Grasshopper and Point of Pines; this lends support to hypotheses based on material culture that both sites shared common recent immigrants from the Kayenta region. However, analyses using the Relethford-Blangero method indicate less variance than would be expected at Point of Pines and the amount of variance expected at Grasshopper, in both cases suggesting no support for recent gene flow into these groups. Rather, between both models, we conclude support for affinities between these groups that did not result from recent gene flow. Rather than focus on discrepancies between the models, we find that together they may present a more nuanced understanding of morphological evidence of past population relationships.

Partial funding for this project was provided by the University of Tennessee Department of Anthropology through the Kneberg-Lewis Scholarship.

Strain-level variation in bacteria across reproduction in wild white-faced capuchin monkeys (*Cebus capucinus*)

ELIZABETH K. MALLOTT

Department of Anthropology, Northwestern University, Department of Anthropology, Dartmouth College

Reproductive success in female primates is constrained by nutrient and energy availability. Recent studies have indicated that shifts in the gut microbiome across reproductive states may be contributing to female energy and nutrient intake. In particular, the bacterial phyla Proteobacteria and Actinobacteria may play a role in lipid metabolism and fat deposition. However, few data exist to link the taxa of bacteria that increase during pregnancy and lactation to specific functions that influence energy uptake, lipid metabolism, and fat deposition. In this study, deep shotgun sequencing of 10 samples from four wild white-faced capuchins (*Cebus capucinus*) is used to examine if there is an increase in strains of bacteria and/or microbial functions related to energy production and lipid metabolism during pregnancy or lactation. Taxonomic, strain, and functional profiling of

ABSTRACTS

adult male (n=2), cycling adult female (n=2), pregnant adult female (n=3), and lactating adult female (n=3) samples was performed. Reproductive status has a significant effect on the functional profile of the samples (PERMANOVA, $F=3.06$, $R^2=0.60$, $p=0.05$) and has a larger impact on the taxonomic composition of the gut microbiome than individual identity (PERMANOVA, reproductive status: $F=1.44$, $R^2=0.39$, $p=0.09$; individual identity: $F=1.38$, $R^2=0.25$, $p=0.14$). Additionally, pregnant and lactating females have higher abundances of *Escherichia* and *Pantoea*, two genera within Proteobacteria. These metagenomic sequencing results will further elucidate the specific functions of the gut microbiome that may influence female primate life history strategies.

Funding was provided by an AAPA Cobb Professional Development Grant, the NSF GRFP program, and the Lewis and Clark Fund for Exploration and Field Research.

New enamel $\delta^{13}\text{C}$ data from wild Ugandan chimpanzees (*Pan troglodytes schweinfurthii*) permits the establishment of a hominoid-specific diet-to-enamel $\delta^{13}\text{C}$ offset value: Implications for fossil hominin dietary reconstructions

MAIRE MALONE and JOHN KINGSTON
Department of Anthropology, University of Michigan

The role of diet and dietary changes in hominoid and hominin evolution is an essential one. The main source of information about diet in the fossil record is the biogenic signal in the bioapatite of tooth enamel. The stable carbon isotope ($\delta^{13}\text{C}$) values of the enamel of extant taxa, and knowledge of their diets, have been used as comparative guides for interpreting the isotopic signatures and diets of fossil organisms. The diets of fossil hominins, however, are generally reconstructed using comparative isotopic data from controlled feeding studies of large bodied ruminants, which have a $\delta^{13}\text{C}_{\text{diet-enamel}}$ offset of 14.1‰ but also have very different digestive physiology than that of hominoids. Without controlled feeding studies in extant hominoids, an applicable $\delta^{13}\text{C}$ offset value between hominoid dietary inputs and enamel outputs has been elusive.

Here we present $\delta^{13}\text{C}_{\text{enamel}}$ values of samples from M2s, P4s, and M3s of seven chimpanzees (*Pan troglodytes schweinfurthii*) from Kibale National Park, Uganda, obtained using a specialized dicing method and analyzed using GC-IRMS. Highlighted within this sample are values from individuals from the Ngogo community, where dietary contents, percent of feeding time spent per item, and those items' isotopic values have been previously documented. A preliminary dietary $\delta^{13}\text{C}$ input value of 27.3‰ is calculated from these dietary data, resulting in a mean $\delta^{13}\text{C}_{\text{diet-enamel}}$ offset value of 12.1‰ for the Ngogo chimpanzees. This new hominoid $\delta^{13}\text{C}_{\text{diet-enamel}}$ offset value will permit

more precise paleodietary reconstructions and in-depth interpretations of relationships between diet, climate, and behavior during hominoid and hominin evolution.

The persistence of silvery gibbons (*Hylobates moloch*) within Ujung Kulon National Park, Banten Province, Java, Indonesia

NICHOLAS MALONE¹, JOHAN ISKANDAR², RUHYAT PARTASASMITA², ENENG N. ROHMATULLAYALY², SIDIK PERMANA² and BUDIAWATI S. ISKANDAR³

¹Department of Anthropology, University of Auckland, New Zealand, ²Departemen Biologi, Universitas Padjadjaran, Indonesia, ³Departemen Anthropologi, Universitas Padjadjaran, Indonesia

In the conservation and tourist site of Ujung Kulon National Park (UKNP) an array of endangered species persists amidst a variety of land-use policies and practices. UKNP's status as a World Heritage site and the refuge of the last 60-70 Javan rhinoceros (*Rhinoceros sondaicus*) ensures its continued prominence and protection. However, encroachment by the approximately 50,000 people residing within the park's buffer zone ($\pm 19,500$ hectares) is commonplace. This research focuses on the Endangered (IUCN Red List) silvery gibbon (*Hylobates moloch*) endemic to West and Central Java. In June-July 2019, we conducted a preliminary survey of silvery gibbon habitat using repeated, line-transect sampling to assess gibbon population parameters on the western slopes of Mt. Honje. Within the Tamanjaya and Legon Pakis management sections, the average group density is 3.65 groups/km². The average group size is 2.55 individuals/group, and population density is estimated to be 9.3 individuals/km². Additionally, 12.5 kilometers of reconnaissance walks were used to estimate the extent of recent, small-scale logging of semi-evergreen rainforest within the park boundary. Finally, ethnographic insights were obtained by participant observation and semi-structured interviews with a variety of stakeholders including rice farmers, local officials and spiritual pilgrims. Gibbon groups range in relative proximity to human settlements, and within the park are not averse to ranging in localities that include the most concentrated forms of human activity. We discuss these findings in relation to recent population viability analyses, and report on the impacts and emerging challenges related to the December 2018 tsunami in the Sunda Strait.

This research is funded by a Faculty of Arts Research and Development Grant (University of Auckland) and an Academic Leadership Grant (Universitas Padjadjaran).

The Effects of Host Taxon, Hybridization, and Environment on the Gut Microbiome of *Callithrix* Marmosets

JOANNA MALUKIEWICZ^{1,2}, REED A. CARTWRIGHT³, JORGE A. DERGAM⁴, CLAUDIA S. IGAYARA⁵,

SHARON KESSLER^{6,7}, SILVIA B. MOREIRA⁸, LEANNE T. NASH⁹, PATRICIA A. NICOLA¹⁰, LUIZ CM. PEREIRA¹⁰, ALCIDES PISSINATI⁸, CARLOS R. RUIZ-MIRANDA¹¹, ANDREW T. OZGA¹², CHRISTIAN ROOS², DANIEL L. SILVA⁴, ANNE C. STONE^{13,14,9} and ADRIANA D. GRATIVOL¹¹

¹Instituto de Medicina Tropical, Universidade de Sao Paulo, ²Primate Genetics, German Primate Center, ³The Biodesign Institute, Arizona State University, ⁴Department of Animal Biology, Federal University of Vicosa, ⁵Guarulhos Municipal Zoo, ⁶Department of Psychology, University of Stirling, ⁷Department of Anthropology, Durham University, ⁸Primate Center of Rio de Janeiro, ⁹School of Human Evolution and Social Change, Arizona State University, ¹⁰Programa de Pos-Graduacao Ciências da Saúde e Biológicas, Universidade Federal do Vale do São Francisco, ¹¹Laboratorio das Ciencias Ambientais, Universidade Estadual do Norte Fluminense, ¹²Halmos College of Natural Sciences and Oceanography, Nova Southeastern University, ¹³Institute of Human Origins, Arizona State University, ¹⁴Center for Evolution and Medicine, Arizona State University

Microbiome studies show that host taxon, diet, and environment influence gut bacteria, but these factors are rarely studied in hybrids and exudivores. Hybridization may perturb host fitness by disrupting host genome and gut microbiome interactions. Increasing anthropogenic hybridization may increase host populations with compromised viability from perturbed gut microbiomes. A number of non-human primates (NHPs) are exudivores. Investigation of exudivore NHP gut microbiomes will provide baseline data to improve conservation, wild management, and exudivore welfare in captivity. To investigate the effects of host taxon, hybridization, and environment on gut microbiota, we conducted 16S V4 ribosomal sequencing of the gut microbiome of marmosets (*Callithrix*), non-human primate (NHP) specialist exudivores that also hybridize. We sampled 59 wild, translocated, and captive pure and hybrid *Callithrix*, including endangered *C. aurita*. Gut microbiome diversity differed significantly between hybrids and non-hybrids, but host environment had the strongest overall effect on the gut microbiome. Captive marmosets showed relatively reduced gut microbiome diversity. Wild *Callithrix* had the highest relative abundance of *Bifidobacterium*, which process host-indigestible carbohydrates, while captive marmosets had the highest relative abundance of Enterobacteriaceae, a family containing several pathogenic bacteria. The wild marmoset gut microbiome was enriched predictively for carbohydrate metabolism functions, while that of captive marmosets was enriched for nucleotide and amino acid metabolism function. Our findings show that carbohydrate metabolism is integral to the

ABSTRACTS

composition and function of the wild exudivore gut microbiome. Further, captivity perturbs the exudivore gut microbiome, raising implications for captive host health and exudivore conservation.

This work was supported by a Brazilian CNPq Jovens Talentos Postdoctoral Fellowship, an American Society of Primatologists Conversation Small Grant, and an International Primatological Society Research Grant.

What shapes the non-human primate gut microbiome? Insights from microbial eukaryotes

ALLISON E. MANN^{1,2}, FLORENT MAZEL¹, MATTHEW A. LEMAY¹, EVAN MORIEN¹, VINCENT BILLY¹, MARTIN KOWALEWSKI³, ANTHONY DI FIORE⁴, ANDRÉS LINK⁵, TONY L. GOLDBERG⁶, STACEY TECOT⁷, ANDREA L. BADEN⁸, ANDRES GOMEZ⁹, MICHELLE L. SAUTHER¹⁰, FRANK P. CUOZZO¹¹, GILLIAN A.O. RICE¹², NATHANIEL J. DOMINY¹², REBECCA STUMPF¹³, REBECCA J. LEWIS⁴, LARISSA WEDELL^{14,15}, KATHERINE AMATO¹⁶ and LAURA WEGENER PARFREY^{1,17}

¹Department of Botany and Biodiversity Research Centre, University of British Columbia, ²Department of Microbiology, Immunology, and Genetics, University of North Texas HSC, ³Estacion Biologica Corrientes (MACN-BR), CONICET, ⁴Department of Anthropology, University of Texas Austin, ⁵Department of Biological Sciences, Universidad de los Andes, ⁶Department of Pathobiological Science, University of Wisconsin-Madison, ⁷School of Anthropology, University of Arizona, ⁸Department of Anthropology, Hunter College of City University of New York, ⁹Department of Animal Science, University of Minnesota, ¹⁰Department of Anthropology, University of Colorado Boulder, ¹¹Lajuma research Centre, Louis Trichardt (Makhado), South Africa, ¹²Department of Anthropology, Dartmouth College, ¹³Department of Anthropology, University of Illinois at Urbana-Champaign, ¹⁴Department of Anthropology, Queens College, ¹⁵Department of Archaeology, University of Cape Town, ¹⁶Department of Anthropology, Northwestern University, ¹⁷Department of Zoology, University of British Columbia

Microbial eukaryotes (i.e., protists and fungi) and macroeukaryotes (e.g., helminths) are important members of the mammalian gut microbiome yet, despite their ecological significance, little is known about the factors that influence their assembly and diversity. Non-human primates (NHP) are a valuable study system for understanding the underlying processes that shape the gut microbiome as they occupy highly variable ecological and dietary niches and live in diverse social systems that range from solitary and pair-bonded family groups to large, multi-level societies. Moreover, as our closest living relatives, understanding the wild NHP gut microbiome provides an important evolutionary context for understanding the human gut microbiome. In this study, we used an 18S rRNA gene-fragment metabarcoding approach to survey the natural diversity of eukaryotes from fecal samples collected from 62 NHP individuals, representing

16 species from Central and South America, Africa, and Madagascar. We find that while protists and nematodes are widespread across NHPs, they are only weakly structured by host phylogeny with no detectable patterns by diet, in contrast to previous reports of NHP gut bacterial communities. Instead we find that the eukaryotic gut assemblage is a mixture of environmental, dietary-derived, and true gut residents, the diversity of which we hypothesize to be the result of host behavior, individual dynamics, and the local environment. The results of this study highlight the importance of cross-species comparative research and the role of eukaryotes in the evolution of the mammalian gut microbiome.

Dietary isotopic ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$) values of muscle tissue from Cayo Santiago macaques sampled before and after Hurricane Maria

EVA M. MANN¹, ALEX DECASIEN¹, MICHAEL L. PLATT⁴, MICHAEL G. MONTAGUE⁴, SUSAN ANTÓN¹, RHONDA L. QUINN^{2,3} and JAMES HIGHAM¹

¹Department of Anthropology, New York University, ²Department of Sociology, Anthropology & Social Work, Seton Hall University, ³Department of Earth and Planetary Sciences, Rutgers University, ⁴Department of Neuroscience, Perelman School of Medicine, University of Pennsylvania

Dietary isotopic analysis of primate tissues is a powerful tool in understanding responses to environmental changes and the utilization of fallback foods by primate populations. Biobanking primate tissues provides comparative samples for current and future populations facing ecosystem disruptions related to climate change. This study analyzed muscle tissue $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values from two cohorts of sampled rhesus macaques from Cayo Santiago, Puerto Rico during the year before and after Hurricane Maria in 2017, as well as food sources collected on the island in 2018 (species=10). Macaque samples included biobanked, RNA-later treated muscle tissues of HH group (n=29) sampled from 2016, and both fresh and RNA-later preserved samples of KK group (n=47) sampled from 2018. We first compared $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values between the 2018 fresh and RNA-later preserved muscle replicates to understand effects on the biogenic dietary isotopic signal. Our results show a significant ($p < 0.001$) decrease in $\delta^{15}\text{N}$ values (3.9‰) for RNA-later preserved tissues, while $\delta^{13}\text{C}$ values did not differ. Comparisons between the HH and KK group $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ values from muscle tissue revealed a slight (0.6‰) but significant ($p < 0.05$) increase in the average $\delta^{13}\text{C}$ value from 2016 to 2018, and no significant difference in the average $\delta^{15}\text{N}$ value. We interpret our results to indicate that the vegetative loss from Hurricane Maria influenced a modest increase in C_4 resource

consumption. Based on behavioral observations and food isotopes, potential food items that were consumed at higher levels included seaweed, C_4 grasses and commercial monkey chow.

Funding to JH and SA from NSF (NSF BCS-1800558), and RLQ (NSF BCS-1455274). CORE Cayo funding from NCCR to CPRC #8-P40-OD012217-25. Funding to MP and MM from NIH (NIH R01MH096875).

Species-specific maturation profiles and transcriptional signatures of human, chimpanzee and bonobo neural cells

MARIA CAROLINA MARCHETTO LOGG, Salk Institute

Comparative analyses of neuronal phenotypes in closely related species can shed light on neuronal changes occurring during evolution. The study of post-mortem brains of nonhuman primates (NHPs) has been limited and often does not recapitulate important species-specific developmental hallmarks. We utilize induced pluripotent stem cell (iPSC) technology to investigate the development of cortical pyramidal neurons following migration and physiological maturation of cells. Our results show differential electrophysiological maturation in human neurons compared to those of chimpanzees and bonobos, suggesting heterochronic changes in human neurons. We also reveal that a pioneer transcription factor exhibited species-specific up-regulation during human neurogenesis and directly regulates the rate of physiological maturity in human neurons. The transcription factor identified shows binding sites that have undergone rapid changes in the human lineage and that are involved in early neurodevelopment. This finding indicates that the rate of physiological maturity in human neurons can be directly controlled by modulating a single, conserved transcription factor, providing evidence for the adaptation of gene regulation as a major contributor to human neoteny. The strategy proposed here lays the groundwork for further comparative analyses between humans and NHPs and opens new avenues for understanding the differences in the neural underpinnings of cognition and neurological disease susceptibility between species.

Evolutionary and phylogenetic insights from a nuclear genome of the extinct giant koala lemur *Megaladapis edwardsi*

STEPHANIE MARCINIAK¹, MEHREEN R. MUGHAL², LAURIE R. GODFREY³, CHRISTINA M. BERGEY^{1,4}, RICHARD J. BANKOFF¹, HERITIANA RANDRIANATOANDRO⁵, BROOKE E. CROWLEY⁶, KATHLEEN M. MULDOON⁷, WEBB MILLER⁴, STEPHAN C. SCHUSTER⁸, RIPAN S. MAHL⁹, ANNE D. YODER¹⁰, EDWARD E. LOUIS JR.¹¹, LOGAN KISTLER¹² and GEORGE PERRY^{1,3,4}

¹Anthropology, Pennsylvania State University, ²Bioinformatics and Genomics Intercollege Graduate Program, Pennsylvania State University, ³Anthropology, University of Massachusetts

ABSTRACTS

Amherst, ⁴Biology, Pennsylvania State University, ⁵Mention Anthropologie et Développement Durable, University of Antananarivo, ⁶Geology and Anthropology, University of Cincinnati, ⁷Anatomy, Midwestern University, ⁸Singapore Centre for Environmental Life Sciences Engineering, Nanyang Technological University, ⁹Anthropology and Animal Biology, Carl R. Woese Institute for Genomic Biology, University of Illinois Urbana-Champaign, ¹⁰Biology and Evolutionary Anthropology, Duke University, ¹¹Conservation Genetics, Omaha's Henry Doorly Zoo and Aquarium, ¹²Anthropology, National Museum of Natural History, Smithsonian Institution, ¹³Huck Institutes of the Life Sciences, Pennsylvania State University

The extinction of megafauna on Madagascar over the past millennium has substantially impacted the island's biodiversity, for example with no surviving endemic animals having average body masses >10kg. Morphological and isotopic analyses of 'subfossil' skeletal remains have helped reconstruct aspects of the biology and behavioral ecology of some of these extinct taxa; yet much remains unknown and uncertainty lingers over particular phylogenetic relationships. As a complementary information source, we generated a nuclear paleogenome sequence (~2x coverage) from the extinct subfossil lemur *Megaladapis edwardsi* (~85 kg body mass). To test among the various competing phylogenetic hypotheses for this taxon, we also needed to generate nuclear genome sequences for two additional extant lemurs, *Eulemur ruffroni* and *Lepilemur mustelinus*. All of these data were then integrated with published sequences from three other lemurs and 46 non-lemur vertebrates. Our phylogenetic results confirm that *M. edwardsi* is most closely related to the Lemuridae (represented by *E. ruffroni* in our analysis); this grouping is supported by 567 out of 771 (74%) gene trees. Meanwhile, our evolutionary analyses identified significant enrichments for convergent amino acid evolution between *M. edwardsi* and extant folivores and herbivores in genes whose protein products degrade plant toxins (with two-toed sloth for "scavenger receptor activity", FDR=0.0018; with a colobine monkey for "hydrolase activity", FDR=0.00535) and absorb nutrients from the breakdown of plant fibers (with horse for "brush border", FDR=0.00216), respectively. Thus, our paleogenomic results are consistent with inferences from various prior non-genomic analyses in suggesting that *M. edwardsi* was likely a specialist folivore.

NSF (BCS-1317163, G.P.; BCS-1750598, L.R.G.),
Ahmanson Foundation (E.E.L.)

From the classroom to the field: A critical review of ethics in human osteological pedagogy and literature.

KATHRYN E. MARKLEIN¹ and STACY DRAKE²
¹Department of Anthropology, University of Louisville, ²Archaeology, Field Museum

Although awareness of ethical considerations inherent to human osteological research has increased in recent topical meeting symposia and published volumes, there still remains general oversight of formal training in bioarchaeological and forensic anthropological ethics at an institutional level. This oversight is captured in the low frequency of "ethics" observed in anthropology undergraduate and graduate programs in the last five years. From the 62 AAPA-published research institutions with biological anthropology graduate programs, 50.0% of undergraduate programs and 33.3% of graduate programs include minimally one course addressing ethical considerations of archaeological/biological research and sampling. Ten universities display both undergraduate and graduate courses/course descriptions with ethics. We propose that this lack of ethics in osteological pedagogy is dialectically related to representations of ethics in our peer-reviewed publications, which presumably epitomize biological anthropology's collective research standards and expectations. Mentions of ethics in forensic anthropology and bioarchaeological research manuscripts, for example in *AJPA*, over the last 50 years have increased at a decadal rate of 300%. Despite this significant increase in peer-reviewed visibility of ethical concerns, "ethics" do not contribute to the methodological essentials of published archaeological and cadaveric research, contrary to observed *AJPA* primatology ($X^2=4.42$, $p<0.05$) and modern DNA ($X^2=13.3$, $p<0.001$) articles, but rather the research shortcomings/limitations of results and discussions. Nevertheless, the significant increase in "ethics" mentions demonstrates growing interest in and consideration for the ethical treatment of human remains in anthropological discourse, and continuously increasing rates of ethical components to published research practices forecast similar improvements to ethics training in the classroom.

Hominin species as anthropological units

JONATHAN MARKS
Anthropology, UNC-Charlotte

One of the most fundamental tenets of the Synthetic Theory is the basic reality of species. Yet since the 1980s, the number of extant primate species has approximately tripled. The number of extinct hominin species has risen dramatically as well. Some of the new hominin taxa sit on the species boundary: notably, Neanderthals and Denisovans. Others, such as *Homo naledi* or *Homo georgicus*, have their reality debated. The debate is more fundamental than "splitting" and "lumping,"

because those practices are strategic, not capricious. Splitter and lumper narratives emphasize different aspects of human prehistory, notably producing narratives of diversity and extinction versus narratives of persistence and cohesion. Biologists working within the Synthetic Theory have long struggled to make zoological sense of hominin taxonomy, on the assumption that paleoanthropological species ought to map onto familiar zoological units, or species. In this paper I argue that paleoanthropological species are not zoological units at all, but "bricolage" in the task of constructing scientific origin narratives. (The term was popularized by Claude Lévi-Strauss to refer to the narrative elements brought together by a mythmaker in creating a compelling and resonant story.) Consequently arguing about the biological reality of *Homo rudolfensis* or *Australopithecus prometheus* is fundamentally misleading. Their reality lies not in the biological realm, but in the anthropological or biocultural; the mistake lies in conflating meaningful units of anthropological origin narrative with zoological species. Moreover, human ancestry and human diversity are connected, through the pseudo-taxonomic practices that produce both ancient species and modern races.

Dietary ethanol in the main food (*Ficus mucosa*) of chimpanzees (*Pan troglodytes*) in a tropical rain forest

ALEKSEY E. MARO¹, AARON A. SANDEL², JOHN C. MITANI³ and ROBERT DUDLEY¹
¹Integrative Biology, University of California, Berkeley, ²Anthropology, University of Texas, Austin, ³Anthropology, University of Michigan, Ann Arbor

Human attraction to ethanol has been hypothesized to be evolutionarily rooted through prolonged ancestral exposure to low dietary concentrations within fermenting fruit. Fermentative yeasts are ubiquitous, vectored by insects and dust motes, and may be present within saccharide-rich substrates without outward signs of decomposition. Obligately frugivorous taxa such as chimpanzees consume large quantities of fruit in relation to their body size, amounting to several kilograms daily. Thus, even low ethanol concentrations potentially add up to a pharmacologically significant dosage, equivalent to multiple standard drinks in human terms. Although ethanol concentrations have been previously documented for primate-consumed fruit, ethanol concentrations within the diet of chimpanzees, our species' nearest relative, have not been systematically examined. Here we look at *Ficus mucosa*, the food item most consumed annually by eastern chimpanzees at Ngogo, Kibale National Park, Uganda. Like most *Ficus* species, *F. mucosa* is pollinated by specialized fig wasps that lay their eggs within the inverted infructescence. Ethanol concentrations were estimated for over 200 figs using

ABSTRACTS

field portable near-infrared spectrometry and gas chromatography. Unripe figs (i.e. those with unhatched wasps) had higher ethanol concentrations (1.1% n=35) than those free of wasps (0.5%, n=150) and hanging figs (preferred by chimpanzees) had higher concentrations (0.8% n=85) than fallen ones (0.4%, n=124). Assays of small sample sizes of several other species of chimpanzee-consumed fruits test positive for presence of ethanol. These results have broader ecological implications for other primate and non-primate taxa and are consistent with prolonged evolutionary exposure to dietary ethanol amongst all hominoid taxa.

Arboreal primate ranging from a new perspective: UAS technology at the landscape scale

CHRIS D. MARSH¹, ROSS HILL¹, MATT NOWAK² and AMANDA KORSTJENS¹

¹Landscape Ecology and Primatology Lab, Bournemouth University, ²Biodiversity Monitoring Unit, Sumatran Orangutan Conservation Program

Unmanned Aerial System (or drone) technology allows the 3-dimensional mapping of forest landscapes, allowing a new perspective of arboreal primate habitat use. Utilizing UASs in primatological studies enables the assessment of canopy use by arboreal primates as well as the identification of discreet forms of anthropogenic disturbance, such as historical selective logging. Combining 3D canopy structure with microclimate measurements, we explore how canopy structure buffers solar radiation and how arboreal species behaviourally thermoregulate within the canopy. Applying future climate change predictions to microclimate models, we can estimate how increased temperatures may affect their behavior, ranging and time-budgets, addressing the conditions that may have led to the adoption of terrestrial locomotion in ape species. We present data on a study of the arboreal primate community in a lowland section of the Gunung Leuser Ecosystem in Northern Sumatra. We present results on how the synergistic effects of 3D canopy structure and microclimates alter the ranging of siamang (*Symphalangus syndactylus*) in low cloud cover ($X^2 = 145.3$, $p < 0.001$) as they try to remain with their thermoneutral zone. We also explore how future climate change may alter habitat suitability for orang-utan (*Pongo abelii*) and siamang, decreasing the availability of prime habitat unequally for each species (O: -15.2%, S: -18%) due to their behavioral and eco-morphological adaptations. We also discuss how UAS technology can be utilized in other future studies.

Funding provided by the Royal Geographic Society, the International Primate Society, the Primate Society of Great Britain and the British Ecological Society

Investigating the Patterns of Periosteal Reactions at Tombos

JENAIL MARSHALL

Anthropology, Purdue University

The skeleton is a major site of bacterial infection for humans; most common chronic bacterial diseases affect the skeleton. The axial and appendicular skeletons are prey to infection by several bacteria; in particular, the bacteria genus *Staphylococcus* are the main causative agents of osteitis, osteomyelitis, osteoperiostitis, and joint infections. The presence of skeletal indicators of infection, both specific and non-specific, is indicative of long-term responses to pathogens. Few studies have investigated the relationship between bone infection and dietary sources of natural antibiotics. This study investigates the frequency of non-specific infection in a region known to consume foods with antimicrobial properties, specifically fermented grains. The skeletal sample used in this study comes from Tombos, which is located in the Third Cataract of the Nile River and was established near the start of the New Kingdom Period (c. 1550-1050 BC). Utilizing two-scoring methods, Standards and the Global History of Health, periosteal lesions were identified macroscopically and scored based on location, size of the lesion, and type of lesion. A comparative analysis was completed on forty-two individuals. The frequency of osteoperiostitis was 30%, with only one individual with osteomyelitis (< 1%). The low level of infection on the skeleton combined with the evidence for many individuals living several decades suggests that the community may have experienced the ameliorating effect of natural antibiotics through the consumption of beer and gruel. This study highlights the importance of understanding the relationship humans have with natural antibiotics occurring due to food consumption and non-specific bone inflammation.

Social and ecological influences on Tsimane infant microbial community assembly

MELANIE A. MARTIN^{1,2}, DANIEL D. SPROCKETT D. SPROCKETT³, DAVID A. RELMAN^{3,4} and MICHAEL D. GURVEN²

¹Anthropology, University of Washington,

²Anthropology, University of Santa Barbara,

³Microbiology & Immunology, Stanford University,

⁴Medicine, Stanford University

Ancestral human infant care practices and caregiver contact were more intensive and constant than are generally observed among industrialized populations today. It is not clear how such intensive practices and shared environmental exposures combine to influence gut and oral microbial assembly in early life. The Tsimane are a forager-horticulturalist population of the Bolivian Amazon. Tsimane mothers nurse infants

on-demand day and night and gradually wean with pre-masticated foods. Environmental exposure to benign and pathogenic microbes is ubiquitous. We examined Tsimane microbial community structure from fecal and salivary samples profiled with 16S rRNA gene amplicon sequencing. Paired fecal (n=288) and salivary (n=119) samples were collected longitudinally from 52 Tsimane mother-infant dyads between 2012-2013, representing one of the largest sample sets of infant microbial assembly in a subsistence-scale population collected to date.

Tsimane infant fecal and salivary communities became more distinct and increased in diversity with age, but their fecal communities remained distinct from adult communities at 18 months of age. Most bacteria shared within mother-infant dyads were found at higher abundance in the mother than non-shared bacteria. About 24% of amplicon sequence variants in younger infants' fecal samples were found in maternal saliva samples, which may suggest maternal oral to infant gut transmission. After adjusting for infant age, dietary diversity was associated with greater gut microbial diversity, while fecal neopterin—a biomarker of intestinal inflammation—was associated with lower diversity. We discuss results in relation to prolonged breastfeeding, pre-mastication, village ecology, and social networks.

Research supported by NSF (NSF BCS 0422690; DDIG 1232370; GRF DGE-114747); NIH (NIH/NIGMS T32GM007276, NIH/NIA R01AG024119, NIH/NICHDK99HD074743); Thomas C. and Joan M. Merigan Endowment (Stanford); Chan Zuckerberg Biohub Microbiome Initiative.

Dietary Diversification Across the Tiwanaku Polity: Isotopic Paleodietary Reconstructions Using Sequential Sampling of Dentine Collagen and Bayesian Methods

MARCOS C. MARTINEZ¹, ALEXANDRA M. GREENWALD², DEBORAH E. BLOM³ and KELLY J. KNUDSON¹

¹School of Human Evolution and Social Change, Center for Bioarchaeological Research, Arizona State University, ²Anthropology Department, University of Utah, ³Department of Anthropology, University of Vermont

We utilize stable isotope measures ($\delta^{13}\text{C}_{\text{collagen}}$ and $\delta^{15}\text{N}_{\text{collagen}}$) of weaning practices, childhood diet, and early adulthood diet from sequential serial samples of paired first and third molar dentine collagen from 10 Middle Horizon (ca. AD 500-1000) individuals that were interred in the sites of Tiwanaku in Bolivia, and Chen Chen in Southern Peru. To better examine the variation in paleodiet of the region, we organize previously published isotopic data from Andean archaeological and modern resources plotted in collagen isotopic space to create an *altiplano* food web. We employ MixSAIR, a hierarchical Bayesian model,

ABSTRACTS

to estimate the proportions of isotopically-distinct dietary resources in the dentinal collagen makeup of diet. Results from the sequential serial samples indicate dietary variability within and between the two sites, as diets shifted from childhood (Chen Chen: mean $\delta^{13}\text{C}_{\text{collagen}} = -13.2\text{‰}$ and mean $\delta^{15}\text{N}_{\text{collagen}} = 6.7\text{‰}$; Tiwanaku: mean $\delta^{13}\text{C}_{\text{collagen}} = -12.6\text{‰}$ and mean $\delta^{15}\text{N}_{\text{collagen}} = 10.7\text{‰}$) to early adulthood (Chen Chen: mean $\delta^{13}\text{C}_{\text{collagen}} = -14.2\text{‰}$ and mean $\delta^{15}\text{N}_{\text{collagen}} = 9.2\text{‰}$; Tiwanaku: mean $\delta^{13}\text{C}_{\text{collagen}} = -12.8\text{‰}$ and mean $\delta^{15}\text{N}_{\text{collagen}} = 10.9\text{‰}$). We examine and discuss the variation between and within individuals across the Tiwanaku polity over the period of first and third molar growth (approx. birth to 22 years) and the relative dietary inclusion of domesticated camelids, freshwater resources, and C_3 and C_4 cultigens.

Funding provided by the School of Human Evolution and Social Change at Arizona State and by the National Science Foundation (9BCS-1317237 to DEB and BCS-1317184 to KJK)

Phenotyping the brain, the face, and their genetic interaction over development

NEUS MARTÁNEZ-ABADÁAS¹, RUBÉN GONZÁLEZ¹, ALEXANDRE ROBERT-MORENO², JIM SWOGER², SUSAN M. MOTCH PERRINE³, KAZUHIKO KAWASAKI³, JOAN RICHTSMEI³ and JAMES SHARPE²

¹Biologia Evolutiva, Ecologia i Ciències Ambientals (BEECA), Universitat de Barcelona, ²EMBL- Barcelona, European Molecular Biology Laboratory, ³Department of Anthropology, Pennsylvania State University

The development of the brain and the face is intimately coordinated through a continuous physical and molecular interaction during morphogenesis. Understanding how dynamic spatio-temporal regulation of gene expression patterns guide this process is crucial to reveal mechanisms that may have contributed to human evolution. Facial retraction and encephalization are modern human traits that may have evolved in response to changes in signaling pathways that are common to the regulation of the development of these systems. Combining methods for visualizing gene expression patterns (Whole-Mount in situ Hybridization) with mesoscopic 3D imaging (Optical Projection Tomography), we are developing methods to quantify changes in the space, time and intensity of gene expression patterns in organ development using mouse models. We analyzed an Apert syndrome mouse model, which carries an FGFR2 mutation that in humans is associated with craniofacial dysmorphology and brain malformations. We compared face and head development in 43 mice (22 wildtype and 21 *Fgfr2*+/*P253R* mutant) between embryonic days 10.5 and 11.5. We also assessed the differential expression of *Dusp6*, a downstream target of *Fgfr2* that is relevant for both brain and craniofacial development. Geometric Morphometrics successfully detected phenotypic differences

between wildtype and mutant embryos. However, traditional landmark-based methods could not be applied to quantify the fuzzy 3D spatial distribution of gene expression domains. We are testing automatic free-landmark methods (auto3Dgm) to produce accurate quantifications of gene expression patterns that can be associated with the observed phenotypic malformations. This knowledge will help reveal genotype-phenotype correspondence in brain/face development driving evolutionary change.

We acknowledge funding from: European Commission (FP7-PEOPLE-2012- 597 IIF 327382), National Institutes of Health (NICHD P01HD078233, NIDCR R01DE02298) and Burroughs Wellcome Fund (2013 Collaborative Research Travel Grant).

Demographic factors influence the relative costs and benefits of chimpanzee intra-group killing

ANTHONY P. MASSARO¹, EMILY E. WROBLEWSKI², DEUS C. MJUNGU³, STEFFEN FOERSTER⁴, KARA WALKER⁴, NISARG DESAI⁵, SHADRACK KAMENYA³, NICOLE M. SIMMONS^{5,6}, REBECCA S. RUDICELL⁷, BEATRICE H. HAHN^{8,9}, ANNE E. PUSEY⁴ and MICHAEL L. WILSON^{1,5}

¹Ecology, Evolution, and Behavior, University of Minnesota, ²Anthropology, Washington State University, ³Gombe Stream Research Centre, The Jane Goodall Institute, ⁴Evolutionary Anthropology, Duke University, ⁵Anthropology, University of Minnesota, ⁶Zoology, Makerere University, ⁷Vaccine Research Center, National Institute of Health, ⁸Medicine, University of Pennsylvania, ⁹Microbiology, University of Pennsylvania

Male chimpanzees aggressively defend group territories and sometimes kill members of neighboring communities. Male coalition strength is important for success in these contests, yet male chimpanzees occasionally kill members of their own community. Here we examine the contexts and consequences of intra-community killing in the Mitumba (median = 3 males, 8 females ≥ 12 years old) and Kasekela (median = 12 males, 19 females ≥ 12 years old) communities of Gombe National Park, Tanzania, and the isolated community at Kyambura Gorge, Uganda (median = 3 males, 6 females ≥ 12 years old). Mitumba chimpanzees ranged more frequently in areas contested with Kasekela when they had more males ($t=5.58$, $df=18$, $p<0.001$), supporting the view that males need one another to obtain food resources. We propose that demographic factors enable alpha males to monopolize access to fertile females, increasing the payoff of killing community members. Consistent with this, killers increased their share of paternities (Chi-square, $\chi^2=8.19$, $df=2$, $p=0.016$). Mitumba had a significantly higher percent of days when only one female was observed mating (t -test, $t=-2.36$, $df=21.8$, $p=0.028$). Paternity assignment demonstrates that alpha males obtained only 7 of 44 (15.9%) of known paternities in Kasekela, but 11

of 14 (78.6%) in Mitumba, and both infants born in Kyambura where mating opportunities are more easily monopolized. Accordingly, weaned individuals have been killed as a result of within-group attacks in the smaller Kyambura ($n=1$) and Mitumba ($n=3-6$) communities but not Kasekela.

Beyond Mickey Mouse: Perpetuating Cartoon Paedomorphosis

MICHAEL P. MASTERS
Anthropology, Montana Tech

As K-selected species that give birth to altricial young, humans have evolved a keen preference for cuteness. Our increased cultural penchants for paedomorphic appeal, or *Kindchenschema* as described by Austrian zoologist Konrad Lorenz, was demonstrated in Stephen Jay Gould's classic 1979 article *Mickey Mouse meets Konrad Lorenz*. Gould documented the evolution of Mickey Mouse's craniofacial morphology and revealed a steady shift toward overtly accentuated paedomorphic traits across this 50-year timespan.

In the current study, craniofacial changes were analyzed in a large sample of 230 human cartoon characters drawn from multiple North American programs spanning an 84-year period (1932 – 2016), to examine whether the accentuation of paedomorphic traits has persisted across a broader range of characters since Gould's study. Following Gould's 1979 methods, digital calipers were used to measure and calculate eye/head, eye/face, and face/head height ratios for each individual in the sample, and regression analyses were carried out to test whether these craniofacial ratios changed over time. Each character's time designation was represented by the year their respective movie or television program first aired, and all characters were randomly selected by a research assistant blind to the study objectives to reduce selection bias.

Results demonstrated that each of the above ratios was significantly correlated with time, and the direction of this change was consistent with a patent shift toward more neotenuous craniofacial traits. This trend, and particularly a marked increase in relative eye height, exemplifies the sustained importance of *Kindchenschema* in North American society.

Extremely robust humeri from coastal Jomon foragers in prehistoric Japan

TADAYUKI MASUYAMA¹ and YOSUKE KAIFU²

¹NA, Tahara City Board of Education, ²Department of Anthropology, National Museum of Nature and Science, Tokyo

Human limb bone shafts grow thicker in response to activity levels experienced by individuals. This knowledge can be used to reconstruct lives of prehistoric people. Previous studies demonstrated that limb bone thickness of the Jomon

ABSTRACTS

people, prehistoric hunter-gatherer-fishers in Japan, vary with period and location. However, further tests are required for these observations because of the relatively small samples analyzed, insufficient examinations of inter-site differences and inter-observer errors in measurements, and the lack of control of possible effect of bone size on its thickness. In the present study, by analyzing relative shaft thickness and focusing on inter-site variability, we examine spatiotemporal variation in humeral shaft thickness using a sample of 797 Jomon individuals. The results show that the humeral thickness increased from the Initial Jomon phase onward; the Jomon humeri are thicker in coastal populations than in inland plain populations; inter-site variation is present even among the coastal groups from the same chronological phase; and the patterns of inter-site variation are different between males and females. Of particular interest is the outstanding thickness seen in the males from the Hobi shellmound site located at the tip of the Atsumi Peninsula. We hypothesize that this was caused by not only fishing in the outer sea, but also active marine transportation by rowing boats.

This work was supported by JSPS KAKENHI (grant number JP18H03596).

Reconstructing environmental variance in the Turkana Basin, Kenya, for the Upper Burgi Member

SILINDOKUHLE MAVUSO¹, WENDY H. KHUMALO², SHANNON WARREN³, CAITLIN CRAIG⁴, ZUBAIR JINNAH¹, DAVID BRAUN⁵ and EMMANUEL NDIEMA⁶

¹School of Geosciences, University of the Witwatersrand, ²Geological Sciences, University of Cape Town, ³Department of Geology, University of Kansas, ⁴Department of Anthropology, University of Victoria, ⁵Department of Anthropology, George Washington University, ⁶National Museums of Kenya, Nairobi, Kenya

The Koobi Fora Formation in north-eastern Turkana Basin, holds Pliocene and Pleistocene records that archive hominin behavioral and biological change over the Pleistocene. This sedimentary sequence comprises various environments of fluvial, lacustrine, and aeolian deposits punctuated with tuffaceous deposits allowing for high resolution temporal boundaries for key evolutionary events. The physical environment that this record represents has traditionally been studied using radiogenic isotopes. Time periods for the members of the formation have been considered to have generally stable environmental contexts. Previous studies have relied on these tuff horizons as key markers of depositional environments. Studies of diachronic environmental change utilize these units as a means of correlating deposits laterally across space. Consequently, this chronostratigraphic framework lacks resolution in understanding key depositional

shifts that occur between tuffaceous deposits as well as the largely lithologically diverse sequence. This study employs sequence stratigraphic model to refine environmental change over time in the upper Upper Burgi Member (~1.9 ma). Here we identify three major environmental shifts across the sub-basin which provide a more refined documentation of temporal changes. In addition, the model allows for the reconstruction of relative lake level changes that may be related to global climatic forcing.

Funding acknowledgments to the Center of Excellence in Palaeosciences, the Human Evolution Research Institute, Advancing Womxn grant, as well as Koobi Fora Research and Training

Phytolith residue on lithics: an unreliable method in determining hominin behavior

DEANNA V. MAYBEE¹, GEORGIA OPPENHEIM², OUMEYMA BEN BRAHIM³, CAITLIN CRAIG⁴, JEANWON KIM⁵, TAMARA CAPPS⁶, RAHAB KINYANJUI⁷, DAVID R. BRAUN⁸ and SARAH HLUBIK⁹

¹Anthropology Department, SUNY Binghamton, ²Department of Anthropology, Wellesley College, ³Muséum National d'Histoire Naturelle, Paris, ⁴University of Victoria, ⁵New York University, ⁶University of North Carolina - Wilmington, ⁷National Museums of Kenya, ⁸Center for the Advanced Study of Human Paleobiology, The George Washington University

Residue analysis, specifically plant microremain analysis, serves as a proxy to understand more about hominin behavior and diet. Accumulation of residual material on lithics is most commonly attributed to a reaction of use. Although residue may remain from processing, it is also possible for residue to be found on lithics when they incidentally encounter a material from the surrounding environment. As phytoliths have some resistance to degradation compared to other residual material, i.e. starches, one objective of this study is to determine if phytoliths recovered from stone tools reflect the depositional environment or material processed with those tools. If the phytoliths recovered reflect the environment, they cannot definitively be correlated with use and thus cannot be used in archaeological contexts in determining past behaviors or diet. Previous studies lacked controlled experimental work to associate residual material as a reaction of use. Initially, siliceous rocks, chert and chalcedony, were knapped to create 48 lithic flakes. Half the lithics were processed with *Phoenix dactylifera*, or palm leaves, and the other half remained unprocessed. The lithics were burned, buried, or both to mimic the effects of deposition and hominin behavior. After environmental exposure, the lithics were sonicated seven times, the sonication liquid was centrifuged, and examined under 250x magnification. In addition to palm phytoliths, other phytoliths were present, indicative of environmental contamination. The results

strongly suggest that the phytoliths recovered are extremely likely to reflect the environment, thus should not be used in archaeological contexts to determine past behaviors or diet.

This research was funded in part by the NSF Archaeology program #1624398 and supplemental REU #1930719.

Characterization of histomorphometric developmental patterns in ribs from a medieval Polish population using Geographic Information Systems software

REBECCA C. MAYUS¹, VICTORIA DOMINGUEZ² and AMANDA AGNEW¹

¹Skeletal Biology Research Laboratory, The Ohio State University, ²Department of Anthropology, Lehman College, City University of New York

Processes surrounding bone development are closely tied to health and biomechanical demand, and histological examination of subadult bone in bioarchaeological contexts therefore offers key insight into conditions experienced in life. Subadult bone growth involves both modeling drift and the onset of remodeling. To date, however, few studies have investigated histomorphometry in juvenile skeletons, leading to an incomplete understanding of these processes. The present research addresses the lack of knowledge about subadult rib histomorphometry using Geographic Information Systems (GIS) software, which allows for detailed examination of spatial relationships of histomorphological features. Rib samples were taken from the medieval (11th-12th c) skeletal collection from Giecz, Poland (n=83). Age-at-death ranged from birth to skeletal maturity. Mid-level ribs were sampled at midshaft, and histological slides were prepared, imaged, and analyzed in the GIS software ArcMap Version 10.3. Frequency and spatial distribution of secondary osteons, drifting osteons, primary vascular canals, and porosity near the endosteal border were assessed. Osteon and drifting osteon prevalence increased predictably with age in both the cutaneous and pleural cortices. Primary vascular canals were retained with greater frequency on the cutaneous cortex. Large pores tended to occur on the endosteal surface of the cutaneous cortex, suggesting rapid trabecularization of cortical bone due to modeling drift as the ribcage expands outward during growth. These results support and expand upon previous examinations of subadult rib histomorphometry, and demonstrate the utility of GIS analyses for investigation of developmental processes.

New adult brain size estimates for juvenile hominins

ROBERT C. MCCARTHY¹, SYED MOHAMMED QADRI¹, SANAMPREET BHULLAR¹, EMILY

ABSTRACTS

ZIMEL², MADELINE PETRIKAS³, DEBORAH L. CUNNINGHAM⁴ and DANIEL J. WESCOTT⁴

¹Biological Sciences, Benedictine University, ²Physical Sciences, Benedictine University, ³Upper School, The Hockaday School, ⁴Anthropology, Texas State University

Brain sizes for Taung (*Australopithecus africanus*), KNM-WT 15000 (*Homo erectus*), Gibraltar 2/Devil's Tower (*Homo neanderthalensis*), and other juvenile hominins have been augmented to facilitate comparisons with adult specimens. Unfortunately, researchers using different samples, methods, 'starting' brain sizes, and developmental age estimates have generated widely-divergent adult predictions. Here we estimated adult brain sizes for 35 juvenile hominin specimens using brain growth data for known-age cross-sectional samples of mountain gorillas (*Gorilla beringei*), chimpanzees (*Pan troglodytes*), and modern humans (*Homo sapiens*). We compared goodness-of-fit of nonlinear asymptotic regression to several growth models (Brody, von Bertalanffy, Logistic, Gompertz, Richards) and LOWESS and piecewise regression using the Akaike Information Criterion. After fitting curves with a self-starting nonlinear asymptotic regression model, we increased juvenile hominin estimates using sex- and species-specific growth parameters. These growth curves predict an earlier attainment of adult brain size than expected based on cross-sectional samples sorted by dental stage. Accordingly, adult brain size estimates tend to be smaller than previous estimates. Estimated adult brain sizes for Gibraltar 2, a 4.6-year-old juvenile Neanderthal, fall short of the frequently-cited value of 1600 cubic centimeters. According to African ape growth models, Taung's brain size growth would have been complete or nearly-complete at-death. In contrast to previous speculation, these growth models demonstrate that KNM-WT 15000, D2700, MH1, and other developmentally-older juveniles had reached adult brain size at-death. Finally, we corrected encephalization quotient values skewed by implausible extrapolations of juvenile brain sizes and used revised brain and body size estimates to reevaluate encephalization in Pleistocene hominins.

This research was supported by the Dr. Scholl Foundation.

Excavations at the Crane Dune Site (41CR61): A Probable Burial Site and Prehistoric Habitation in West Texas

BRITTANY S. MCCLAIN, ROBERT LASSEN and TIMOTHY GRIFFITH
Archaeology, AmaTerra Environmental, Inc.

In West Texas, the documentation of isolated burials or cemeteries is relatively limited as a result of harsh environmental conditions, erosional factors, and/or prior disturbances by relic collectors. As such, ornamental objects associated with burials, such as pendants, are extremely

uncommon and rarely documented. During the excavations of a stabilized sand dune for the Crane Dune site (41CR61), a burial pit feature with associated human molar and carved bone pendant was recovered during investigations prior to the widening of Highway 385 in Crane County, Texas. Initially, excavations focused primarily on exposing and recording features consisting of rock-lined ovens in shallow basins, as well as deeper cooking pits without rocks. However, instances of a turquoise pendant recovered near a burial feature and probable human skeletal material adjacent to potential burial features were identified throughout the site.

This site dates to the Late Prehistoric and Late Archaic, and is suggestive of an intensive occupation. Artifacts from the site include dart and arrow points, occasional groundstone and ceramic sherds, lithic debitage, and faunal material ranging from rodents to bison.

This presentation provides the preliminary results and documentation of the continued excavations and bioarchaeological investigations of the project. This includes the discussion of four potential burials, associated ornamental objects, and documentation of spatial patterning and burial positioning. This work at the Crane Dune site has further implications within bioarchaeology and will enhance the limited knowledge of mortuary traditions within an under-studied region, while continuing to provide a wealth of archaeological data in West Texas.

The role of stable hydrogen isotope analysis of bone collagen in refining dietary interpretations at prehistoric Paquimé (Casas Grandes), Mexico

COURTNEY MCCONNAN BORSTAD¹, ADRIANNE OFFENBECKER¹, STEPHEN TAYLOR² and M. ANNE KATZENBERG¹

¹Anthropology & Archaeology, University of Calgary, ²Applied Geochemistry - Isotope Science Laboratory, University of Calgary

Previous isotopic analyses at prehistoric Paquimé indicated meat consumption varied between individuals, but the contribution of plant proteins to these values was not clear. Trophic level interpretations can also be complicated in arid environments because of the physiological effects of water-stress on stable nitrogen isotope tissue values. Collagen stable hydrogen isotope values, which reflect drinking water and dietary hydrogen sources, increase with each trophic level and can also be used to compare the relative amounts of dietary plant and animal protein between individuals.

In order to refine our previous interpretations, 71 human individuals from Paquimé were analyzed for their collagen stable hydrogen isotope values. After accounting for the exchangeable hydrogen in the samples, the stable hydrogen isotope

ratios range from -18.8 to +30.6 per mil. We also estimated the isotopic values of meteoric precipitation and of herbivore tissues using the stable oxygen isotopes from tooth enamel from the same individuals. Plant-based diets will correlate more closely with these estimates than those that included more animal protein.

The results show that while most individuals at Paquimé incorporated some meat into their diet, plant proteins remained important. Young adults appear to have consumed more animal protein than adolescents and older adults, but other characteristics associated with social differentiation do not correspond to any particular dietary pattern.

This study demonstrates the benefit of incorporating stable hydrogen isotope analysis into research questions about protein sources. By refining isotopic knowledge about past diet, we are better able to understand human omnivorous adaptations to semi-arid environments.

This research is supported by the Social Sciences and Humanities Research Council of Canada.

Cranial variation in a historic Icelandic population and a modern 'U.S. White' population

SAMANTHA M. MCCRANE
Anthropology, University of Florida

Despite widespread recognition that racial terms do not correspond to ancestral populations, these are still readily utilized for identification purposes on body donation paperwork and missing person's reports. This study compares within and between group cranial shape variation among two "White" populations: 41 Icelandic crania from the Harvard Peabody Collection and 50 U.S. White crania from the William W. Bass Donated Skeletal Collection. A landmark-based morphometric approach reveals statistically significant shape differences between U.S. White and Icelandic crania overall, as well as within the face, neurocranium, and basicranium specifically. U.S. White individuals are found to have relatively larger crania than Icelandic individuals, with broader faces, taller and more narrow neurocrania, and shorter, less posteriorly projecting basicrania. Temporally defined subsets within the Icelandic sample also differ significantly in their cranial morphology. The shape variation observed among U.S. White and Icelandic crania is compared to previously identified Northwest to Southeast clinal trends for European populations. The direction of variation is contrary to previous findings for most measures. Neutral evolutionary processes resulting from migration and admixture, and/or environmental plasticity during development, are considered as likely candidates for producing the observed patterns of cranial variation. These findings suggest that racial terms such as "White" mask essential phenotypic variation, and that with larger, more varied samples

ABSTRACTS

different "White" populations may be able to be distinguished. These results also broaden our understanding of how migration has shaped morphological variation in Americans of European descent and can act as a model for understanding other ancestral groups.

Social and spatial correlates of disease prevalence in sympatric western lowland gorillas and central chimpanzees

PHILIP MCELMURRAY¹, DAVID MORGAN^{2,3}, DELON NGOTENI³, JEAN ESPOIR MAGEMA³, JUVEY WAWA³, SEVERIN NDAOSSOBA³, DAVID KONI³ and CRICKETTE SANZ^{1,3}

¹Department of Anthropology, Washington University in St. Louis, ²Lester E. Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo, ³Congo Program, Wildlife Conservation Society

Over the last fifty years, precipitous declines in western lowland gorilla (*Gorilla gorilla gorilla*) and central chimpanzee (*Pan troglodytes troglodytes*) populations have been attributed to habitat loss, poaching, and infectious diseases. Respiratory pathogens, lesion-causing bacteria, and emerging diseases such as Ebola and anthrax have been of particular concern with regard to these coexisting apes. Certain aspects of gorilla and chimpanzee sociality and ranging could affect disease spread dynamics of various pathogens depending upon mode of transmission. In this study, we predicted that differences in gorilla and chimpanzee social grouping and home range usage would influence patterns of within- and between- population prevalence of respiratory diseases and lesions. We used longitudinal health monitoring of four groups of gorillas and one community of chimpanzees in northern Republic of Congo conducted from January 2008 to July 2019 to test whether frequency of symptoms was related to group stability, home range size, and range overlap. Prevalence of respiratory disease and lesions varied over time and in relation to within and between-group social interactions. Respiratory outbreaks spread more consistently among gorillas who tend to live in polygynous family groups which show high degrees of range overlap. Whereas in the chimpanzees, the emergence and spread of lesions through individuals within the community was insular and reflective of their fission-fusion subgroups and highly territorial behavior. Understanding how differing social dynamics, range use, and interspecies interactions affect disease prevalence is imperative to effectively conserving remaining ape populations in the Congo Basin.

Arcus Foundation, Lincoln Park Zoo, St. Louis Zoo, US Fish and Wildlife Service, Nouabalé-Ndoki Foundation

Retzius lines: an inconstant biorhythm in human teeth

GINA MCFARLANE¹, DEBBIE GUATELLI-STEINBERG², CAROLINA LOCH³, SOPHIE WHITE³, ROSIE PITFIELD¹, PRISCILLA BAYLE⁴, BRUCE FLOYD⁵ and PATRICK MAHONEY¹

¹School of Anthropology, University of Kent, ²Department of Anthropology, The Ohio State University, ³Departement of Oral Sciences, University of Otago, ⁴De la Préhistoire à l'Actuel: Culture, Environnement et Anthropologie, Université de Bordeaux, ⁵School of Social Sciences, University of Auckland

Human permanent teeth retain evidence of an underlying biorhythm as Retzius lines in enamel. The periodicity of these lines varies between humans but is generally assumed to remain constant within an individual. As such, Retzius periodicity (RP) is incorporated into calculations of subadult age at death in forensic and archaeological contexts, and used to explore variation between hominin species related to the overall pace of life history. Yet, it has never been truly established if RP remains constant along the entire permanent tooth row. Recent research suggest shifts in RP can occur between deciduous and permanent teeth of the same individual. Here we calculate RP (n=129) for South African teeth from the Newcastle Collection and for British teeth from the UCL/Kent collection. Multiple permanent tooth types were present from n=37 individuals and both anterior and posterior types from n=22. Only thin sections that were not oblique were included.

We report first evidence that RP does not always remain constant along the permanent tooth row. When all teeth were analyzed together, RP was significantly higher in anterior (mean RP = 9.88) compared to posterior teeth (mean RP = 8.56). Paired teeth from the same individuals also revealed a significant downwards shift from anterior to posterior teeth. Although not all individuals demonstrated a change in RP, many decreased by at least two days along the tooth row. These findings call into question the reliability of assuming RP calculated from one tooth can be used to represent an individual.

Study undertaken as part of The Biorhythm of Childhood Growth project funded by The Leverhulme Trust (grant number RPG-2018-226). The Royal Society provided an equipment grant (grant number RG110435).

Developing a Tool for Investigating Diachronic Change in Pastoralist Settlement and Land-use in East Turkana Kenya through the use of Historic Aerial Imagery

CONNOR MCFAYDEN¹, CODY WILLNERD¹, PHILIP KYULE², MEDINA LUBIA², MATTHEW DOUGLASS^{1,2}, YI QI¹, EMMANUEL NDIEMA² and DAVID BRAUN³

¹College of Agricultural Sciences and Natural Resources, Univ of Nebraska, ²Archaeology, Kenya

National Museums, ³CASHP, George Washington University

Daasanach Pastoralists on the eastern shore of Lake Turkana, far northwestern Kenya, are experiencing great change, much of it related to the effects of climate variability and an increasingly globalized world. While the modern era reflects major change to traditional practices, pastoralism has been practiced in the region for a very long time (c. 4500 years), and in effect has demonstrated deep resiliency under variable environmental and social circumstances. To explore this issue, we rely on historic aerial imagery from satellites and planes covering the last 70 years. These images provide varied resolutions with which to characterize changing distributions of settlement and vegetation cover. When coupled with remote sensing data, these images provide an opportunity for longitudinal study of changing relationships between people and the land. Here we present on the use of automated feature extraction to characterize changing distributions of settlements through time. Preliminary results demonstrating changing patterns of settlement and land use in relation to climate variability and external development in the study area.

NSF CNH2 # 1924322 NSF REU #1930719 NSF ARCH #1624398

Functional description of the primate nuchal musculature with a focus on positional behaviors

FAYE MCGECHIE¹, NEYSA GRIDER-POTTER², THIERRA K. NALLEY³ and CAROL V. WARD¹

¹Pathology and Anatomical Sciences, University of Missouri, ²Department of Human Sciences, Osaka University, ³Department of Medical Anatomical Sciences, Western University

One of the most understudied regions of primate anatomy is the neck. How soft tissues of the neck vary across primate taxa is relatively unknown, yet is important for understanding function, head carriage, and locomotion. Here, we explore the hypothesis that the dorsal neck musculature is related to postural and locomotor behaviors. We collected and dissected 26 primate cadavers from 17 different genera representing each major primate clade. We hypothesize that trunk and neck posture, as well as suspension and neck rotation all influence the morphology of the neck muscles. We qualitatively described and compared the attachment sites of the dorsal neck, back, and shoulder muscles of taxa that display contrasting behaviors and quantified muscle mass. Using the dissection data combined with contrast enhanced CT data, we constructed 3D models to visualize the *in situ* attachment sites of this complex region for further analysis. Dissections demonstrated that among nonhuman apes, hylobatids lack cranial attachments of the trapezius and rhomboideus. Additionally, strepsirrhines demonstrate anatomy that is more like nonprimate mammals

ABSTRACTS

in the distribution of the trapezius, rhomboideus, and semispinalis muscles. Results of phylogenetic regressions indicate that neck muscle masses are best predicted by body size, but also demonstrated significant results for both postural and locomotor behaviors as predictors of muscle mass overall ($p < 0.05$). This study represents the first comprehensive description of the epaxial musculature of the neck in primates. Future work will focus on quantifying biomechanically-relevant variables such as physiological cross-sectional area using novel fascicle-tracking methods and estimating muscle moments.

This work was funded by the Leakey Foundation, the American Association of Anatomists, the University of Missouri, and the National Science Foundation.

Cases of Precocious and Delayed Puberty in Romano-British Females

CANDACE MCGOVERN

Department of Archaeology, University of Reading

Puberty is the period in which an individual becomes capable of reproduction and is the result of endocrine and physiological changes; however, pubertal timing can be influenced by a range of factors including nutrition, health and genetics. In modern populations, 95% of girls enter stage 1 between the ages of 8.5 and 13 years with peak height velocity (PHV) occurring at 12 years and menarche at 13 years.

To explore pubertal timing, a sample of 136 females between the ages of 10 and 25 from 11 Romano-British urban centres were placed into six pubertal stages. Determining menarche from skeletal remains is established once PHV is reached but prior to the phalangeal epiphyses fusing and is associated with the ossification of the iliac crest. Among Romano-British women, menarche occurred between the ages of 11 and 16 years of age with a mean age of 14 years. However, three individuals were more than 2 years removed from the mean. A 20 to 25-year-old female from Baldock was determined to be delayed as they were in the Deceleration stage despite 97.7% ($n=42/43$) of the age group reaching Maturation or Completion. Additionally, two individuals were classified as having early onset or precocious puberty since they reached the Transition or PHV stage early, at 11.1 and 11.7 years respectively. Age at menarche can be reflective of a variety of diseases; therefore, skeletal pathology was also examined. This can be used to further understand pubertal timing and pathologies in past populations.

Developmental defects of deciduous teeth can be linear too: an analysis of enamel hypoplasia in juvenile great apes

KATE MCGRATH^{1,2}, CARSTEN WITZEL³, ELIZA ORELLANA-GONZÁLEZ⁴, UWE KIERDORF³, HORST KIERDORF³ and EMMY BOCAEGE⁵

¹UMR 5199 PACEA, Université de Bordeaux, ²Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, ³Department of Biology, Universität Hildesheim, ⁴UMR 5060 IRAMAT – CRP2A, Université Bordeaux Montaigne, ⁵Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent

Linear hypoplastic defects of enamel are horizontal grooves on the tooth surface, representing disruptions to enamel secretion in response to disturbances during development. Compared to permanent teeth, much less is known about hypoplastic defects in deciduous teeth. Localized hypoplasia of the primary canine (LHPC) has been described in hominoids, appearing as roughly circular depressions on the labial surface. LHPC has been linked with compromised somatic development and crypt fenestration and/or localized trauma to developing teeth. We report enamel hypoplasia prevalence in a collection of juvenile wild-captured great apes (*Gorilla gorilla*, *Pan troglodytes*, *Pongo* spp.). LHPC prevalence is higher than previously reported: 11 of 12 observable individuals have LHPC on the lower deciduous canines, and 7/12 have LHPC on the upper deciduous canines. LHPC presence, but not morphology, matches across antimeres. Previous studies suggested that linear defects do not occur in deciduous teeth of hominoids, but 4/12 individuals have linear hypoplasia on their upper and/or lower deciduous canines. Linear defects, with or without pits, also occur on the deciduous incisors (5/10 individuals). One individual has localized defects resembling LHPC on the central incisors. Confocal imaging shows exposed Tomes' pit processes in the floors of both defect types, signaling that matrix secretion ceased abruptly. Linear deciduous defects are shallower than those in permanent teeth from the same taxa, which might make the former harder to reliably identify 'by eye'. Ongoing surface characterization will allow these features to be compared between populations and better understood in terms of formation processes.

This project has received funding from the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No 798117.

Residential mobility or Little Ice Age environments? Interpreting bone carbonate $\delta^{18}\text{O}$ values of early to mid 19th c. Philadelphia burials

ELIZABETH A. MCGUIRE¹, KIMBERLEE MORAN², MAJA ŠEŠELJ¹ and RHONDA L. QUINN³

¹Department of Anthropology, Bryn Mawr College, ²Department of Chemistry, Rutgers University - Camden, ³Department of Sociology, Anthropology and Social Work, Seton Hall University

Residential mobility and diet are commonly inferred from oxygen ($\delta^{18}\text{O}$) and carbon ($\delta^{13}\text{C}$) isotopic values of human skeletal remains from historical contexts. However, climatic conditions and geographic variability in food sources through time must be considered to create temporally-specific isoscapes. Rib samples representing nineteen individuals recovered from the burial ground of the First Baptist Church of Philadelphia, dating from the early to mid 19th century, were analyzed for $\delta^{18}\text{O}$ and $\delta^{13}\text{C}$ values from bone carbonate. The estimated ingested water values, ranging from -10.9 to -15.7‰, are lower than expected for the Philadelphia area and instead fall within the rainfall and river water isoscapes of upstate New York, northern New England, and Europe. $\delta^{13}\text{C}$ values span -15.0 to -11.1‰; this range is lower than published bone carbonate $\delta^{13}\text{C}$ values from contemporaneous US burials and suggests little to no C_4 foods in the diet. We suggest possible origins from the northern US and Europe and also discuss the influence of local climatic conditions during the Little Ice Age.

This research was funded by the Frances Velay Fellowship and by funding provided to RL Quinn by the National Science Foundation (NSF BCS-1455274)

The impact of stochastic events on ring-tailed lemur (*Lemur catta*) demography at the Beza Mahafaly Special Reserve

KATHLEEN M. MCGUIRE¹, MICHELLE L. SAUTHER¹ and FRANK P. CUOZZO²

¹Anthropology, University of Colorado Boulder, ²Lajuma Research Centre, Louis Trichardt (Makhado), South Africa

The occurrence and frequency of stochastic events, such as droughts, floods, and cyclones, can influence primate demographic parameters. Accounting for these events is thus essential for estimating future population dynamics, especially in species that are currently endangered in the wild. Ring-tailed lemurs (*Lemur catta*) are experiencing declines in their wild habitats with populations becoming smaller and more fragmented. The ring-tailed lemurs living at the Beza Mahafaly Special Reserve (BMSR) are one of the last intact populations in Madagascar. We used age-structured survival data on over 630 individual ring-tailed lemurs living at BMSR from 2003 to 2014 to estimate the annual population growth rate (λ) across these 11 years. We also used these data to estimate future population size

ABSTRACTS

30, 50, 75, and 100 years into the future using the popbio package in R. Average annual population growth rate across the 11 years indicates that the population is relatively stable ($\lambda=1.035$). However, during the 2005-2006 years of notable cyclones, we observed significant reductions in the BSMR population (lowest: $\lambda=0.825$). Furthermore, the frequency of these events has been increasing over time, and if this continues, the population might not have adequate amount of time to recover between events. Our population projection models indicate that the BSMR population could experience severe decline in numbers in a matter of decades (30-50 years; <90 individuals), which could not only threaten the genetic diversity of ring-tailed lemurs but also the persistence of populations of this species in the wild.

Funding for this study was provided for by the National Science Foundation BCS 0922465.

Living in Dust and Smog: Identity, Inequality, and Pollutant Exposure during England's Industrial Revolution

SARA A. MCGUIRE¹, ALI POURMAND² and WILLIAM J. PESTLE³

¹Department of Anthropology, The Ohio State University, ²Neptune Isotope Lab, Department of Marine Geosciences, Rosenstiel School of Marine and Atmospheric Science, University of Miami, ³Department of Anthropology, University of Miami

The consequences of industrialization in England include an increase in social inequality, increased exposure to pollution, and the deterioration of urban environments. The environments in which individuals lived and worked during this period varied as a consequence of region and biosocial identity (e.g. age, sex, and socioeconomic status). This study examines subsets of two historic English populations (rural Barton-upon-Humber, $n = 40$; urban South Shields, $n = 60$) from the Industrial period to determine how identity and the inequality inherent in England's class system caused differences in individual exposure to industrial pollutants. Trace element and isotopic (Pb, Sr) analyses were used to examine exposure to trace element pollutants that transfer into and store within bone (arsenic, barium, and lead), as well as to assess mobility. The preliminary results of elemental analysis for 93 individuals were contrasted according to age, sex, and local environment (urban vs rural) using T-tests. Overall, the trace-element values fall within the range for dangerous exposure levels (arsenic = 1.26 ± 0.28 ppm; barium = 66.41 ± 4.64 ppm; lead = 34.38 ± 3.08 ppm). Moreover, urban samples have significantly higher values for arsenic ($p = 0.038$), while rural samples have significantly higher values for lead ($p = 0.001$). However, both groups exhibit dangerous exposure levels to these pollutants. As such, this research provides evidence

that exposure to pollutants may not have been confined to the industrial city, and that at least the individuals from Barton-upon-Humber were not as protected by the supposedly idyllic countryside.

This research was funded by OSU's Department of Women's, Gender and Sexuality Studies Coca-Cola Critical Difference for Women Research Grant and OSU's Alumni Grant for Graduate Research and Scholarship.

Mapping juvenile children's salivary aldosterone and cortisone responses during athletic and non-athletic competition

TIMOTHY S. MCHALE¹, WAI-CHI CHEE², CAROLYN R. HODGES-SIMEON¹, DAVID T. ZAVA³, GRAHAM ALBERT¹, KA-CHUN CHAN⁴ and PETER B. GRAY⁵

¹Anthropology, Boston University, ²Department of Education Studies, Hong Kong Baptist University, ³ZRT Laboratory, ⁴Department of Psychology, University of Hong Kong, ⁵Anthropology, University of Nevada, Las Vegas

Aldosterone and cortisone are two understudied adrenal biomarkers associated with the regulation of physical and psychological stress. However, aldosterone and cortisone responses in juvenile children engaged in competition have not been described. We examined acute reactive responses of aldosterone and cortisone among Hong Kongese children, aged 8-11 years, during (1) a soccer match against unknown competitors ($N = 84$, high physical and high psychological stress condition), (2) soccer scrimmage against teammates ($N = 81$, high physical and low psychological stress condition), (3) a table tennis competition ($N = 22$, low physical and low psychological stress condition), and (4) a mixed-sex, team, math competition ($N = 45$, non-physical, high psychological stress condition). We hypothesized that aldosterone and cortisone levels would significantly vary with respect to the type of competition. As predicted, aldosterone levels significantly increased in boys during the soccer match and soccer scrimmage. Cortisone approached a significant increase for the soccer match ($p = 0.055$) and significantly decreased during the soccer scrimmage, likely indicating that competitors experienced high psychological stress during the soccer match and low psychological stress during the soccer scrimmage. Aldosterone and cortisone did not significantly change during table tennis contests. Counter to expectations, aldosterone and cortisone levels significantly decreased, rather than increased as predicted, consistent with a relaxed psychological state for math competitors. This finding also provides support that aldosterone is not only sensitive to physical stress (e.g., regulation of blood pressure), but may also vary with respect to decreases in psychological stress.

This work was supported by a Wenner-Gren dissertation fieldwork grant (#9239).

Observer error and dental metrics

MASON MCKINNEY, ANDREA SBEI and MARIN A. PILLOUD

Anthropology, University of Nevada, Reno

Dental metrics can be used to address research questions related to primate evolution, sexual dimorphism, biological distance analysis, biological stress, and the biological profile in forensic anthropology. As these measurements tend to be small, it is important to know the level of inter- and intra-observer error in recording these data. In this study, we address the role of experience in observer error of dental metrics. Two students were trained on the recordation of dental metric data using Paleo-Tech digital dental calipers calibrated to 0.01 mm. Data were collected on mesiodistal and buccolingual dimensions on a set of five dental casts five times each; time was recorded to the nearest half minute for each dental arcade. The absolute value of the average difference was calculated for each measurement to assess intra- and inter-observer error. The inter-observer error was also calculated between the first recording session and the last.

Intraobserver error rates ranged from 0.09 to 2.19 mm. One observer had high error rates among anterior teeth, whereas the other had higher rates among posterior teeth. The average time spent on each cast ranged from 23 to 10 minutes. On average, the time spent was reduced by seven minutes by the last session. The average interobserver error for the first recordation session was 0.35 mm and for last session, it was 0.29 mm. However, a t-test did not find the difference significant ($p=0.09$). These results show that additional practice can improve observer error rates and lead to significantly faster data collection.

Male sleep is shorter and more fragmented than female sleep in a semi-electric, non-industrial, rural population of Kaqchikel Maya

LEELA MCKINNON¹, DAVID R. SAMSON¹, CHARLES L. NUNN^{2,3} and PABLO A. NEPOMNASCHY⁴

¹Department of Anthropology, University of Toronto Mississauga, ²Department of Evolutionary Anthropology, Duke University, ³Duke Global Health Institute, Duke University, ⁴Maternal and Child Health Laboratory, Faculty of Health Sciences, Simon Fraser University

Background: Humans rely on sleep for a host of functions related to survival and reproduction, including immune response, memory consolidation, cellular maintenance, and emotional regulation. However, the factors that affect sleep duration and quality are not fully understood. Many factors appear to play a role in sleep, including sex and gender, access to electricity, and pattern of

ABSTRACTS

subsistence activities. The current study presents a sleep report from a semi-electric, non-industrial, rural, agricultural population of Kaqchikel Maya in the southwestern highlands of Guatemala.

Methods: Data were obtained using the CamNtech Motionwatch8 actigraph, a small, non-invasive wearable device that provides objective sleep measures in natural living environments. Analysis of four cohorts describes sleep duration, latency, fragmentation, and central phase measure in adolescent girls, adult women, menopausal women, and men, and aims to broaden our understanding of sleep differences associated with sex and reproductive status in a semi-electric, rural population.

Results: Adolescent girls were found to have the longest sleep duration (average= 7.07 hours, SE= 0.1), lowest fragmentation (average= 22.85%, SE= 1.05) and shortest sleep onset latency (average= 0.15 hours, SE= 0.017). In contrast, men were found to have the shortest sleep duration (average= 5.98 hours, SE= 0.23) and lowest sleep quality measured by fragmentation (average= 35.98%, SE= 1.69%), efficiency (average= 76.4%, SE= 1.32%), and sleep onset latency (average= 0.23 hours, SE= 0.03).

Significance: These findings will increase our understanding of variation in sleep patterns in a rural, agricultural population.

This research was supported by the Social Sciences and Humanities Research Council of Canada and Duke University.

Examination of the aye-aye (*Daubentonia madagascariensis*) genome reveals lineage-specific *Alu* element subfamilies

ADAM T. MCLAIN

Biology and Chemistry, SUNY Polytechnic Institute

The aye-aye (*Daubentonia madagascariensis*) is an arboreal, nocturnal lemur and the sole surviving taxon in the genus *Daubentonia*. Aye-ayes last shared a common ancestor with other lemurs ~55 million years ago, after the initial colonization of Madagascar by the common ancestor of all extant lemur species. The sequencing of the aye-aye genome presents an opportunity to examine the status of primate-specific mobile genetic elements called *Alu*. *Alu* elements, non-autonomous retrotransposons ~300 base pairs in length, are widely studied as phylogenetic and evolutionary markers, as well as for their association with various genetic diseases in humans. Over time, older *Alu* elements break down and stop replicating, becoming, in effect, genomic fossils that are useful in the construction of phylogenetic trees. Examination of *Alu* elements in the aye-aye genome allows for a better understanding of the evolutionary history of this lineage. This analysis also provides information on the relationship between *Daubentonia* and other lemur species as

well as *Alu* subfamily activity in a deeply diverged genus. Computational examination of the aye-aye genome identified 301,529 total *Alu* elements, of which 12,330 are long enough (>250 base pairs) to be considered potentially active elements. This indicates a low level of activity for *Alu* in the evolutionary history of the aye-aye genome. This study also identified an endemic and active but very small subfamily of *Alu* elements specific to the aye-aye that are likely to prove useful in future population genetic and evolutionary studies.

This research was supported by start-up funds provided by SUNY Polytechnic Institute.

Determination of Sex Ratios Using the Proximal Femur from Midnight Terror Cave, A Commingle Skeletal Deposit

ERIKA L. MCMULLIN

Anthropology, California State University, Los Angeles

The development of interest in human sacrifice in the 1990s coincided in the Maya area with the rise of the hypothesis that warfare caused the Classic Maya Collapse. This impacted the sacrifice question as victims were assumed to be young, adult males captured in battle. Because of the scarcity for large assemblages related to sacrifice, this assumption has never been tested. Midnight Terror Cave contains over a hundred individuals but very few skulls suitable for sexing. My thesis project uses a variety of sexing methods on different bones to develop an approximate sex ratio to test the warfare hypothesis. This poster discusses one method approach I am using, measuring the proximal femur. The method was outlined by Albanese et al. (2008) by finding three measurements: greater trochanter (GT) to fovea capita (FC), GT to the lesser trochanter (LT), and LT to FC. The measurements produce a triangle which can be used to assess and determine sexual dimorphism between individuals. My results showed that out of nine right-femurs, all were female ($p < 0.1$), and out of six left-femurs, five were female and one was male ($p > 0.8$). Thus, the results suggest that females have an important role in human sacrifice at MTC collection although more data is needed to conclude how large their role was.

New discoveries from Rusinga Island's Kiahera Formation, with implications for catarrhine phylogeography

KIERAN P. MCNULTY¹, THOMAS LEHMANN², LAUREN A. MICHEL³, KIRSTEN E. JENKINS⁴ and DANIEL J. PEPPE⁵

¹Anthropology, University of Minnesota,

²Paläomammalogie, Senckenberg-Forschungsinstitut und Naturmuseum,

³Earth Sciences, Tennessee Tech University,

⁴Anthropology, Tacoma Community College,

⁵Geosciences, Baylor University

Fossils from Rusinga Island, Kenya, are known primarily from the so-called Fossil Bed Member of the Hiwegi Formation, dated to ca. 18.1 Ma. These include at least five catarrhine species and a similar number of strepsirrhine primates. The Kiahera Formation, dated to ca. 18.3-18.7 Ma, is thought to share a similar faunal community with the Hiwegi Formation, but there are substantially fewer specimens from this older unit, making it difficult to verify this claim. Here, we report three major discoveries from our 2019 field season targeting Kiahera Formation outcrops. First, more than a dozen soft-tissue specimens were found preserved on the Gumba Peninsula, representing the first such assemblage in nearly a century of research on Rusinga. Second, at least four hundred fossils were found preserved in the remains of a hollow tree trunk located in the Gumba Red Beds. Results from comparative analyses demonstrate that these specimens broadly sample the faunal community – albeit within a single size class – and include taxa that are otherwise very rare in collections. Comparisons to the assemblage from Whitworth's tree trunk suggest that these new fossils were accumulated by a much smaller mammalian or avian predator. Finally, a new primate specimen found in Kiahera deposits near Wayando Hill suggests similarities to small catarrhines from Tinderet and Napak localities. Its presence on Rusinga, first reported here, points to continuity between Rusinga's primate community and those from older deposits in East Africa.

This research was sponsored by grants from the Leakey Foundation (to LAM) and National Science Foundation (BCS #1241807 to KPM).

Testing the role of body size in the transition from semi-digitigrady to plantigrady in primates: a case study using the calcanei of *Theropithecus oswaldi*

ELLISON J. MCNUTT

Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California

Plantigrady (i.e., heel-striking) is an important precursor to upright, stable bipedalism. While the extant apes all display some degree of plantigrade foot postures during walking, extant monkeys display semi-digitigrade foot postures. Understanding the drivers behind this difference has been difficult. It has been hypothesized that increases in primate body size correspond with a shift toward more plantigrade postures. However, given the bias between foot posture and body size within extant primates (i.e., apes are generally larger and plantigrade, monkeys are generally smaller and semi-digitigrade) this hypothesis has been difficult to test. Building on previous work relating comparative kinematic data with calcaneal morphology, this study addressed this problem using 3D geometric morphometric analyses comparing calcanei from a large-bodied fossil monkey, *Theropithecus oswaldi*

ABSTRACTS

($n=9$), to a sample of extant primates from 11 genera. The distal calcanei of *T. oswaldi* display intermediate anatomy between semi-digitigrade monkeys and plantigrade apes, including: a larger, flatter posterior articular facet than those found in other monkeys; a smaller, less medially projecting anterior tubercle; and a more vertically oriented calcaneocuboid joint. Proximally, *T. oswaldi* appear similar in anatomy to extant monkeys apart from a relatively longer posterior tuber and a slightly expanded plantar region of the proximal tuber—traits found in more plantigrade primates. Although *T. oswaldi* retains many of the anatomies found in extant semi-digitigrade monkeys, the presence of several characteristics more commonly associated with plantigrade apes provide some support for the hypothesis that increases in body size drive changes in foot posture.

This research was supported by the National Science Foundation, grant number 1730822.

Getting under their skins: New insights into primate baculum/baubellum preservation

RYAN T. MCRAE^{1,2}, JULIA BOLDRICK³ and ANDREA R. ELLER⁴

¹Anthropology/CASHP, George Washington University, ²Human Origins Program, Smithsonian Institution's National Museum of Natural History, ³Vertebrate Zoology, Smithsonian Institution's National Museum of Natural History, ⁴Anthropology, Smithsonian Institution's National Museum of Natural History

Despite their evolutionary, functional, and behavioral significance, the baculum and baubellum (respectively, the male and female genital bones) are understudied. Previous publications on the presence/absence, morphology, and functional significance of these skeletal elements are sparse, often lacking in taxonomic breadth. The collections at the Smithsonian Institution's National Museum of Natural History (NMNH) provide an ideal resource to survey these bones across the order Primates, which we demonstrate are often left preserved in study skins. To our knowledge, documenting bacula/baubella presence in primate skins has never been attempted. NMNH skeletal collections list a single primate baculum (*Theropithecus gelada*) while literature suggests bony element presence in at least half of primate genera. Here, we document the presence/absence of both genital bones for every nonhuman primate taxon within NMNH holdings. Among currently accepted primate genera (about 73), the NMNH skin collections contain 5581 individuals from 66 genera. Preliminary results ($n=300$) indicate a preserved bony element in about 5% of specimens. Visualization techniques include radiograph and CT scanning of study skins to determine bony element preservation, allowing for the collection of new data for morphological comparison. Although much is known about the

sexual behavior and soft-tissue morphology of primates relative to other mammals, the bacula/baubella of many species are not well described. New insights on genital bone presence/absence, combined with phylogeny and behavioral data, will allow for further investigation of evolutionary and ecological pressures on the bones' presence and morphology.

Postcranial sex estimation for unidentified migrants along the U.S. Southern Border

STEPHANIE MEDRANO¹, MOLLY KAPLAN¹, KATE SPRADLEY¹, GILLIAN FOWLER² and CRIS HUGHES³

¹Anthropology, Texas State University, ²School of Life Sciences, University of Lincoln, ³Department of Anthropology and Institute for Genomic Biology, University of Illinois Urbana-Champaign

Sex estimation is a critical part of the biological profile that greatly assists in the identification of unknown individuals. With increasing numbers of Central Americans and Mexicans crossing the U.S. southern border, the need for sex estimation criteria that encompasses the biological variation of unidentified migrants remains critical. The current research addresses whether univariate analyses of postcranial measurements can be used to develop accurate sex classification criteria for unidentified migrants from varied regions in Latin America. Utilizing a combined sample of 314 (201 males, 113 females) known-sex Central American and Mexican individuals from the Forensic Anthropology Foundation of Guatemala, Operation Identification, the Pima County Office of the Medical Examiner, the Universidad Nacional Autónoma de México, and Universidad Nacional Autónoma de Yucatán, analysis of variance was conducted on 42 postcranial measurements to generate sectioning points to serve as sex estimation criteria. In order to test classification accuracies, 16 measurements with significant F-values were applied to a test sample of 30 known-sex individuals not included in the original analyses. Classification accuracies for the test sample were above 80.00% for eight of the 16 measurements, with humerus epicondylar breadth performing best at 96.00%. Classification accuracies were overall better for males than females. Univariate classification criteria are crucial for forensic cases where trauma and taphonomy may render elements incomplete, which is often the case for unidentified migrants. The applicability of broader-encompassing sex estimation criteria for unidentified migrants will prove relevant to ever-changing U.S. demographics. Future studies seek to assess multivariate postcranial sex estimation criteria.

Subadult Femoral Growth Velocity Across the Late Pre-Hispanic and Postcontact Transition in Northern Peru: Biological Stress, Canalisation, Resilience, and Adaptation

CAROLINE K. MEEK, HAAGEN D. KLAUS and DANIEL H. TEMPLE

Sociology and Anthropology, George Mason University

Studies of subadult human growth provide windows upon ontogeny, biological stress, and cultural dynamics - particularly when contextualizing the biocultural effects of adaptive transitions, such as European contact in the Americas. In this work, patterns of subadult growth velocity were examined between A.D. 500-1750 in the Lambayeque Valley Complex on the north coast of Peru. Multiple lines of bioarchaeological indicators and ethnohistoric evidence demonstrate widely negative impacts from European conquest in the region. Therefore, we hypothesize that subadult growth velocity declined. Following established equations, we calculated subadult femoral growth velocity curves from maximum femoral length in a sample of 258 individuals between the ages of 0 to 12 ($n=103$ late pre-Hispanic; $n=155$ postcontact). We reject our hypothesis as no differences were observed between late pre-Hispanic and postcontact growth curves. The results are, however, consistent with a growing number of studies on terminal adult stature and subadult/adult body mass from this area of Peru. The growth curves suggest that somatic growth in this Andean population is strongly developmentally canalised and resistant to external perturbation. Postcontact patterns may relate to biocultural resilience and successful buffering of native populations against some childhood biological stressors stemming from conquest. One notable outlier is the depressed growth curve from the precontact Late Moche period (A.D. 550-850). Political fragmentation, social turbulence, and environmental instability during this era may have negatively affected subadult growth velocity.

This work was funded by grants to HDK from the National Science Foundation, Wenner-Gren Foundation, National Geographic, and George Mason University since 2004.

Paleoecological context of early *Homo erectus* from the Omo-Turkana Basin: Insights from stable Isotopes

SAHLESELASIE MELAKU^{1,2}, ASHLEY S. HAMMOND^{3,4}, KEVIN T. UNO⁵, DAVID B. PATTERSON^{6,7} and MARYSE BIERNAT⁸

¹Cultural Heritage Collection and Laboratory Services, Authority for Research and Conservation of Cultural Heritage (ARCCH) Addis Ababa, Ethiopia., ²Paleoanthropology and paleoenvironment program, Center for Human Evolutionary Studies, Addis Ababa University, Ethiopia., ³Division of Anthropology, American Museum of Natural History, New York, USA., ⁴Department

ABSTRACTS

of Anthropology, New York Consortium in Evolutionary Primatology (NYCEP), New York, USA.,⁵Lamont-Doherty Earth Observatory, Columbia University, Palisades, New York, USA.,⁶Department of Biology, University of North Georgia, Dahlonega, GA, USA.,⁷Center for the Advanced Study of Human Paleobiology, The George Washington University, Washington, DC, USA.,⁸Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University, Tempe, U.S.A.

Early evidence for *Homo erectus* in Africa is documented in the Omo-Turkana Basin in the Upper Burgi Member of the Koobi Fora Formation (East Turkana) and Upper Member G of the Shungura Formation. This study investigates the paleoecological context of early African *Homo erectus* in these regions using stable carbon and oxygen isotopic analysis of tooth enamel from associated large mammals.

Our dataset consists of stable carbon ($\delta^{13}\text{C}$ values $n=269$) and oxygen ($\delta^{18}\text{O}$ $n=191$ values) isotope ratios of fossil tooth enamel from 269 herbivore teeth (18 taxa) compiled from new samples from Area 13 (Upper Burgi Member) at East Turkana and published values dating to the same period from across the Omo-Turkana Basin.

The $\delta^{13}\text{C}$ results indicate most large mammals had a C4-dominated diets, with exception of some mixed C3/C4 feeders. C3-dominated diets are rare. Among the large mammal communities, the family Equidae recorded a largely C4-dominated diet. Alcelaphini was the only bovid with consistent C4-dominated diet throughout the basin ranging from a pure C4 grazer to hypergrazer. Together, the Equid and Alcelaphini data suggest the presence of abundant C4 grasses. *Homo sp.* show a mixed C3-C4 dietary signals. The $\delta^{18}\text{O}$ values among the different mammalian lineages display a wide spectrum from water-dependent to water-independent taxa. These results agree with previous studies indicating the prevalence of C4 grasses at 2.0 Ma during the first appearance of *Homo erectus* in the Omo-Turkana Basin.

Research supported by National Science Foundation (BCS-1424203; BCS-1624398, DDRI-1424203, REU supplement 1930719), Lamont-Doherty Earth Observatory, Wenner-Gren Foundation, and the National Museums of Kenya.

The first cranium of *Australopithecus anamensis*

STEPHANIE M. MELILLO¹, ANTONINO VAZZANA², STEFANO BENAZZI², TIMOTHY M. RYAN³, BEVERLY Z. SAYLOR⁴, LUIS GIBERT⁵, ALAN DEINO⁶, MULUGETA ALENE⁷, NAOMI E. LEVIN⁸, MARK D. PEAPLE⁹, SARAH J. FEAKINS⁹, BENJAMIN BOUREL¹⁰, DORIS BARBONI¹⁰, ALICE NOVELLO¹⁰, FLORENCE SYLVESTRE¹⁰, STANLEY A. MERTZMAN¹¹ and YOHANNES HAILE-SELASSIE¹²

¹Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology,

²Department of Cultural Heritage, University

of Bologna, ³Department of Anthropology, Pennsylvania State University, ⁴Department of Earth, Environmental and Planetary Sciences, Case Western Reserve University, ⁵Departament de Mineralogia, Petrologia i Geologia Aplicada Facultat de Ciències de la Terra, Universitat de Barcelona, ⁶Berkeley Geochronology Center, ⁷School of Earth Sciences, Addis Ababa University, ⁸Department of Earth and Environmental Sciences, University of Michigan, ⁹Department of Earth Sciences, University of Southern California, ¹⁰Aix-Marseille University, CNRS, IRD, INRA, Collège de France, CEREGE, ¹¹Department of Earth and Environment, Franklin and Marshall College, ¹²Department of Physical Anthropology, Cleveland Museum of Natural History

Australopithecus anamensis is the oldest undisputed hominin in the fossil record. Until recently, the species was known primarily from jaws and teeth. Despite this spotty anatomical coverage, there has been broad consensus that *A. anamensis* is the most primitive representative of the genus and the anagenetic ancestor of *Australopithecus afarensis*.

A newly discovered cranium from Woranso-Mille (MRD-VP-1/1) was dated to 3.8 million years ago and assigned to *A. anamensis* based on canine, maxilla and temporal bone morphology. Following virtual reconstruction, we conducted comparative and phylogenetic analyses to characterize morphological affinities and evaluate hypotheses about evolutionary relationships, for the first time using cranial features.

In some respects, our comparisons support previous work portraying *A. anamensis* as a plesiomorphic extension of *A. afarensis*. The structure of the MRD face is characteristic of the genus *Australopithecus*, whereas neurocranial features are shared with more primitive hominins. However, we also identify unexpected morphology in MRD that is variably present in robust australopithecids and *Australopithecus africanus*. This work contributes to the characterization of *A. anamensis* as a species and provides a morphological link between the earliest "putative" hominins and the australopithecids.

Our phylogenetic analyses largely confirm accepted cladistic topology. These results indicate that craniofacial features newly documented in MRD convey the same information about phylogenetic position as previously documented dentognathic features. Our results further suggest that *A. anamensis* possessed more derived features than previously recognized. In conjunction with other lines of evidence, this finding challenges the widely accepted hypothesis of *A. anamensis*-*A. afarensis* anagenesis.

This research was supported by the CMNH; W. J. and L. Hlavin, T. and K. Leiden, and E. Lincoln; MPI-EVA; NSF (BCS-1124705, BCS-1124713, BCS-1124716, BCS-1125157 and BCS-1125345); ERC (ERC-724046-SUCCESS)

The Effects of Taphonomic Distortion on Fluctuating Asymmetry Analysis in a Historic Hispanic Population

RAPHAELA M. MELORO¹, JOSEPH T. HEFNER² and VALERIE B. DELEON¹

¹Department of Anthropology, University of Florida, ²Department of Anthropology, Michigan State University

Fluctuating asymmetry (FA) analysis is often considered a powerful tool for examining developmental stress in past populations, giving insight into population health. FA analyses are, however, highly sensitive to error, with small deviations in measurements having large impacts on overall results. We hypothesize that taphonomic distortion may also have a significant impact on the results of FA analysis. To examine the effects of burial position on fluctuating asymmetry, this study analyzed three-dimensional landmark coordinate data collected from ectocranial surface scans of a mixed-sex sample of Hispanic adult crania ($n=45$) from the mid-19th century Alameda-Stone cemetery located in Tucson, Arizona. Thirty landmarks, spanning much of the face and neurocranium, were collected in two replicates for each specimen. Landmarks located on the cranial base were omitted due to damage in this region on most of the crania. Data collection and analyses were conducted in R statistical software using the Geomorph package. Burial position was recorded as the side to which the cranium leaned, and the degree to which it leaned. Sex-based differences in levels of asymmetry were not found to be significant, and sexes were pooled for further analysis. Although burial position appeared to have a significant effect on the asymmetric component of shape, there was no generalizable pattern of taphonomic distortion. These findings highlight the difficulty of controlling for taphonomic distortion in bioarchaeological analyses of fluctuating asymmetry.

Determining the rate of co-occurrence in three species of neotropical primates and its indicative effects on group behavior

AARON J. MENCIA

Department of Biological Sciences, Florida Atlantic University

Some species go through social adaptations in response to environmental pressures that drive them to interact with other species. These polyspecific associations are common among primates; driving factors behind mixed-species associations include increased foraging efficiency and decreased predation risk. The semi-habituated species living in the primary and reclaimed lowland rainforest at La Suerte, Costa Rica provides an opportunity to study three different New World monkeys, white faced capuchins (*Cebus capucinus*), mantled howler monkeys (*Alouatta palliata*), and Central American spider

ABSTRACTS

monkeys (*Ateles geoffroyi*). The objective of my study is to observe variation in behavior in relation to mixed species occurrences and determine mixed species relationships. I hypothesized that species would express more stress behaviors during interspecies associations. Additionally, species with dietary overlap would show more agonistic behaviors and larger species, such as spider monkeys, would initiate agonistic behaviors and more sedentary species, such as howler monkeys, would receive more aggressive interactions. Observations were conducted using 20 minute continuous focal samples for a cumulative duration of 25 hours. Activity budget of species in single and multi-species groups were compared in an excel data base. Results of the study yield no differences in each species behaviors during heterospecific and conspecific events. Additionally, implications of species heterospecific relationships are inconclusive. However, further data collection may reveal that species associations would be a behavior that contrasts among differing habitats.

Correlation Between Saw Blade Width and Kerf Width

MELISSA D. MENSCHER and JAMES T. POKINES
MS Forensic Anthropology, Boston University

Previous studies of saw mark analysis primarily focused on using qualitative methods to determine saw class and addressed their potential for identifying suspect saws utilized in cases of dismemberment. The present study examined the extent to which metric analysis can correlate saw blades with saw marks based on measurements of kerf width. A sample of 56 partially defleshed white-tailed deer (*Odocoileus virginianus*) long bones were utilized as proxy for human remains. The specimens were cut using a variety of new and used commercially available saws, including 11 hand-powered and 5 mechanical-powered saws. A total of 500 false start kerfs were measured using digital calipers to ascertain whether their minimum kerf width measurements could be used to determine the type of saw used to produce those cuts. Two experiments were performed, with the first test examining the kerf widths of false starts produced on specimens restrained using clamps, while the second test analyzed the kerf widths of false starts produced on minimally restrained specimens.

Statistical analysis using Hierarchical Linear Modeling found that the average kerf width (mm) was statistically significantly larger for comparatively thicker blades ($p < 0.001$), with average kerf width 29% larger than blade width. Additionally, variables other than saw blade thickness influence kerf width; for example, the average kerf width was statistically significantly larger for

used blades compared to new blades ($p = 0.007$). However, a comparison of hand to mechanical saws ($p = 0.50$) and unrestrained cuts ($p = 0.45$) were not statistically significantly different.

Funding for this project was provided by the MS Forensic Anthropology program at Boston University School of Medicine.

Comparative analysis on the differential role of population history and selection during human morphological diversification in South America

LUMILA P. MENÉNDEZ

Evolutionary Anthropology, Konrad Lorenz Institute for Evolution and Cognition Research

Recent South American populations have been described as presenting larger morphological variation than the one expected due to their recent diversification. However, there is no agreement on the possible causes behind it. Previous comparative anatomy studies have described craniometric changes when comparing specimens from different chronological periods (early, middle, and late Holocene) and from various ecogeographic environments (lowlands/highlands, Andes/Amazonia, East/West). Such variation was either interpreted as the result of genetic drift and/or regional adaptations due to accelerated evolutionary rates. However, the application of a comparative evolutionary approach that allows evaluating the role of different processes in several regions is crucial to gain a more exhaustive local understanding. Therefore, the objective of this presentation is to evaluate the craniometric changes occurred at different regions of South America (Argentina, Brazil, Chile, Colombia, Peru) from the early to the late Holocene. For this, a database with 30 linear measurements that was previously collected by Dr. Héctor Pucciarelli in more than 3000 specimens was used. The samples were grouped into two chronological groups: early/middle Holocene and late Holocene. We calculated Lynch's δ as well as Moran's I to test the neutral hypothesis. The results obtained show that in some regions, as a result of geographic isolation, random factors such as genetic drift could have been dominant (i.e. Chile), while other areas ecological factors such as altitude, climate, and diet were most relevant (i.e. Pampa, Peru). It is concluded that an interdisciplinary approach combining continental and local perspectives would improve current interpretations.

This research was possible thanks to a Postdoctoral Fellowship from the Konrad Lorenz Institute for Evolution and Cognition Research.

Modelling the realized distribution patterns of the Critically Endangered mongoose lemur (*Eulemur mongoz*) in Ankarafantsika National Park: Signals of a specialized biogeographic pattern?

FERNANDO M. MERCADO MALABET^{1,2}, TRAVIS S. STEFFENS^{3,4}, MEGAN L. AYLWARD⁵, JEAN-CLAUDE RAZAFIMAMPIANDRA⁶, FINARITRA T. RANDIMBIARISON⁶ and SHAWN M. LEHMAN¹

¹Department of Anthropology, University of Toronto, ²School of the Environment, University of Toronto, ³Department of Sociology and Anthropology, University of Guelph, ⁴Planet Madagascar, ⁵Department of Anthropology and Archaeology, University of Calgary, ⁶Department of Animal Biology, University of Antananarivo

The persistence of rare species in disturbed environments depends on various aspects of their ecology, including their capacity to occupy a wide breadth of biogeographic conditions. This relationship implies that species that occupy small and fragmented geographic ranges across a specialized breadth of biogeographic conditions are more vulnerable to extirpation from the threats of habitat loss, fragmentation, and stochastic perturbations. Little is known about the biogeography and distribution ecology of the Critically Endangered mongoose lemur (*Eulemur mongoz*). We observed that *E. mongoz* are primarily distributed in a river valley located in the western portion of Ankarafantsika National Park (ANP). Outside this valley, the species is rarely observed. We hypothesize that the restricted distribution of *E. mongoz* to this valley and other similar localities around the park is attributed to the availability of biogeographic conditions specific to these sites. To examine the sources of this biogeographic pattern we used MaxEnt v3.4.1 to develop a species distribution model (SDM) using: (1) presence-only data collected between 2015 and 2019, (2) seven independent background covariates, and (3) a record of survey effort. The results from our model (AUC = 0.89) provide preliminary support for our hypothesis. The probability of occurrence of *E. mongoz* was highest in tall hardwood forests located in close proximity to freshwater sinks. Moreover, occurrence hotspots occupy a small proportion of the park, fragmented by grasslands and dry mixed forest habitats. Our biogeographic model provides some of the first ecological explanations of why *E. mongoz* has a restricted distribution in ANP.

Financial support provided by the Schools of the Environment and Graduate Studies at UofT, The Ontario Government, NSERC, Primate Conservation, Inc. (PCI#1566 and PCI#1582), Global Wildlife Conservation LCAF, and IUCN-SOS.

ABSTRACTS

Fracture Healing in Unintentional and Abuse-Related Fractures in Children: Considerations of Identity in the Context of Physical Abuse

DIANA L. MESSER^{1,2,6}, BRENT ADLER³, FARAH W. BRINK⁴, HENRY XIANG⁵ and AMANDA M. AGNEW⁶

¹Division of Anatomy, The Ohio State University, ²SNA International, In support of DPAA Hawaii, ³Department of Radiology, Nationwide Children's Hospital, ⁴Center for Family Safety and Healing, Nationwide Children's Hospital, ⁵Center for Pediatric Trauma Research & Center for Injury Research and Policy, Nationwide Children's Hospital, ⁶Skeletal Biology Research Lab, School of Health and Rehabilitation Sciences, The Ohio State University

Untreated healing fractures in physically abused children may be discovered during radiographic survey and accurate time since injury estimation can be essential for identification and characterization of abuse. Timelines of fracture repair are primarily derived from unintentional fractures in otherwise healthy children and applied to children suffering physical abuse and other forms of maltreatment. However, potential differences in healing between abuse-related and unintentional fractures has been largely unexplored. This study provides a preliminary evaluation of the relationship of abuse status to fracture healing through a retrospective analysis of radiographically visible features of fracture healing in a modern pediatric population. In total, 176 radiographic follow-ups from 56 patients with humeral fractures (abuse-related: 19, unintentional: 37) were assessed in patients under the age of two years. Subperiosteal new bone and callus formation were assessed radiographically using modified parameters based on Walters *et al.* (2014). Kruskal-Wallis H tests were performed to determine if there were significant differences in fracture healing time between abuse-related and unintentional fractures. Over half the abuse-related fractures were associated with multiple fractures. Subperiosteal new bone formation was observed earlier in abuse-related fractures, but this was not statistically significant ($p=0.310$). All levels of callus matrix occurred earlier in abuse-related, but only one level reached statistical significance. Intermediate callus occurred approximately 7 days earlier in abuse-related fractures ($p=0.057$) than unintentional fractures. These results suggest that there may be differences in healing between abuse-related and unintentional fractures and that the context of abuse should be considered when applying fracture healing timelines

This research was supported by the Center for Injury Research and Policy at Nationwide Children's Hospital through Grant Number 1R49 CE002106 from the Centers for Disease Control and Prevention.

An anthropologist's experiment self-aligning with the OEI course design rubric: What does it take to get an online biological anthropology course taught state-wide?

RACHEL L. MESSINGER¹ and SHAWN VALCARCEL²

¹Life Sciences Department, Moorpark College, ²Professional Development Team, California Virtual Campus-Online Education Initiative

With online instruction becoming increasingly prevalent in biological anthropology, it has become more important than ever to make sure that students have access to high quality courses. The California Virtual Campus-Online Education Initiative (CVC-OEI) was initiated to ensure access to high quality distance education courses, and to help students succeed in those courses. Among the resources created by the CVC-OEI are the OEI Course Design Rubric, the OEI consortium which includes the OEI exchange, and the CVC-OEI Course Design Academy. For a course to be taught on the exchange, it must be approved or "badged" by the CVC-OEI Course Design Academy as being in alignment with the OEI Course Design Rubric, which describes the best practices for distance education courses. The hypothesis being tested was if an instructor can "self-align" an online biological anthropology course to the rubric without going through the Course Design Academy. The results after the course was submitted deemed it incomplete in several areas, but mostly minor changes had to be made to bring the course into alignment. The most substantial changes involved clarifying unit objectives, design changes related to content presentation, and ensuring each assignment had clear objectives and a grading rubric clearly associated with it. Changes related to accessibility were by far the most time-consuming. Overall, the study of biological anthropology and the student experience were enhanced by aligning to the OEI Course Design Rubric. This project offers lessons therein for instructors of online biological anthropology courses related to best practices.

Anatomic extremes of the postcranial axial skeleton of *Australopithecus* and *Paranthropus robustus*

MARC R. MEYER¹, SCOTT A. WILLIAMS^{2,3} and MICHAEL FONG¹

¹Anthropology, Chaffey College, ²Center for the Study of Human Origins, Department of Anthropology, New York University, ³New York Consortium in Evolutionary Primatology

Recent discoveries from *A. anamensis* at Assa Issie (4.2 Ma) and *A. afarensis* from Woranso Mille (3.6 Ma) in Ethiopia, along with later fossils of *A. sediba* from Malapa and *P. robustus* from Drimolen in South Africa preserve rare aspects of vertebral anatomy from opposite poles of the postcranial axial skeleton (C1-C3; S5).

Here we use 2D geometric morphometrics to focus these understudied anatomic regions across extant primate taxa (20 genera, N=518) and find a set of previously unrecognized functional signals that may be used to model extinct hominin postural and locomotor behaviors.

Uncinate process morphology in *A. sediba* provides an arboreal signature not observed in early *Australopithecus* from Ethiopia, and signals a stiffening of the cervical region function where the pectoral girdle mirrors the role of the pelvic girdle, possibly for shoulder support and/or gaze stabilization during climbing, although not to the degree in suspensory primates.

At the opposite axial pole, we find expansion for the gluteus maximus across fossil hominins, as well an expanded origin for the sacrotuberous ligament, which prevents nutation and stabilizes the sacroiliac joint during bipedal locomotion. Moreover, expansion of the caudalmost sacral element (S5) in hominins provides greater insertion area for the perineum, which would strengthen the pelvic floor in erect posture and bipedal locomotion. We discuss the special significance of this development in pregnancy, where the pelvic floor is responsible for resisting gravity in hominins, replacing the supportive role of ventral structures such as the abdominals and pubis in gravid quadrupeds.

Leakey Foundation research grant (to SAW)

Multiple traumas: health care among an Early Medieval community in Italy (Selvicciola, 4th-8th centuries AD)

ILEANA MICARELLI^{1,2}, ROBERT R. PAINE¹, MARY ANNE TAFURI¹ and GIORGIO MANZI¹

¹Department of Environmental Biology, Sapienza, University of Rome, ²Department of Classics, Sapienza, University of Rome

Trauma defects observed among members of archaeological communities is a topic of interest in bioarchaeology. The determination of the cause and effect of traumatic episodes is essential; trauma might be accidental or intentional, while discriminating between multiple injury events and single event with multiple fractures is challenging. The effects of such events may include changes in the individuals' life, as well as, caring efforts by the community. While assessing the skeletal collection from the Early Medieval necropolis of Selvicciola, an older male revealed a unique pattern of healed injuries. From these defects, we recognised two events and recorded six fractures. The first event includes well healed fractures of the nasal bone, right clavicle, scapulae and right ribs. The second event relates to the healing of the right femoral neck (unfused to the head). This fracture happened months before his death, as testified by only 2 mm of new bone formation on femur neck. This last fracture might have been due to osteoporosis combined with an accident.

ABSTRACTS

The result of our investigation shows that he was disabled for much of his life. Even if community level care was not detected in the archaeological record of this case study, the bioarchaeological approach reveals that the implication of a man's survival was strictly dependent by community care and value for human life. Knowledge of herbal medicine, dealing with infection and anatomical issues were probably crucial. Critically, his survival suggests that community health care was a significant part of Early Medieval Italian life.

Harris Lines as Indicators of Physiological Stress in the Middle Holocene Cis-Baikal

LAUREN M. MICHELMAN and ANGELA R. LIEVERSE

Archaeology and Anthropology, University of Saskatchewan

Harris lines (HL) are thought to represent osteological indicators of physiological stress during early life but are often critiqued regarding validity in the reconstruction of life histories. Recent research attempted to challenge critiques including lack of standardized observational methods, loss of HL due to bone remodeling, and uncertainty if physiological stress is tied to HL formation.

Including only individuals aged 0 – 25 years at time of death, this study attempted to determine differences in HL presence and severity in three mortuary populations from the Middle Holocene Cis-Baikal (Russia). Of the three populations, two date to the Early Neolithic (EN) (7500 – 7000 cal. BP) and one to the Late Neolithic – Early Bronze Age (LN – EBA) (5600 – 3700 cal. BP); they are divided by the Middle Neolithic (7000–5600 cal. BP) during which time no evidence of formal cemetery use exists in the region. Previous research demonstrated EN individuals experienced more frequent and repetitive stress events likely reflecting reduced access to or availability of resources.

Despite an expectation that EN individuals would display higher prevalence and severity of HL than LN – EBA individuals, this study found the opposite. Rather than HL severity being tied to individual mortuary populations, age at death appears to be a determining factor. Using comparative data regarding alternative indicators of physiological stress in these populations, this study continues to challenge critiques regarding HL validity while contributing to understandings of overall health in the Middle Holocene Cis-Baikal.

Funding provided by: The Northern Scientific Training Program, The Baikal Archaeology Project (a SSHRC Major Collaborative Research Initiative) and the Arthur Silver Morton Travel Scholarship.

Integration of the hominoid spine, part II: The effects of lordosis on integration of the cervical and lumbar vertebrae

EMILY R. MIDDLETON¹ and CATALINA I. VILLAMIL²

¹Anthropology, University of Wisconsin-Milwaukee, ²School of Chiropractic, Universidad Central del Caribe

Lordosis in the cervical and lumbar regions of the vertebral column produces the characteristic sinusoidal shape of the hominid spine. These curves are considered key skeletal adaptations to bipedal locomotion given that they align the axial skeleton with the hips and knees for a stable center of gravity. Nonhuman apes, on the other hand, lack lumbar lordosis and instead possess short, stiff lower backs adapted to resisting compression during below-branch suspensory behaviors. Here we investigate whether extant hominoids share a common pattern of integration across the cervical and lumbar regions of the spine related to upright body postures or whether the functional demands of different locomotor modes led to variation in patterns of covariation across taxa. To investigate these hypotheses, we calculated four measures (variance of eigenvalues, mean evolvability, mean conditional evolvability, and mean integration) across pairs of cervical and lumbar vertebrae in a large sample of *Homo* (n=151), *Pan* (n=92), and *Hyllobates* (n=77). Results indicate that all three taxa have similar levels of integration across the upper typical cervical (C3-C5) and lumbar vertebrae. However, *Hyllobates* has stronger integration of C6 and C7 with the lumbar than does either *Homo* or *Pan*, and *Hyllobates* also has the lowest evolvability and conditional evolvability among the three taxa. Thus, the functional demands of orthograde appear to lead to numerous similarities across the extant hominoids in terms of cervico-lumbar integration, and bipedality does not appear to have increased coordination across the cervical and lumbar vertebrae in humans relative to other apes.

Funding provided by the Wenner-Gren Foundation, Leakey Foundation, New York University, and an American Association for Anatomy Postdoctoral Fellowship.

Troubles in Tuva: demographic patterns of interpersonal violence in a Late Antique nomadic community from Southern Siberia (2nd-4th c. AD)

MARCO MILELLA¹, GINO CASPARI^{2,3}, YULIJA KAPINUS⁴, JEGOR BLOCHIN⁵, TIMUR SADYKOV⁵ and SANDRA LÄSCH¹

¹Institute of Forensic Medicine, Department of Physical Anthropology, University of Bern (Switzerland), ²Department of Archaeology, University of Sydney (Australia), ³Institute of Archaeological Sciences, University of Bern (Switzerland), ⁴Volga-Ural Center for Paleoanthropological Research, SSGPU (Russian Federation), ⁵Institute for the History of Material

Culture, Russian Academy of Sciences, St. Petersburg (Russian Federation)

Since the emergence of nomadic pastoralism in Eastern Eurasia, warfare became a cultural characteristic of steppe nomads – not only directed towards sedentary cultures, but also among different nomadic tribes. Few bioarchaeological data are available for this contexts dating to Late Antiquity, hampering a discussion of the type of violence characterizing these societies.

Here we present a study of skeletal trauma in Late Antique skeletal sample from Tunnug 1 (Tuva, Siberia – 2nd-4th c. AD), and address following research questions: a) which type of trauma are present? b) which demographic distribution characterizes the observed evidence?

The skeletal injuries were macroscopically diagnosed according to forensic criteria. Differences among sexes and age classes in frequency and type of trauma were tested by means of generalized linear models. The sample includes 78 individuals of both sexes and different age classes (44 adults, 34 subadults, 22 males and 10 females).

17 individuals (21%) show perimortem trauma, mostly represented by sharp-force trauma and in 14 cases suggesting multiple strikes. In 6 cases cutmarks at the level of the cervical vertebrae point to the slicing of the throat. No significant association was found between sex, biological age, and presence or and type of injuries.

Our results indicate a remarkable amount of violence experienced by this population, especially through raids. Also, they suggest that overkill and executions were relevant components of aggressive behaviors among Late Antique steppe nomads.

Variation in male reproductive success on Cayo Santiago: evidence for reproductive senescence in rhesus macaques

KRISTA M. MILICH^{1,2}, ANGELINA RUIZ-LAMBIDES³, ELIZABETH MALDONADO³ and DARIO MAESTRIPIERI²

¹Anthropology, Washington University in St. Louis, ²Institute for Mind and Biology, University of Chicago, ³Caribbean Primate Research Center, University of Puerto Rico

Sexual selection theory predicts that male primates are mainly limited in their reproductive potential by access to fertile females. Within nonhuman primate groups, alpha males can have better access to mates and are therefore expected to produce more offspring until they are no longer dominant, which usually corresponds with age. Little is known about male reproductive senescence independent of rank changes in primates, although a large body of literature on this topic exists for men. Here, we examine variation in the reproductive success of high-ranking

ABSTRACTS

male rhesus macaques on Cayo Santiago. We compare the number of offspring sired by high-ranking males using a generalized linear model. Male age ($F=7.79$; $p=0.0125$), group stability ($F=22.55$; $p=0.0002$), and the interaction of these two variables ($F=14.71$; $p=0.0013$) significantly accounted for the number of offspring produced that year. The low reproductive output for the older males was not a result of lower mating effort – older males consorted with females on many of the days they were observed. Both the number of days consorting ($F=19.96$; $p=0.0003$) and the interaction between the number of days consorting and the male's age ($F=9.01$; $p=0.0080$) were significantly associated with variation in the number of offspring sired. This interaction was such that the amount of time a male spent consorting with females impacted the number of offspring he produced until a certain age when the likelihood of producing an offspring became very low regardless of mating effort. Our results provide novel evidence of reproductive senescence in high-ranking male nonhuman primates.

CPRC supported by NIH grant 8 P40 OD012217 from the National Center for Research Resources and Office of Research Infrastructure Programs. Study partially funded by NIH grant R01-HD067175 to DM.

Disputing Patriarchy: A Bioarchaeological Analysis of the Power of Ancient Maya Women

KATHERINE A. MILLER WOLF

Department of Anthropology, University of West Florida

In archaeological reconstructions of the past, patriarchal models of social structure dominate discourse and can limit the interpretations of ancient women, drawn from skeletal remains, to their social roles in marriage or motherhood. A contextualized bioarchaeological analysis reconstructs the identities of women who wielded considerable power and gravitas extending beyond traditional gender roles. Skeletal, isotopic, and biodistance data are drawn from archaeological samples (including ~1200 individuals) recovered from large urban centers and isolated settlements throughout the Maya region during the Classic Period (400-900 AD) and serve to re-evaluate reified and somewhat stagnate models of patriarchal social structure for archaeological populations.

The results highlight the royal, ritual, and household mortuary contexts in which women are principal tomb occupants, where post-marital residence patterns deviate from a patrilocal pattern, and grave furniture mark women not as wives and mothers, but as queens, dynastic founders, shamans, and matriarchs, worthy of ritual, sacrifice, and mortuary monuments in their honor. Analysis of the contexts and skeletal remains of female burials demonstrate statistically

significant rates of migration (10-40%), various patterns of biological kinship and post-marital residence, and a milieu of ancient Maya women holding significant power and place in society.

Funding was provided by the National Science Foundation BCS-1207533, Arizona State University, Indiana University East, and the University of West Florida.

Patterns of extra-group paternity in gelada monkeys (*Theropithecus gelada*) at Guassa, Ethiopia: A comparison with other polygynous nonhuman primates

CARRIE M. MILLER¹, NOAH SNYDER-MACKLER², NGA NGUYEN^{3,4}, PETER J. FASHING^{3,4}, JENNY TUNG⁵, EMILY E. WROBLEWSKI⁶, MORGAN L. GUSTISON⁷ and MICHAEL L. WILSON^{1,8}

¹Department of Anthropology, University of Minnesota, ²Department of Psychology, University of Washington, ³Department of Anthropology and Environmental Studies Program, California State University, Fullerton, ⁴Center for Evolutionary & Ecological Synthesis, Department of Biosciences, University of Oslo, Oslo, Norway, ⁵Department of Evolutionary Anthropology, Duke University, ⁶Department of Anthropology, Washington University in St. Louis, ⁷Department of Integrative Biology, University of Texas, ⁸Department of Ecology, Evolution, and Behavior, University of Minnesota

Since the advent of DNA fingerprinting in the 1980s, studies have repeatedly revealed mismatches between the mating system inferred from social behavior and actual genetic relationships. Here we examine the occurrence of extra-group paternities (EGPs) in gelada monkeys (*Theropithecus gelada*) at Guassa, Ethiopia. Geladas aggregate in herds that contain a varying number of units. Each unit contains several females, a leader-male (thought to dominate breeding), and (sometimes) one or more follower-males. We found that leader-males do obtain a majority (80%; $n = 70/88$ offspring) of paternities (one-way ANOVA: $F = 34.68$, $P = 1.9e^{-6}$, $d.f. = 1$, $N = 34$ males). However, we also found that EGPs occurred in most units. EGPs occurred more often when offspring were: (a) the first successful conception for a mother; (b) conceived when three or more females were synchronously cycling at the time of conception; (c) conceived in the 90 days after a new leader-male had taken over a unit, during which time social relations often appeared unstable; (d) conceived in a one-male unit (i.e., no follower-males); and (e) conceived during the birthing season rather than the mating season. Compared to published data for other nonhuman primates, Guassa geladas had a relatively high rate of EGPs (Guassa: 19% EGPs), compared both to nonhuman primates

in general (median = 7% EGPs, range = 0–67%; $n = 48$ populations) and polygynous primates in particular (median = 13.5% EGPs, range = 0 – 65%, $n = 10$ populations).

This research was funded by the Leakey Foundation, the Wenner-Gren Foundation, and the University of Minnesota.

The paracingulate sulcus is present in the medial frontal cortex of great apes

ELAINE N. MILLER¹, CHET C. SHERWOOD¹ and WILLIAM D. HOPKINS²

¹Center for Advanced Study of Human Paleobiology, The George Washington University, ²Department of Comparative Medicine, University of Texas, MD Anderson Cancer Center

Since the divergence between great apes and hominins, the human brain has undergone gyralsulcal reorganization and significant expansion in areas including the frontal lobe. We investigated sulcal organization in the medial frontal cortex with a particular focus on the paracingulate sulcus (PCGS). The PCGS runs dorsal and parallel to the cingulate sulcus in an area associated with functions such as mentalizing and counterfactual thinking. Until recently, the presence of the PCGS was thought to be a structural feature that is unique to the human brain. However, upon closer examination, the PCGS has been observed in chimpanzee brains (*Pan troglodytes*). To better understand the evolutionary origins of sulcal anatomy in the medial frontal cortex, we examined high-resolution MRI scans for the presence or absence of the PCGS in orangutans (*Pongo pygmaeus*), gorillas (*Gorilla gorilla* and *Gorilla beringei*), and bonobos (*Pan paniscus*). We found that the PCGS is present in either the left hemisphere, the right hemisphere or both hemispheres in 56% (14/25) of orangutans, 34% (17/50) of gorillas, and 44% (8/18) of bonobos. These data suggest that the PCGS was present in the last common ancestor of all great apes and humans.

The Lewis N. Cotlow Fund

Dietary practices over the life-course: gender and food in two urban Eastern Zhou communities (ancient Zhengnan City, China)

MELANIE J. MILLER^{1,2}, YU DONG³, KATE PECHENKINA⁴, WENQUAN FAN⁵ and SIÂN HALCROW¹

¹Anatomy, University of Otago, New Zealand, ²Archaeological Research Facility, University of California, Berkeley, ³Institute of Cultural Heritage, Shandong University, ⁴Anthropology, Queens College, New York, ⁵Anthropology, Henan Provincial Institute of Cultural Relics and Archaeology

Dietary practices are deeply intertwined with biocultural factors and can reveal aspects of human behavior not found in other archaeological or historical sources. Stable isotope analysis

ABSTRACTS

of human tooth and bone samples allow bioarchaeologists to study human diet from discrete periods of life and can provide fine-grained dietary histories of individuals. Previous research on the Eastern Zhou Dynasty identified differences in dietary patterns between adult females and males, interpreted as the emergence of male-biased inequality during this time period. To fully understand the development of this pattern of sex-based dietary difference it is critical to investigate infant and child feeding practices, as dietary patterns may have begun in childhood, and nutritional differences can have consequential effects on health outcomes later in life. We studied two mortuary communities from the ancient Zhengnan city (Xinzheng, China) using a life-course approach: we sampled an early forming tooth from 23 individuals using incremental dentin sampling, which records breastfeeding, weaning and childhood diet, and also analysed a bone sample for carbon and nitrogen isotope data, which records adulthood diet over the final decade of life. We found that dietary differences between males and females began in childhood, with boys consuming greater amounts of millets than girls. However, all children also showed diets that contained more C_3 foods (wheat, soybeans) than their later adulthood diets, indicating important dietary changes over the lifetime. These patterns suggest that certain C_3 foods, such as wheat, may have been integrated into Eastern Zhou culture and cuisine as foods for children.

Funding was provided by: University of Otago Research Grant, the Royal Society New Zealand Marsden Fund (18-UOO-123), and the National Natural Science Foundation of China (41703003).

Exploring Sexual Dimorphism of Ancestral Cranial Nonmetric Traits in Modern European Americans

SAVANNAH R. MILLS and SEAN D. TALLMAN
Anatomy and Neurobiology, Boston University

The present study analyzes cranial nonmetric traits used in forensic ancestry assessment on contemporary skeletal remains of modern European Americans in order to determine if there are statistically significant differences between males and females in trait expression. Research on cranial nonmetric traits for ancestry estimation has largely ignored the effects of sexual dimorphism on trait expression; however, there is growing evidence that some traits may be impacted by sex, among other variables. The seventeen cranial nonmetric traits described in Hefner and Linde (2018) and the six mandibular morphoscopic traits described in Berg (2008) were scored on 97 females and 113 males from the Texas State University Donated Skeletal Collection in San Marcos, Texas. Chi-square tests were used to analyze if there are statistically significant cranial nonmetric trait expressions between males and females. From these tests,

the results indicate that 14 out of the 23 cranial and mandibular nonmetric traits are statistically significantly different between the sexes, with a p -value less than 0.05. Gonial angle flare is the most significant feature, while the zygomaticomaxillary suture is the least significant feature. Additionally, correspondence analyses show the relationship between each cranial nonmetric trait score, that demonstrated significance, and both sexes. Ultimately, this research demonstrates that several nonmetric traits used in ancestry estimation are affected by sex; thus, it may be beneficial to develop sex-specific ancestry models for nonmetric traits.

Funding for this project was provided by the Program in Forensic Anthropology at the Boston University School of Medicine.

Human bone health at Taumako, ca. 700 – 300 BP Southeast Solomon Islands

JUSTYNA J. MISZKIEWICZ¹, HALLIE R. BUCKLEY², NATHALIA R. DIAS GUIMARAES¹, MEG M. WALKER¹, LAWRENCE KIKO³ and REBECCA L. KINASTON²

¹School of Archaeology and Anthropology, Australian National University, ²Department of Anatomy, University of Otago, ³Archaeology Unit, The Solomon Islands National Museum

Previous genetic and bioarchaeological studies have revealed complex past human migration patterns and widespread metabolic disease in the remote regions of the Pacific. However, ancient human bone physiology through the life-course remains to be investigated in this part of the world. Here, we report the first reconstructions of human bone health in relation to age-at-death, sex, and lower limb skeletal function in a ca. 700 – 300 BP sample ($n = 69$) from Taumako, Solomon Islands.

Posterior femur cortical histology was examined for remodeling events in 34 young, 13 middle-aged, and 22 old adults, representing 42 females and 27 males. Intriguingly, bone vascularity (per $\sim 14 \text{ mm}^2$), determined from Haversian canal densities, was significantly ($p = 0.04$) higher in females (19.37) when compared to males (17.34). This pattern was consistent when adjusted by femoral robusticity ($p < 0.01$), and within the young sub-group only when corrected by femur midshaft circumference ($p = 0.022$). As expected, osteon population densities, indicating the amount of remodeled bone per 2.05 mm^2 , were significantly ($p = 0.014$) higher in young males (14.84) when compared to young females (11.57).

These results are somewhat at odds with traditional life-course paradigms in bone health. The young Taumako females may have achieved peak bone mass earlier than males, and maintained good bone health in later adulthood. As

this island is one of linguistically and genetically distinct "Polynesian outlier" cultures in the Pacific, hereditary aspects and male frailty at the site may contribute to our results.

Australian Research Council, Discovery Early Career Researcher Award (DE190100068)

Chewing through trauma: Normal and pathologic shape variation in cercopithecoid skulls

D. REX. MITCHELL¹, CLAIRE A. KIRCHHOFF², SIOBHÁN B. COOKE³ and CLAIRE E. TERHUNE¹

¹Department of Anthropology, University of Arkansas, ²Department of Biomedical Sciences, Marquette University, ³Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Pathologic signs arising from disease or injury are a ubiquitous feature of the vertebrate skeleton. The morphology of the adult primate craniofacial apparatus differs significantly among species and between sexes, yet studies examining skull morphology have largely excluded specimens exhibiting any sign of pathology. Potential associations between morphology and pathology have therefore received little attention. Here, we employ a geometric morphometrics approach combined with pathologic data for the dentition and temporomandibular joint (TMJ) to investigate relationships between pathology and craniomandibular morphology. We analyze cranial, mandibular, and TMJ shape across six species of cercopithecoid primates ($n=318$): *Cercopithecus mitis*, *Colobus polykomos*, *Macaca fascicularis*, *Nasalis larvatus*, *Papio anubis*, and *Theropithecus gelada*. Significant associations were identified between shape and a variety of dental and TMJ pathologies (e.g., pulp cavity exposure, antemortem tooth loss, TMJ osteoarthritis), but associations were not necessarily consistent across all taxa. Conditions such as osteoarthritis, pulp cavity exposure, and dental abscesses were frequently associated with larger temporalis muscles and molars situated more anteriorly. Pulp cavity exposure more often occurred alongside a deeper mandibular corpus and relatively higher condyle in *C. mitis*. Furthermore, these relationships weren't always consistent between sexes. Our results suggest that certain bone morphologies and muscle distributions may adversely influence intrinsic biomechanical movements, resulting in higher rates of compromised masticatory anatomy. Alternatively, compensatory mechanisms may alter development after the onset of certain conditions. The relationships identified here may be mediated by contrasting aspects of life-history, diet, and/or social organizations between taxa.

Funding has been provided by the National Science Foundation NSF BCS-1551722 (CAK) NSF BCS-1551669 (SBC) NSF BCS-15511766 (CET)

ABSTRACTS

Flowers born to blush unseen: The biological and cultural context of fetal and perinatal mortality in 18th-19th century South Shields, England

DELANEY MITCHELL and ELIZABETH CRAIG-ATKINS

Department of Archaeology, University of Sheffield

A group of 41 fetuses and perinates were interred between AD 1768-1818 just beyond the southern boundary of St Hilda's Church cemetery, South Shields, UK. This study undertook a holistic archaeological and anthropological examination of this burial group to illuminate the biological and cultural context of perinatal mortality in 18th-19th century England.

A Bayesian age-at-death distribution was generated based on a modern reference population of individuals who died in the perinatal period, creating accurate demographic data to produce an aging method based on long-bone development tailored to this archaeological population. Two peaks were identified – one at 27-29 weeks gestation which coincides with a peak in stillbirth and premature birth observed in modern populations, and another at 38-42 weeks, most likely caused by death during or soon after full-term birth. Limited disparity between skeletal and dental age suggests maternal diet was sufficient to buffer intrauterine growth from the effects of physiological stress; however, two individuals buried together, most likely twins, were both small for their dental age.

The funerary context revealed widespread use of coffins and containers, suggesting a deliberate effort to provide individualized and 'proper' burial to even the youngest members of society, countering any suggestion that their grouping outside the cemetery boundary was clandestine. This study demonstrates the value of the study of fetuses and infants as a physical manifestation of the complex health, religious, economic, and social factors that shaped growing Industrial towns.

Do we still evolve? The "shifting trade-off model" of biological evolution in response to medical and technological transitions

PHILIPP MITTEROECKER

Dept. of Theoretical Biology, University of Vienna

Throughout human history, cultural transitions repeatedly altered human lifestyle, the conditions of survival and reproduction as well as the modes of biocultural inheritance. Cultural changes thus have been important drivers of biological evolution in our species. With the advancement of agriculture, housing, medicine, and other technologies, natural selection has been continually reduced. It is thus tempting to assume that biological evolution in humans has reduced or even stopped as a result of reduced natural selection. I will show

that this is not true: by shifting existing fitness trade-offs, reduced selection pressures have even triggered new evolutionary changes. Many anatomical, physiological, and behavioral traits have evolved by trading off fitness for different functions, life stages, or environmental conditions. The resulting "evolutionary compromises" optimize average fitness in a population and may also entail individuals that appear to be maladapted for one or more of the involved functions. Relaxation of one of the opposed selective forces, e.g. by technological or medical advancements, disrupts the evolved equilibrium and induces a novel evolutionary trend. I will outline this theory and illustrate it with examples from childbirth and immune function. Extending the model to trade-offs between ecological and sexual selection, I will use global demographic and biometric data to demonstrate how relaxed ecological selection throughout the last centuries has affected the pattern of sexual dimorphism in human body height. Finally, I will briefly discuss ethical and political challenges involved in this research.

Supported by the Austrian Science Fund (FWF) grant P29397.

Inter-cuspal fluctuating asymmetry of deciduous second molars is not different than their permanent homologues in contemporary New Mexicans

EMILY MOES and HEATHER JH. EDGAR

Department of Anthropology, University of New Mexico

Variation in fluctuating asymmetry (FA) between dental homologues in the same individual is attributed to differences in developmental timing. Previous research on traditional dental FA metrics predicts that FA in the first permanent molar (M1) will be greater than in the deciduous second molar (dm2) because M1 may be more affected by environmental stressors, since they develop after birth. The dm2 begins development at approximately 30 weeks *in utero*, and its homologue, the M1, begins development at 4.5 months. This project examines FA, as a measure of developmental instability, in inter-cuspal distances of dm2 and M1. Inter-cuspal FA has not been previously reported in research on dental FA. Inter-cuspal FA is a novel method by which we can examine developmental instability within a specific age. The sample consists of dental casts of 76 contemporary New Mexican children (males: n=33; females: n=43) with bilateral maxillary and mandibular dm2 and M1. FA was calculated using 15 metrics of inter-cusp distances, including those used to map the occlusal polygon. Results indicate no difference between FA in dm2 and M1 (average FA (mm): dm2=1.02; M1=0.98; p=0.49). Therefore, children in this sample likely experienced similar amounts of developmental instability within the last month of fetal development as in the latter half of their first year. This would indicate that

dm2 may not be as developmentally stable as previously thought. Alternatively, it is possible that individuals experienced greater stress during development of dm2, resulting in FA similar to M1.

The ontogeny of pelvic sexual dimorphism in *Macaca mulatta*

ELIZABETH A. MOFFETT

Biomedical Sciences, Rocky Vista University

It is currently unknown whether the demands of parturition in skeletally immature females influence modeling of the bony pelvis. It is likely that hormones involved in birth and parturition may influence adult pelvic form in females, especially among females who give birth prior to reaching skeletal maturity. The current study explores the effects of age and parity on pelvic form in *Macaca mulatta*. In this species, the mean age at first birth for females is 5.6 years, with the median age being 5. However, skeletal maturity is reached modally at age 6. 3-D pelvic landmarks were collected on male and female pelvis (n=153) from Cayo Santiago – parity and age at death was known for all individuals. Principal Components Analysis was performed on coordinates. Pelvic shape was statistically significantly different between adolescent and adult females, while this was not true of the males. Among females, pelvic shape is significantly correlated with age but not number of offspring. Results indicate that significant bone remodeling occurs in females during late adolescence, during which many females of this species give birth, while this is not the case in males. It is likely that hormones such as estrogen and progesterone in late adolescence influence final pelvic form among female *M. mulatta*.

This research was funded by the Wenner-Gren Foundation and Louis B. Leakey Foundation.

The relationship between tree-fall canopy gaps, tree phenology, diet, and lemur behavior in Masoala National Park, Madagascar

MONICA MOGLEWSKY^{1,2}, NATALIE VASEY^{1,2,3}, ANTONIN ANDRIAMAHAIHAVANA⁴ and ZAFIMAHERY RAKOTOMALALA⁴

¹Earth, Environment & Society, Portland State University, ²Environmental Science & Management, Portland State University, ³Department of Anthropology, Portland State University, ⁴Department of Animal Biology, University of Antananarivo

In Madagascar, researchers have documented extensive spatial, seasonal, and annual variability in fruit availability. Tree-fall canopy gaps, hereafter called gaps, are numerous within Madagascar's evergreen tropical rainforests and may contribute to this variability by increasing productivity of trees near their edges. In this study we aimed to address the potential of gaps to serve as food-dense feeding sites for two frugivorous lemur,

ABSTRACTS

Eulemur albifrons and *Varecia rubra*. We collected data from September 2017 through February 2018 at Andranobe Forest, Masoala National Park, Madagascar. We recorded phenology for 303 transect trees bi-weekly. We also recorded phenology of 1448 trees visited by either lemur species during focal animal sampling conducted during daylight hours. For all trees, we recorded the distance to the nearest gap, gap area, tree diameter at breast height (DBH), tree height, and local vernacular name. We fitted general linear mixed-effects models, one each for percent young tree leaves and percent tree fruit as dependent variables. As fixed effects, we included tree type (transect, visited by *E. albifrons*, visited by *V. rubra*), tree DBH, and distance to the nearest gap as fixed effects. Our results indicate that gaps contribute a small but significant amount to the overall variation in the abundance of young leaves and fruit available for *E. albifrons* and *V. rubra*. Given the relationship between gaps and food availability, conservation management plans that account for fluctuations in food availability caused by disturbances have a greater probability of succeeding in saving critically endangered species.

Re-evaluation of the phylogenetic relationships of *Australopithecus sediba*

CARRIE S. MONGLE¹, DAVID S. STRAIT² and FREDERICK E. GRINE³

¹Division of Anthropology, American Museum of Natural History, ²Department of Anthropology, Washington University in St. Louis, ³Departments of Anthropology and Anatomical Sciences, Stony Brook University

It has been suggested that *Australopithecus sediba* may be an ancestor of *Homo* because it possesses a mosaic of derived *Homo*-like and primitive australopithecine-like traits. However, an alternative hypothesis proposes that the majority of the purported *Homo*-like craniodental characters can be attributed to the juvenile status of the type specimen, MH1. Here, we conduct an independent character assessment of the craniodental morphology of *Au. sediba*. Morphological characters that have been questioned on the basis of ontogeny were treated as missing data for *Au. sediba*. Existing character data were analyzed using both standard parsimony and Bayesian techniques. In addition, we conducted a series of Bayesian analyses constrained to only produce trees that include *Au. africanus* and *Au. sediba* as sister taxa. By comparing the most credible tree obtained by the constrained analysis to those produced by the unconstrained analyses, we directly evaluated the hypothesis of a sister relationship between *Au. africanus* and *Au. sediba*. Parsimony analyses recover *Au. sediba* as the sister taxon to the clade containing *Homo* + *Kenyanthropus*, while the Bayesian analyses place *Au. sediba* in a polytomy with *Kenyanthropus* at the base of *Homo* + *Paranthropus*. However,

comparisons between the constrained and unconstrained trees were inconclusive and did not strongly favor the placement of *Au. sediba* in a clade with *Homo* as opposed to the hypothesized sister relationship with *Au. africanus*. This suggests that additional data, such as postcranial characters and new fossils preserving adult craniodental morphology, are required to resolve the phylogenetic relationships of *Au. sediba*.

This research was supported by a grant by the Wenner-Gren Foundation for Anthropological Research (Gr. 9120).

Body-society interactions during childhood in post-medieval Leeds, England: Metabolic disease, lead exposure and allostatics

PAULA A. MONGUI¹, JANET MONTGOMERY¹, JULIA BEAUMONT², ANWEN C. CAFFELL^{1,3}, REBECCA L. GOWLAND¹ and CHRIS J. OTTLEY⁴

¹Archaeology, Durham University, ²School of Archaeological Sciences, University of Bradford, ³Osteoarchaeology, York Osteoarchaeology, ⁴Earth Sciences, Durham University

Metabolic disease in bioarchaeology has been associated with poor diet and living conditions, but lead (Pb) poisoning can also act as a primary or contributing factor. This relationship was explored using the allostasis framework in a post-medieval population (Victoria Gate, Leeds, England), where documentary evidence suggested an already high allostatic load due to precarious living conditions. The skeletal remains of 14 individuals (8 non-adults, 6 adults) were analysed macroscopically using established criteria to evaluate metabolic disease. Teeth from 10 individuals were sampled for Pb trace element analysis using ICP-MS. Four non-adults were identified with scurvy, 5 with active rickets, and 3 with metabolic disease comorbidity. Five adults had residual rickets. Pb mean concentration was 15.5 mg/Kg, and Pb exposure was consistent during childhood. No correlation between level of Pb exposure and age-at-death, or presence/severity of disease was found. The results suggest a variety of social and environmental factors influenced health, further supported by the wider variation in Pb concentration in adults with residual rickets. Pb concentration was below average for post-medieval England, but correlation with Pb blood values indicates serious physiological disruptions to normal bodily functions. Pb exposure contributed to allostatic overload, but it was not the main factor of disease burden. It is likely disease and pollution had inter-generational consequences, which were then further compounded by the dire living conditions. Thus, the altered homeostasis would have been easily disrupted. The main limitations of this study are the small sample size and lack of comparative studies.

Janet Montgomery, Durham University

Human enamel-dentine junction morphology evolves neutrally and tracks population history

TESLA A. MONSON

Anthropology, Western Washington University

Teeth have been studied for more than a century and are still providing insights relevant to human evolution. The morphology of the enamel-dentine junction (EDJ) captures important aspects of tooth development and is incredibly informative, because it is not subject to the same extent of wear as the outer enamel surface and thus preserves more morphology in worn specimens, particularly fossils. The EDJ has been well-studied in hominids but has yet to be comprehensively explored in modern humans. This study used μ -CT biomedical imaging to assess EDJ morphological variation in a sample of late Holocene modern humans (N=161) from archaeological populations spanning all continents except Antarctica. Global variation in human EDJ morphology was compared to the statistical expectations of neutral evolution and 'Out of Africa' modeling of trait evolution, focusing on left mandibular first molars. Significant correlations between phenetic variation and neutral genetic variation indicate that EDJ morphology has evolved neutrally in humans. There are significant differences in EDJ morphology across human populations, particularly in positioning of the hypoconid, and EDJ morphology reflects population history. Global distribution of EDJ morphology does not reflect the expectations of the 'Out of Africa' model, emphasizing that multiple factors may contribute to EDJ variation including geographic dispersal and body size. This study dramatically increases our knowledge of human dental variation and contributes to our understanding of dental development more broadly with important applications to studies of population history, population movement, and social structure in archaeological human populations.

This work was funded by the Swiss National Science Foundation, SNF Grant #CR3213_166053

The Genetics of Malaria Resistance in Ancient Rome

HANNAH MOOTS¹, DAVID PICKEL², ALESSANDRA SPERDUTI^{3,4}, MARGARET L. ANTONIO⁵, ZIYUE GAO^{6,7}, ALESSIA NAVA^{3,8}, PERE GELABERT⁹, MICHAELA LUCCI⁹, FRANCESCA CANDILIO^{10,11}, SUSANNA SAWYER⁹, VICTORIA OBERREITER⁹, MAURO RUBINI^{12,13}, LUCA BONDIOLI¹³, ALFREDO COPPA⁹, RON PINHASI⁹ and JONATHAN PRITCHARD^{14,6,7}

¹Anthropology, Stanford University, ²Classics, Stanford University, ³Servizio di Bioarcheologia, Museo delle Civiltà, ⁴Anthropology, Università L'Orientale Napoli, ⁵Biomedical Informatics, Stanford University, ⁶Howard Hughes Medical Institute, Stanford University, ⁷Genetics, Stanford University, ⁸DANTE Laboratory for the study of Diet

ABSTRACTS

and Ancient Technology, Sapienza Università di Roma, ⁹Department of Evolutionary Anthropology, University of Vienna, ¹⁰Dipartimento di Biologia Ambientale, Sapienza Università di Roma, ¹¹School of Archaeology, University College Dublin, ¹²Dipartimento di Archeologia, Università di Foggia, ¹³SABAP-LAZ, Ministero dei Beni e delle Attività Culturali, Rome, ¹⁴Biology, Stanford University

Malaria is known to have afflicted the Romans since at least the 2nd century CE, and possibly centuries earlier. Recent paleo-biomolecular evidence and numerous ancient literary sources confirm the malaria pathogen's ancient presence and hint at the disease's devastation. Given this growing body of knowledge, archaeologists and ancient historians increasingly are taking the disease into consideration when studying ancient Rome. Yet much remains unknown about the disease's changing prevalence over time and its impact on the population. Research on modern populations has made clear that malaria has been a major selective force in human history, shaping human genomes and resulting in high frequencies of malaria resistant alleles in regions where the disease has long been endemic. Information on the frequency of these alleles in the past would complement existing lines of evidence regarding malaria's historical impact in Italy, a history that spans two millennia, up until the disease's ultimate elimination there in the 20th century.

In this study, we examine the frequencies of known malaria resistance alleles using time-series data from Rome and central Italy, which includes 127 individuals and spans the last 12,000 years. We take a closer look at the timing and context of these allele frequency changes, exploring how selection, migration, or both might be driving these allele frequency changes. We also examine the changing disease ecology of ancient Rome and how this may have played a role in the trends observed.

The population genetics of within-host *Mycobacterium tuberculosis*

ANA Y. MORALES-ARCE, REBECCA B. HARRIS, ANNE C. STONE and JEFFREY D. JENSEN
Center for Evolution and Medicine, Arizona State University

The within-host evolutionary dynamics in *Mycobacterium tuberculosis* (TB) populations, and consequent development of resistance to antibiotics, remain unclear. This partly owes to the fact that the underlying biological characteristics of TB (e.g., clonality, compact genomes, and a lack of recombination) render standard population genetic approaches based on Wright-Fisher (WF) assumptions largely inappropriate. Regardless, it is empirically observed that drug-resistance rapidly and independently evolves across the globe. This rapid adaptation, in spite of lacking variation, represents something of a paradox to date. Utilizing an approximate Bayesian (ABC)

approach based upon within-host site frequency information, we demonstrate an ability to disentangle the relative contributions of these evolutionary processes. Our preliminary analyses suggest that a mutation rate on the order of $\sim 1e-8$ / site / replication, along with significant progeny skew owing to clonality as well as widespread purifying selection, well explain observed polymorphism and divergence in this important human pathogen. This inference is currently being applied to patient samples from the state of Alaska where TB incidence was highest in the US in 2018. We propose that a consideration of these evolutionary processes will be informative for future epidemiological studies and treatment strategies.

Locomotor vs. non-locomotor signals in bony labyrinth: insights from fossil and modern anthropoid primates

NAOKI MORIMOTO¹, YUTAKA KUNIMATSU², MASATO NAKATSUKASA¹, MARCIA S. PONCE DE LEÓN³, CHRISTOPH P. E. ZOLLIKOFER³, HIDEMI ISHIDA¹, TOMOHIKO SASAKI⁴ and GEN SUWA⁵

¹Laboratory of Physical Anthropology, Kyoto University, ²Faculty of Business Administration, Ryukoku University, ³Anthropological Institute and Museum, University of Zurich, ⁴The Kyoto University Museum, Kyoto University, ⁵University Museum, University of Tokyo

The bony labyrinth of the inner ear is relatively well preserved in extant and fossil primates. The bony labyrinthine morphology has been thought to contain relevant information about locomotor modes. Its morphology is complete already at birth, and it remains almost unchanged during postnatal period. The bony labyrinth thus has special relevance when tracking phenotypic evolution. Here we track the evolution of the bony labyrinth of anthropoid primates during Mio-Pliocene, which is the time period that gave rise to the extant great apes and humans. We use methods of landmark-based geometric morphometrics to analyze labyrinthine morphology in a wide range of extant and fossil anthropoids (a total of $N = 133$ specimens from 7 fossil and 62 extant primate taxa), including New World and Old World monkeys, apes, and humans; fossil taxa are represented by *Aegyptopithecus*, *Epiplioptithecus*, *Nacholapithecus*, *Oreopithecus*, *Ardipithecus*, *Australopithecus*, and *Homo*. The results show that the morphology of the anthropoid bony labyrinth conveys a statistically significant phylogenetic signal and is constrained by body size allometry rather than locomotor adaptations. Although labyrinthine variation is often interpreted in terms of locomotor adaptation, our results suggest that alternative explanations need to be explored, such as craniofacial developmental constraints.

Higher ventilatory response to hypoxia associates with higher oxygen saturation and lower hemoglobin concentration among ethnically Tibetan women residing above 3500m in Nepal

ESTEBAN A. MOYA¹, JAMES J. YU¹, SIENNA R. CRAIG², CHRISTINA A. BUCHANAN³, FRANK L. POWELL¹, TATUM S. SIMONSON¹ and CYNTHIA M. BEALL⁴

¹Section of Physiology, Division of Pulmonary, Critical Care, and Sleep Medicine, Dept. of Medicine, University of California San Diego, ²Department of Anthropology, Dartmouth College, ³Recreation, Exercise & Sports Science Department, Western State Colorado University, ⁴Department of Anthropology, Case Western Reserve University

Populations living at high altitudes show a variety of adaptations to low oxygen (O_2). Compared to Andean highlanders, Tibetans show a higher hypoxic ventilatory response (HVR) and lower hemoglobin concentration ([Hb]). We aimed to test the hypothesis that HVR values correlate positively with arterial O_2 saturation (SpO_2) and negatively with [Hb] measured noninvasively (Masimo Pronto-7, San Diego, CA) in 370 ethnically Tibetan women, lifelong residents above 3000m, in Upper Mustang, Nepal with an average age of 60 ± 9.3 (SD) years. We measured ventilation (V_t) 5 minutes after a decrease in inspired O_2 , which lowered SpO_2 from an average of $91 + 4.2$ to one of $78 + 5.0\%$ (SD) to calculate HVR ($HVR = -\delta V_t / \delta SpO_2$). HVR averaged $0.20 + 0.15$ (SD) (L/min/%) and correlated directly with SpO_2 ($r = 0.392$; $p < 0.0001$) and negatively with [Hb] ($r = -0.106$, $p < 0.041$) and age ($r = -0.282$; $p < 0.0001$). The average HVR we measured is lower than that reported for Andean Aymara women with an average age of 40 years (0.32 L/min/%), and Tibetan women with an average age of 38 years (0.70 L/min/%), all residing at 3,800 – 4,065m (Beall et al., 1997). These differences may arise from the effect of age on HVR, since the women in the present study were 20-22 years older; differences in experimental protocols and altitudes may contribute also. These findings demonstrate we have more to learn about sources of variation within and among indigenous high-altitude populations.

Supported by NSF award 1831530 to CMB and NIH 1R01HL145470 to TSS.

Indigenous American and African Interaction in Puerto Rico, A Comparative Analysis

ELSA M. MUELLER¹, LIJUAN CHEN¹ and JADA BENN TORRES^{1,2}

¹Department of Anthropology, Vanderbilt University, ²Vanderbilt Genetics Institute, Vanderbilt University

The high amounts of Indigenous American ancestry found among the Puerto Rican general populace has instigated a debate on the interactions and supposed extinction of native

ABSTRACTS

populations within the Caribbean. Although some historical narratives detail the interactions between European settlers and Indigenous peoples, much less is known about the interactions between Indigenous and African-descended peoples, specifically the extent of Indigenous and African admixture in Puerto Rico. To this end, we used whole mitochondrial sequences in order to examine the potential for Indigenous American and African interaction and to illuminate more about the histories of both Indigenous and African peoples in the wake of European colonization of the Americas.

Building on previous work, we expanded our sample from 31 to 53 Afro-Puerto Ricans. Based on sequence data we found that 14 were identified as possessing an Indigenous American haplogroup with a distribution as follows: A2=57%, B2=21%, C1=14%, D1=7%. We performed a series of Fischer-Friedman analyses that showed significant differences in Indigenous haplogroup distribution when compared to sampled populations in Cuba and the Dominican Republic ($p < .05$), with a similar distribution to that of sampled populations of Venezuela and Mexico. The distribution of Indigenous American haplogroups within Afro-Puerto Ricans relative to subsets of larger populations with Indigenous ancestry suggests that Afro-Puerto Ricans have comparable haplogroup distributions to that seen in other groups regardless of identification as African-descendants. Further research is recommended to examine the extent of the interaction between Indigenous populations and specific Afro-descended groups throughout the Americas.

The research was supported by a grant from the Office of Equity, Diversity, and Inclusion at Vanderbilt University.

Correlations between structural properties of cortical and trabecular bone in the human limbs

BRAM MULDER¹, JAY T. STOCK^{1,2,3}, JAAP P.P. SAERS¹, SARAH A. INSKIP¹, CRAIG CESSFORD¹ and JOHN E. ROBB¹

¹Department of Archaeology, McDonald Institute for Archaeological Research, University of Cambridge, ²Department of Anthropology, University of Western Ontario, ³Department of Archaeology, Max Planck Institute for the Science of Human History

Cortical and trabecular bone adapt to mechanical loading, and their structural properties are frequently employed in the interpretation of past behavior. To analyze tissue differences in functional adaptation, cortical and trabecular bone were analyzed in a sample that was composed of adults from a medieval friary, hospital, and parish. From each individual, one tibia and femur ($n = 108$), and both humeri ($n = 115$) were scanned using micro-computed tomography. Trabecular

architecture was evaluated in each epiphysis, while diaphyseal geometry was analyzed at femoral and tibial midshafts, and 35% of the humerus.

Cortical area and bone volume fraction correlated strongly and consistently, explaining 25%-40% of the variation, while total subperiosteal area was poorly related to trabecular architecture. Anisotropy frequently correlated with cortical parameters in females, but not in males, and this varied with anatomical location. Correlations between trabecular architecture and torsional rigidity were only moderate in males and insignificant in females.

The contrast between good correlations in measures of bone content and poor correlations in its spatial distribution, suggest that cortical and trabecular bone may in part be modelled by similar processes, while local loading and tissue differences cause divergences in structural quality. This indicates that diaphyseal geometry and trabecular architecture are unlikely to reflect behavior similarly. Moreover, sexual dimorphism differs substantially between the tissues, and is dependent on anatomical location, which complicates a straightforward interpretation of sex differences in past populations. Such comparative analyses are needed to unravel how the tissues may complement each other in interpreting past behavior.

As part of the After the Plague project, this work received funding from the Wellcome Trust.

Modeling human evolution with brain organoids carrying ancestral genetic variations

ALYSSON R. MUOTRI

Pediatrics/Cellular & Molecular Medicine, UC San Diego

The evolutionarily conserved splicing regulator *NOVA1* plays a key role in neural development and function. *NOVA1* also includes one of the few fixed protein-coding differences between modern human and archaic hominin genomes. In the RNA binding domain of *NOVA1*, modern humans carry a specific nucleotide substitution. To investigate the functional significance of this amino acid change in humans, we re-introduced the archaic allele into human pluripotent cells and followed their development through cortical organoids. Reintroducing the archaic *NOVA1* in a human genetic background induced molecular and cellular alterations in cortical organoids. Levels of synaptic markers and synaptic protein co-associations correlated with altered electrophysiological properties in organoids expressing the archaic version. Our results suggest that the human-specific substitution in *NOVA1* may have had functional consequences for our species' evolution.

PalaeoChip: An eDNA targeted enrichment approach for reconstructing human palaeoecosystems

TYLER J. MURCHIE¹, MELANIE KUCH¹, ANA DUGGAN¹, MARISSA LEDGER², KEVIN ROCHE³, JENNIFER KLUNK⁴, EMIL KARPINSKI⁴, DIRK HACKENBERGER⁵, TARA SADOWAY⁶, ROSS MACPHEE⁷, DUANE FROESE⁸ and HENDRIK POINAR^{1,5}

¹Anthropology, McMaster University, ²Archaeology, University of Cambridge, ³Archaeology, University of Bourgogne Franche-Comté, ⁴Biology, McMaster University, ⁵Biochemistry, McMaster University, ⁶Toronto, University Health Network, ⁷Division of Vertebrate Zoology/Mammalogy, American Museum of Natural History, ⁸Earth and Atmospheric Sciences, University of Alberta

Two major limitations in palaeoenvironmental metagenomics are DNA loss during extraction and the carryover of enzymatic inhibitors. PCR metabarcoding can overcome some degree of inhibition, but this technique can be vulnerable to differential amplification rates and a subsequent bias in taxonomic profiles, especially if there was substantial DNA loss with overly thorough inhibitor removal treatments. Alternatively, sedimentary ancient DNA extracted with techniques designed to maximize ancient DNA recovery are prone to the carryover of enzymatic inhibitors, which can result in failed PCR amplifications or failed adapter ligation during library preparation, impeding shotgun and targeted enrichment strategies.

Here, we report on a new sedimentary ancient DNA extraction protocol paired with targeted enrichment for reconstructing past environments. Our approach averages a 14.6-fold increase in on-target plant and animal DNA compared to a commercial soil extraction kit, and a 22.6-fold increase compared to a PCR metabarcoding approach. To illustrate the effectiveness of our PalaeoChip protocol, we present results of plant and animal presence from permafrost samples and the new potential evidence for the late survival (ca. 9685 BP) of mammoth (*Mammuthus* sp.) and horse (*Equus* sp.) in the Klondike Region of Yukon, Canada. Our approach translates to a more diverse and sensitive dataset with increased sequencing efficiency of human ecologically informative sedaDNA.

Extending our understanding of human long bone mechanobiology through life history theory

ALISON A. MURRAY¹, JONATHAN CK. WELLS² and JAY T. STOCK^{3,4}

¹Department of Anthropology, University of Victoria, ²Institute of Child Health, University College London, ³Department of Anthropology, Western University, ⁴Department of Anthropology, Max Planck Institute for the Science of Human History

ABSTRACTS

Mechanical properties of the human skeleton are often used to interpret variation in habitual loading in the past. An essential component of the interpretation of biomechanical properties is the standardization of data to body size, to remove the influence of allometric scaling on mechanical interpretations of the data. Body size, however, is more than a confounding factor in our interpretation of bone mechanical properties, it is also a measure of energetic investment that reflects fundamental variation in life-history strategies. Variation in human body size is known to correspond with population differences in maturational rates, age at maturity, and mortality. Differences in body composition are also important. In this paper we investigate these relationships among a group of pre-menopausal women, aged 19-40, of varying physical activity levels and phenotypes. The results demonstrate that long bone cross-sectional geometry is influenced by variation not just in ground impact loading, but also by functionally-related muscle mass and its ability to generate force, rather than by the direct loading imposed by body mass. The fat mass component of body mass has little impact on limb bone CSG properties, indicating the importance of body composition rather than simply total mass. Overall body size is heavily influenced by life history strategy, and thus reflects energetic investment in skeletal growth, and this information is indirectly reflected in raw CSG property variation. We therefore predict that significant differences in bone mechanical properties will occur both with shifts in habitual activity, but also relative to changes in life history strategy.

This study was funded by the European Research Council under ERC Grant Agreement n.617627 (to JTS).

Fossils in the Museum. Non-formal classes for school children and students about fossils and their stories

SARAH MUSALIZI, CHRISTOPHER SSEBUYUNGO, MICHEAL TATYABALA and VICENT NGABIRANO
Museums and Monuments, National Museum of Uganda

Uganda is among the East African sources of human and environmental histories over time. A spectrum of fossils recovered and published recent ones; the 20 million-year-old Napak Monkey and *Ugandapithecus*, among others. It is widely known that for a long period of time fossilization processes have endowed Uganda with oil resources comprising between 1.2 and 1.7 billion barrels of oil. Over 10 billion USD investment is anticipated to last between 50 and 70 years in phases of exploration, field development, production and field abandonment and thus employment. This is among stories stressed to the school children and students during the study of fossils in the Museum. A lot of field work has been carried out in the Albertine Rift, Northeastern Uganda (Karamoja Region) and some parts of Eastern

Uganda around Mt. Elgon which have yielded thousands of fossils. These fossils are communicated to the public through exhibitions, guided tours and scientific publications. Here, we present the methodology used to diffuse the evolution story at the National Museum of Uganda, Kampala. Focus study sessions for school children and students where informal theoretical and practical sessions are done to extend the knowledge about evolution. Students have an oral introduction and then split for self-discoveries in the displays and later gather to discuss their finds. Demonstrational activities where a field environment (especially for 5-15 year olds) is created and they are given space and tools to search for fossils, and suggestions about documenting and communicating them to audiences at their schools where exhibitions are organized.

Balancing Research, Education, Conservation and Sustainable Use of the 3.6 Million Years Old Hominin Footprint Site G and S at Laetoli in northern Tanzania

CHARLES M. MUSIBA¹, MECKSADECK M. MWAMBUNGU², JOSHUA MWANKUNDA², ANATOLY N. ZAITSEV³, ANTON I. SAVCHENOK³, AUDAX Z. MABULLA⁴, CASSIAN C. MAGORI⁵, KERSTEN BERGSTROM⁶, ALEX PELISSERO⁷ and SEWASEW ASSEFA⁸

¹Department of Anthropology, University of Colorado Denver, USA, ²Department of Cultural Heritage, Ngorongoro Conservation Area Authority, Tanzania, ³Department of Mineralogy, St. Petersburg State University, Russia, ⁴National Museums of Tanzania, Ministry of Natural Resources and Tourism, ⁵Department of Anatomy, Saint Francis University College of Health and Allied Sciences, ⁶Department of Anthropology, Texas A&M University, USA, ⁷Department of Anthropology, Colorado State University, USA, ⁸Department of Anthropology, University of Wisconsin - Madison, USA

Designated archaeological World Heritage Sites (AWHS) play a major role in shaping the socio-economic, stewardship, conservation and their sustainable use in many countries. Many African countries now recognize that apart from constructing national and socio-cultural identities, archaeological World Heritage Sites can propel the socioeconomic growth for communities surround them. If properly managed, AWHS have the capacity of becoming centers of excellence and sustainable tourism. For many years, management of archaeological heritage sites and the designation of some of the AWHS in Africa were completely based on European colonial models; focusing on research and conservation and completely neglecting the communities surrounding them. Laetoli, a World Heritage Site serves as a best example where not only local communities, but also local experts in the past were totally ignored when the 1995-96

conservation efforts to rescue the hominin footprints at Site G were implemented. As a result the conservation efforts produced unintended consequences that have led to a complete deterioration of the G-prints. Here we present the current state of preservation of the Laetoli hominin G prints based on the 2011, 2014, and 2016 re-excavation and physical (including geochemical) observations of the footprints tuff 7 at the northern- and southern ends of the G trail where tuff discoloration and sediment dissolution has decreased the scientific value of the prints. Furthermore, we will also discuss some conservation efforts being carried out by the Ngorongoro Conservation Area Authority to develop Laetoli World Heritage Site as a research, educational, cultural and tourism center accessible to all.

Funding for the 2011, 2014 and 2016 re-excavation was provided by the Ngorongoro Conservation Area Authority (NCA), the University of Colorado Denver (ORS and the CLAS-CRISP Grants).

Faunal abundances in Area 13 from the Upper Burgi Member of East Turkana

LEAH K. MYERHOLTZ¹, ASHLEY S. HAMMOND^{2,3}, CHRISTOPHER SMITH^{3,4,5} and SHARON KUO⁶

¹Department of Anthropology, Ohio University, ²Division of Anthropology, American Museum of Natural History, ³Division of Anthropology, New York Consortium in Evolutionary Primatology (NYCEP), ⁴The Graduate Center, City University of New York, ⁵Center for Anatomy and Functional Morphology, Icahn School of Medicine at Mount Sinai, ⁶Department of Anthropology, Penn State University

Reconstructing the paleoenvironment of East Turkana is crucial for understanding the evolution of fossil taxa. However, the East Turkana environment likely varied substantially among different subregions in the Upper Burgi Member (UB; 2.62-1.87 Mya) due to the positioning of the main water sources. The UB paleoenvironment in Area 13, located within the Ileret subregion, is especially interesting given the number of *Homo* fossils recovered there but remains poorly understood. Here we assess whether faunal abundance in Area 13 differs from other contemporaneous Upper Burgi communities within East Turkana.

During the 2017-2019 seasons of the Koobi Fora Field School, taxonomically identifiable fossils were collected from Area 13 and compared with UB faunal counts in the East Turkana Database from the following collection areas: Koobi Fora (KF), Ileret (IL), and Karari (KR). A Fisher's Exact test was used to determine whether Area 13 was unique compared to surrounding and nearby subregions. Overlapping cases between Ileret and Area 13 in the East Turkana Database were removed from the Ileret counts. The bone walk data from Area 13 did not differ significantly from the KF subregion ($p=0.33$) nor the KR subregion ($p=0.07$), but did differ significantly

ABSTRACTS

from the IL subregion ($p < 0.05$), largely due to the large numbers of fish and reptiles in Area 13, suggesting proximity to a water source for that specific area. Future work should consider variation within Each Turkana subregions and how paleontological collection methods may bias the available data to a primarily mammalian terrestrial ecosystem.

This research was supported by the National Science Foundation (IRES-OISE 1358178) and would not be possible without the support of the National Museums of Kenya.

A lorisoid-like distal humerus from the middle Miocene at Napudet, Kenya

LYDIA C. MYERS¹, GABRIELLE A. RUSSO¹ and ISAIAH O. NENGO²

¹Anthropology, Stony Brook University, ²Turkana Basin Institute, Stony Brook University

Napudet is a middle Miocene (13 Ma) site in the Turkana Basin, Kenya, best known for yielding ape fossils. Here, we describe a lorisoid-like distal humerus from Napudet, which potentially represents the first small-bodied primate from the site. We evaluated the taxonomic and functional affinities of the distal humerus in a comparative sample including extant lorisoids, other small-bodied mammals, and Miocene galagids. Extant taxa were allocated to locomotor groups (i.e., vertical clingers and leapers (VCL), volant (flying and gliding), terrestrial and arboreal quadrupeds, and slow climbers). Humeral measurements were collected in order to calculate morphological indices with established functional relevance. The distal humerus exhibits general primate features, including a prominent medial epicondyle, and some galago-like features, such as a wide zona conoidea and a shallow olecranon fossa. In basic morphology the distal humerus resembles Miocene galagid distal humeri, though it is larger than distal humeri from many extant and extinct galagids, and more similarly-sized to extant lorisoids like *Perodicticus*. Preliminary quantitative results are mixed, with some values for the distal humerus falling within the VCL group to the exclusion of other locomotor groups, while other values overlap ranges of multiple locomotor groups. Without additional (especially craniodental) remains, taxonomic assignment is not possible at this time. Regardless, this fossil is important in characterizing primate diversity at Napudet in the middle Miocene, suggesting that along with larger-bodied apes, there was at least one lorisoid-like primate.

Funding sources: National Geographic Society, The Leakey Foundation, National Science Foundation, Turkana Basin Institute, and Stony Brook University (OVPR, and Department of Anthropology Undergraduate Research and Travel Award).

Differences in how women walk while carrying infant-sized loads

MARCELLA J. MYERS¹, LANA PROKOP², MACKENZIE ESS¹, TAYLOR GENTZ¹ and LAKEN MULLER¹

¹Biology, St Catherine University, ²Nutrition and Exercise Science, St Catherine University

Understanding the locomotory consequences of child carrying is necessary to make informed predictions about dyad and group movement patterns in first humans as well as contemporary human populations. Although the influence of child size has been studied, the effect on walking kinematics depending upon carrying position and method is not well-researched. To address this gap, we designed a study to determine within-person differences in self-selected walking speed and gait kinematics for reproductive age women (18-25 yrs) under four randomly ordered free-walking conditions: 1) no load (NL), 2) carrying an infant manikin (5 kg) on the hip (HL), 3) carrying the manikin on a hipseat carrying device (Hippychick) (HSL), and 4) carrying the manikin in a carrier (Ergobaby) worn on the participant's front (FL). Kinematic data were collected from inertial sensors (ADPM) and a gait analysis mat (GAITRite) participants walked across during each of 4 laps per condition. A general linear model showed: stride length was shorter compared to NL for HL ($p = 0.014$) and HSL ($p = 0.003$), while cadence and speed did not differ across conditions; swing time as %stride was smaller for all three carrying conditions ($p < 0.0001$) compared to NL; pelvic coronal ROM was similar between NL and HL but dropped significantly for FL ($p = 0.003$) and HSL ($p < 0.0001$); and pelvic transverse ROM was smaller for all three carrying conditions ($p < 0.0001$) compared to NL. Thus, aspects of pelvic rotation, stride length, and swing time are affected by infant-sized loads, in some cases depending upon load position, even when speed stays fairly consistent.

Health and Disease in Pre-Columbian Amazon Societies: Everyday Life in the Teeth and Bones of Volta Grande of the Xingu River, Brazil

LETICIA M. MÜLLER¹, HILTON P. SILVA¹ and RENATO KIPNIS²

¹Graduate Program in Anthropology, UFPA, ²Scientia Scientific Consulting

The vast Amazon territory has been occupied for millennia by human groups with different cultures, economies, and socio-environmental relations. Poor preservation of bones and teeth in the archaeological context of rainforests is well known and as a result there are few studies analyzing skeletal material from most of these areas. However, in some specific contexts preservation does occur and this material is helpful in investigating health status and aspects of socio-ecologic practices. In this research, 12 adult burials recovered from

five archeological sites located along the middle Xingu River, Volta Grande region, Pará, Brazil, were investigated. The burials were located in or below anthropogenic soil (Amazonia dark earth), associated to occupations dated to the last millennium before European contact. Studies of the material culture of these sites point to a long history of occupation, and a wide variety of styles of ceramic material in the anthropogenic soil. The poor preservation hampered the identification of age and sex of all individuals. Teeth analysis shows a high prevalence of tartar, wear of the occlusal surfaces, cavities, and tooth loss during life, compatible with horticultural practices. In the bones, abscess and periodontitis were identified. Despite the difficulties, this is one of the first studies of oral health of pre-contact populations in this area of the Amazon basin.

Research partially funded by CAPES/Brazil

Digitizing typologies: A morphometric archive of lithics projectile point collections from Florida

MARCELINA L. NAGALES¹, KATHRYN O. MIYAR² and SAM M. WILFORD²

¹Scientific Computing, Florida State University, ²Bureau of Archaeological Research, Florida Department of State

North American projectile point/knife (PPK) typology and classification varies widely across cultural groups, time period, geographic locale, and archaeological interpretation. The Florida Bureau of Archaeological Research has compiled a digital archive of 3D PPKs to facilitate virtual research that would otherwise be confined to the curatorial facility. Comprising of sixteen PPKs from the Southeastern United States, high-resolution 3D scanning and photogrammetric methodologies were tested to create highly accurate 3D renderings. The HDI LMI 109A scanner with FlexScan software used blue light scanning to create black and white 3D models that were rasterized with images taken of the physical object using Meshlab. The NextEngine Ultra HD scanner with stereographic cameras and LED light along with ScanStudio Software were utilized to create 3D models with color. Due to the stationary nature of the scanners, however, environmental factors affected the visual aspect of the 3D model; therefore, photogrammetry techniques were utilized, allowing for model modification in response to light exposure factors. Through these synthesized models, users can manipulate and rotate the scanned virtual renderings as well as conduct morphometric assessments and measurements. It is our hope to continue to build this archive to include a broader representation of Southeastern lithic technology and apply this methodology to other artifact types and typologies.

ABSTRACTS

Identifying facial mites on captive prosimians

MCKENZIE D. NALLEY, DAVID C. DENTON, SAMANTHA E. COTHERN, CARMEN M. CROMER, QUENTIN D. WATTS and LISA M. PACIULLI

Biological Sciences, NC State University

Demodex mites have been characterized on a wide range of mammals, but little is known about mites in non-human primates (NHP). The relationship between mite proliferation and host skin irritation is well known, but what happens between the time an individual has “demodicosis” and before is unknown. In this study, captive prosimian facial hair was examined for mites. The research question was, Do healthy lemurs have facial mites? It was hypothesized that because lemurs are primates like humans, and healthy humans have facial mites, then healthy lemurs will have facial mites, too. The study was conducted on prosimians housed at the Duke Lemur Center in Durham, NC. The hair including the follicle was plucked from sixteen facial regions on animals anesthetized for physicals. The hairs were placed on glass slides with mineral oil to prevent desiccation. The hair follicle was then analyzed under a microscope for the presence of mites. Of the 24 slides analyzed from two fat-tailed dwarf lemurs (*Cheirogaleus medius*) and one gray mouse lemur (*Microcebus murinus*) thus far, none had *Demodex* mites. However, a dust mite and unknown pieces of invertebrate exoskeleton were found on the mouse lemur’s midsagittal sinciput region. These findings may be due to the nocturnal and solitary nature of the species, contamination, and/or improper sampling. Research is still being conducted on other prosimians to sample for *Demodex* mites on healthy captive lemurs. Understanding the prosimian skin microbiome is critical for conservation, as it correlates with increased immunity and life spans.

NC State Department of Biological Sciences and Office of Undergraduate Research

Using camera traps to study the impacts of disturbance on the abundance of two lemur species in southeast Madagascar

PAMELA R. NARVÁEZ-TORRES¹, DEVIN CHEN¹, OLIVIA TIAFINJAKA², EDWARD E. LOUIS JR.³ and STEIG E. JOHNSON¹

¹Department of Anthropology and Archaeology, University of Calgary, ²Faculté des Sciences, de Technologies et de l’Environnement, Université de Mahajanga, ³Conservation Genetics Department, Omaha’s Henry Doorly Zoo and Aquarium

Human activities are greatly threatening the persistence of tropical ecosystems, including their flora and fauna. In Madagascar, lemurs are at especially high risk of population declines and extirpations due to human disturbance. We used camera traps to evaluate the potential effects of exotic species and vegetation structure on the abundance of two lemur species,

the greater dwarf lemur (*Cheirogaleus major*) and the red-fronted lemur (*Eulemur rufifrons*) in Kianjavato, Madagascar. We hypothesized that higher disturbance (lower percentage of canopy cover and higher abundance of individuals of exotic species) will present a lower abundance of lemurs. We collected data from May-August 2019 in five forest fragments. To determine the abundance of lemur (*C. major* and *E. rufifrons*, species with at least 80 records) and introduced species (*Rattus rattus* and *Canis lupus familiaris*), we used 30 arboreal (average height=10m), and 30 ground cameras (average height=0.05m). The cameras were positioned within a 700m grid and operated for 30 days per location. We estimated species abundance as the number of individuals recorded at each event (i.e., within 30 minutes) and summed for each camera location. Canopy cover was measured at each location using a densiometer. We found that areas with a higher percentage of canopy cover presented a higher abundance of *C. major* (GLMM: $z=2.39$, $p=0.017$) and *E. rufifrons* ($z=4.12$, $p<0.001$). However, exotic species abundance did not significantly predict lemur abundance. Canopy cover’s decline can cause decreases in the abundance of lemurs, eventually affecting ecosystem functioning, particularly via key roles played by seed-dispersing species.

This study was supported by the Natural Sciences and Engineering Research Council of Canada, Global Wildlife Conservation, the American Society of Primatologists, Primate Conservation Inc., and the Animal Behavior Society

Short-term wasting, linear faltering, and Type X Collagen

DANIEL J. NAUMENKO^{1,2}, NABEEL AFFARA³, DAVID B. DUNGER⁴, KEN K. ONG^{4,5}, ANDREW M. PRENTICE⁶, SOPHIE E. MOORE^{6,7} and ROBIN M. BERNSTEIN^{1,2}

¹Department of Anthropology, University of Colorado, Boulder, ²Institute of Behavioral Science, University of Colorado, Boulder, ³Department of Pathology, University of Cambridge, ⁴Department of Paediatrics, University of Cambridge School of Clinical Medicine, ⁵MRC Epidemiology Unit, University of Cambridge School of Clinical Medicine, ⁶MRC Unit The Gambia, London School of Hygiene and Tropical Medicine, Banjul, The Gambia, ⁷Department of Women and Children’s Health, King’s College, London

Growth faltering is linked to several short- and long-term sequelae, especially in early life. Frequently defined as negative deviations in length-for-age z-score, faltering can also be applied to other anthropometric dimensions (e.g., wasting in weight). It has recently been suggested that stunting is in part the result of repeated rounds of wasting, implying that stunting is a negative adaptation to undernutrition, and that growth faltering in one dimension can negatively impact other growth dimensions. If growth is linked across multiple anthropometric

dimensions, then wasting is predicted to covary with faltering, and significant short-term wasting is predicted to correspond to lower biomarkers of bone formation, indicating slowed linear growth over the same time period. We use data from the HERO-G (Hormonal and Epigenetic Regulators of Growth) cohort study, which tracked alternate day growth in rural Gambian infants across the first year of life, to compare a real-time linear bone growth biomarker (degraded product of Type X collagen, CXM) with short-term wasting (weight loss) patterns across three weeks. CXM was measured in dried blood spots collected from infants determined to be at risk of entering a faltering event, based on infant temperature, appetite, and morbidity (F: 19, M: 24). CXM was lower when measured during a short-term wasting event ($16.47\pm0.99SE$) than during normal growth ($22.072\pm1.73SE$). As CXM decreased, there was a significant increase in the likelihood that it was sampled during a faltering event, regardless of overall growth rate. This suggests that bone growth slows during short-term weight loss events.

Funded by the Bill and Melinda Gates Foundation (OPP1066932)

Daily-resolved maternal diet and early feeding history from histologically-defined compositional profiles of human dental enamel by laser-based mass spectrometry (LA-ICPMS)

ALESSIA NAVA^{1,2}, FEDERICO LUGLI^{3,4}, LUCA BONDIOLI², STEFANO BENAZZI^{3,5}, ALFREDO COPPA⁶, EMANUELA CRISTIANI¹, CHRISTOPHER DEAN⁷, DAVID EVANS⁸, ANGELA HELBLING⁸ and WOLFGANG MÜLLER⁸

¹DANTE - Diet and ANcient TEchnology Laboratory – Department of Oral and Maxillo Facial Sciences, Sapienza University of Rome, ²Bioarchaeology Service, Museum of Civilization, Rome, ³Department of Cultural Heritage, University of Bologna, Ravenna, Italy, ⁴Department of Chemical and Geological Sciences, University of Modena and Reggio Emilia, Modena, Italy, ⁵Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, ⁶Department of Environmental Biology, Sapienza University of Rome, Rome, Italy, ⁷Earth Sciences, Natural History Museum, London, UK, ⁸Institute of Geosciences, Goethe University Frankfurt, Frankfurt am Main, Germany

Maternal diet during pregnancy, breast feeding and the onset of weaning are key determinants for human development, which also correlate with the societal role of women, access to food resources, infant growth and adult health.

The spatial variation of trace elements (Sr, Ba) in deciduous teeth can reveal such dietary transitions for past societies during the early phases of an individual’s life, while Pb and Zn are proxies for environmental pollution and mineralization, respectively.

ABSTRACTS

Here we show how spatially-resolved mass spectrometry (LA-ICPMS) coupled with enamel histology can be used to reconstruct dietary change at daily resolution, as reflected by the trace elemental variations along the enamel-dentine-junction in enamel. Six deciduous teeth - five canines and one second molar - from five modern and archaeological individuals were analyzed. The well-known feeding history of the two modern individuals (mod.1, mod.2) is exploited as a benchmark to reconstruct those of both an early 20th century specimen (mod.3) and two archaeological specimens (arch.1, arch.2) from two Imperial Roman graveyards.

Our results show that Sr/Ca ratios correlate closely and Ba/Ca ratios to a lesser extent with mode and time of the known nursing histories of mod.1 and mod.2. This allows us to use their dietary models to interpret the other unknown feeding histories. In mod.3, a short period (~25 days) of exclusive breast feeding is followed by a switch to bottle-feeding. The Roman individuals display an internally rather similar nursing history where exclusive breastfeeding for 3-4 months is followed by the introduction of supplementary food.

European Research Council (ERC), ERC Starting Grant Project HIDDEN FOODS, G.A. No. 639286; ERC Consolidator Grant Project SUCCESS, G.A. No 724046; NERC Capital equip fund CC073

Sniffing out decomposition: Investigating the reliability of human remains detection dogs

KRISTEN M. NAWN

Anthropology, Humboldt State University

The purpose of this study was to investigate the reliability of trained Human Remains Detection (HRD) dogs (*Canis familiaris*). HRD dogs are trained to locate deceased individuals, typically in conjunction with law enforcement agencies, by using their enhanced olfactory systems to detect scents and alert their human handlers. Limited research has been conducted on the strengths and weaknesses of these dogs and their abilities to locate human skeletal remains. This study focused on a North Carolina organization that trains HRD dogs. Data were collected by observing training exercises and documenting canine behavior and human-canine interactions. An experiment was conducted in July-August 2018, which tasked five dogs with locating human bone samples buried under four common regional North Carolina soil types. It was hypothesized that even though a canine may not have been previously exposed to a specific soil through training, their enhanced olfactory abilities and adaptability to new environments would enable them to quickly increase efficiency, suggesting that dogs trained in one environment can be widely deployed. The teams had a 20% success rate

(8/40 correct indications) and results indicated that canines responded quicker and more reliably to the soil most local to their training region but were sometimes able to readily locate remains in unfamiliar soils. The variation in response time for each canine could relate to breed or training. Additional research is needed to fully evaluate training needs of the appropriate deployment of HRD dogs, especially during disaster situations when forensic teams may be called to unfamiliar areas.

The Powerhouse Project: Encouraging Community Stewardship in Anthropology Students

NADIA C. NEFF^{1,2}, HEATHER M. BROOKSHIER¹, DAWN M. MULHERN¹ and LANGSTON SHUPE-DIGGS¹

¹Anthropology, Fort Lewis College, ²Anthropology, University of New Mexico

The Powerhouse Project focused on engaging undergraduate anthropology students in community stewardship through the creation of a lasting collaboration between Durango, Colorado based Fort Lewis College Anthropology Department (FLC), a small liberal arts undergraduate institution, and the Powerhouse Science Center and MakerLab (PSC), a community center focused on providing accessible non-formal science education. This collaboration was developed through faculty involvement in the PSC education committee which led to the implementation of an FLC undergraduate internship program at the PSC. The implementation of this program began during the 2018-19 academic year through the creation of a three-pronged outreach program focusing on human and primate evolution, culture and archaeological development:

- pop-up modules built using MakerLab 3D printed, laser cut and screen-printed materials along with scaffolded and scaled lesson plans
- a week-long anthropology kids science camp
- a semester-long homeschool program

Lessons and materials for each program were developed by undergraduate interns supervised by faculty. This collaboration was designed to train undergraduate students in the development and dissemination of scaled lessons, provide students access to high quality lessons outside of formal education, expose K-12 students to the science of anthropology, forge ties with community institutions, and provide anthropology undergraduates with practical experience that will lead to career opportunities and future successes. This program has resulted in a lasting collaboration between the PSC and FLC, an increase in K-12 student knowledge and excitement in anthropology, FLC student involvement in, and ability to plan and execute lessons, and paid employment in museum education.

Issues and Ethical Considerations in Molecular Paleopathology

ELIZABETH A. NELSON^{1,2}, ALYSSA C. BADER^{3,4}, DEBORAH A. BOLNICK^{5,6}, JANE E. BUIKSTRA⁷, KEOLU FOX⁸ and COURTNEY HOFMAN⁹

¹Institute for Archaeological Science, University of Tübingen, Germany, ²Archaeogenetics, Max Planck Institute for the Science of Human History, Germany, ³Anthropology, Sealaska Heritage Institute, Alaska, ⁴Department of Anthropology, University of Illinois at Urbana-Champaign, ⁵Department of Anthropology, University of Connecticut, ⁶Institute for Systems Genomics, University of Connecticut, ⁷Center for Bioarchaeological Research, Arizona State University, ⁸Department of Anthropology, University of California San Diego, ⁹Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma

The study of ancient disease is an interdisciplinary endeavor, with contributions from anthropology, medicine, microbiology, and molecular biology. Today, many researchers in paleopathology seek not only to identify and describe ancient disease, but also to undertake more comprehensive investigations of past population health and disease, providing a greater understanding of ancient disease within bio-cultural, socio-political and environmental contexts. The power of such in-depth analyses, made possible through multidisciplinary involvement and methodological advances, has been demonstrated in the application of molecular methods. However, in the wake of the ancient DNA revolution, little consideration has been given to the social implications and narratives that follow molecular-based paleopathological work, and ethical standards have yet to be firmly established.

We present social, cultural, political and bioethical considerations for molecular-based paleopathology. We review relevant principles of viral sovereignty and privacy for study populations existing in biomedical and infectious disease research, and consider their application to molecular paleopathology. Furthermore, we discuss principles and suggest guidelines essential for ethical project design and scientific practice, including contextualizing research, sample collection, responsible scientific collaborations and community engagement, and thoughtful interpretation and communication of results. These recommendations are important to counter contextually shallow research designs where biocultural aspects of human-pathogen interactions and evolution are not fully considered. We call instead for a focus on anthropologically-relevant contributions, where the biocultural context may be further illuminated through a deeper understanding of ancient disease. We suggest this approach produces more robust results and better serves the interests of descendant groups.

ABSTRACTS

Do the regions of the spinal column record stress differently? An analysis of growth stunting in the vertebral neural canal

JENNIFER S. NELSON¹, EMILY HOLLAND², LESLEY HARRINGTON¹ and HUGO F.V. CARDOSO³

¹Department of Anthropology, University of Alberta, ²Department of Anthropology, Brandon University, ³Department of Archaeology, Simon Fraser University

The diameters of the vertebral neural canal (VNC) are used as an indicator of non-specific stress during early childhood because VNC growth occurs during the first years of life and cannot experience catch-up growth once fusion has occurred. Most studies that assess the VNC prioritize measurements of the lumbar region, as these vertebrae undergo post-natal growth over the longest period, and therefore have the greatest potential for growth disruption. This study explores the validity of such a focus by comparing the levels of growth stunting (defined by z-score ≤ -2) in the cervical, thoracic, and lumbar VNC diameters of 56 subadult individuals from a documented skeletal collection. Data from 50 adult individuals provided a standard for VNC diameters by which to generate z-scores for the subadults. ANOVA was used to assess for differences in the mean z-scores for each vertebral region of those individuals who were identified as stunted. No significant difference between means in the level of growth stunting was identified in the anterior-posterior diameter ($p = 0.157$).

Growth stunting in the transverse diameter of the cervical ($z = -2.94$, $p = 0.011$) and lumbar ($z = -3.03$, $p = 0.002$) regions differed significantly from the thoracic region. Although the lumbar region shows more stunting, on average, than the thoracic region as expected, this study found that growth stunting is also evident in the cervical region. These findings indicate that a focus on the lumbar region alone could overlook growth stunting recorded by the earlier developing cervical vertebrae.

Funding for this project was provided by SSHRC - Social Sciences and Humanities Research Council of Canada

Relative encephalic artery size and re-estimating brain metabolism in the tarsier

LATICHA L. NELSON¹, THIERRA K. NALLEY², NEYSA GRIDER-POTTER³ and JASON ORGAN⁴

¹Graduate School of Medical Sciences, Western University of Health Sciences, ²Medical Anatomical Sciences, Western University of Health Sciences, ³Graduate School of Human Sciences, Osaka University, ⁴Department of Anatomy, Cell Biology, & Physiology, Indiana University School of Medicine

Tarsiers are capable of extreme axial rotation of the cervical spine, and regularly rotate their heads 180 degrees from the forward-facing position. Previous work indicates that tarsiers have cervical features that facilitate these rotational

movements while reducing the risk of injury to the vertebral artery, an important component of the brain's vascular supply. Tarsier vertebral arteries are small relative to body mass and brain size, but how this affects other encephalic arteries has not been investigated. Previous estimates of tarsier brain metabolic requirements (19-30 pBGU/BMR%) using bony proxies to measure arterial size are surprisingly similar to estimates for humans (22-32 pBGU/BMR%). In this study, we examine the relative ratio of vertebral to internal carotid/promontory artery size and reevaluate models of tarsier brain metabolism using direct measurements of encephalic vessels. We measured cross-sectional areas of the internal carotid and promontory arteries from a contrast-enhanced microCT scan of a single wild-caught Philippine tarsier (*Carlito syrichta*). We compared these values to those reported for a sample of euarchontans ($n = 139$). Results demonstrate that tarsiers do not have an enlarged internal carotid to compensate for their small vertebral artery. However, the predicted metabolic energy requirements for our individual, computed using vascular cross-sectional measurements instead of bony proxies, falls below human percentages (17 pBGU/BMR%) and within the ranges for other nonhuman primates. Our findings indicate that tarsiers do not have unusually large brain metabolic requirements.

Patterns of Free-Standing Water Drinking Among Wild Chimpanzees (*Pan troglodytes*) at Gombe National Park, Tanzania

RACHEL S. NELSON¹, ELIZABETH V. LONSDORF², KAITLIN R. WELLENS³, KAREN A. TERIO⁴ and CARSON M. MURRAY¹

¹Center for the Advanced Study of Human Paleobiology, George Washington University, ²Department of Psychology, Franklin and Marshall College, ³Department of Biology, Trinity Washington University, ⁴Zoological Pathology Program, University of Illinois

For a long time, it was believed that African great apes were innately hydrophobic, such that consuming free-standing water was not a substantive part of their hydration strategies; instead it was believed that great apes met their hydration requirements through the water content of their diets. However, early work by Nishida (1980) demonstrated a seasonal variation in chimpanzee water intake at Mahale National Park, Tanzania, that suggested water intake increases during times of water stress. Since this study, the drinking patterns of wild chimpanzees at other study sites are still not well-studied. The present study presents an unparalleled long-term dataset on chimpanzee mothers and offspring to quantify the patterns of drinking among chimpanzees (*Pan troglodytes*) at Gombe National Park, Tanzania; lactating mothers and dependent offspring are likely under more extreme hydration

burdens than their conspecifics due to the water content of milk production and an abrupt challenge to offspring when they are weaned. The Gombe chimpanzees present an interesting study population in which to investigate this question as it has extremely pronounced seasonality, and individuals here have varying access to free-standing water. Using behavioral data on mothers and offspring collected from 1975 to 2016, we quantified drinking patterns based on offspring age and season. Free-water consumption was higher during the dry season than the wet season ($t(10) = -9.12$, $p < 0.00001$). There was also a higher proportion of drinking during weaning ($X^2(7) = 332.07$, $p < 0.00001$). These data demonstrate chimpanzees increase their water consumption when placed under various hydration burdens.

Population, Race, or Racism?: slippery usage of the population concept in studies of health inequities in minoritized communities

ROBIN G. NELSON

Anthropology, Santa Clara University

The term "population" is often employed as an uninterrogated referent for a biologically valid group of organisms, and contrarily as a seemingly self-explanatory and naturalized grouping of individuals based on culture, geography, and/or ethnicity. In this paper, I conduct a thematic analysis on 50 studies each from biological anthropology, demography, and public health published between 2000-2019. I investigate variability in contemporary uses of this term in papers that identify a "population" as a primary locus of analysis. Usage of this term in these fields clusters thematically in several categories ranging from people living in discrete geo-spatial locations to individuals with shared socio-economic histories. Thematic analyses demonstrate that a lack of specificity in the use of the term "population" transcends disciplines and is often rooted in a race concept. Race and population are used interchangeably in studies investigating health disparities even though races are not biological units. This imprecision has resulted in slippage between the terms "race" and "population," and an inability or unwillingness to identify racism as a primary underlying factor preceding commonly recognized components in models of the social determinants of health.

The circle game: is seasonal workload responsible for birth seasonality?

ILONA NENKO¹, AGNIESZKA MICEK² and GRAZYNA JASIENSKA¹

¹Department of Environmental Health, Jagiellonian University Medical College, ²Department of Nursing Management and Epidemiological Nursing, Jagiellonian University Medical College

ABSTRACTS

Human birth seasonality is common in many populations. While social and climatological factors are usually suggested to be responsible for this phenomenon, energetic factors that influence female fecundity should be also considered. Physical activity causes decline in ovarian hormone levels, less frequent ovulations, and consequently, a lower probability of conception. In the past, farm work was highly seasonal and labour-intensive. In rural Poland, high energy expenditure during harvest and haying season (July-August) remained in contrast to fall and winter when women had lower involvement in agricultural work. Such variation has the potential to affect seasonal birth rate through suppressing ovarian function. Moreover, seasonal patterns in births may gradually change because of changes over time in an important exposure i.e. workload. However, despite of evidence that physical work suppresses ovarian function, few previous studies have convincingly shown that seasonal workload may also influence birth rate.

We test the relationship between seasonal workload and seasonality of births using parish records from a village in Southern Poland. We examine whether monthly number of births changed over a 200-year period from 1783 to 2005. The whole period was divided into 20-year bins and seasonality in each time period was assessed.

We have not observed predicted differences in birth seasonality over time. The highest occurrence of conceptions was observed between March-June and lowest frequency of conceptions was observed between September-December. Our results did not confirm that seasonal workload affected probability of conception and we did not observe predicted changes in seasonality pattern over time.

This study was supported by Salus Publica Foundation and National Science Centre (grant no. 2016/21/D/NZ8/01306).

The ontogeny of endocranial shape asymmetry in humans and apes

SIMON NEUBAUER¹, PHILIPP GUNZ¹, NADIA A. SCOTT^{1,2}, JEAN-JACQUES HUBLIN^{1,3} and PHILIPP MITTEROECKER⁴

¹Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ²Konrad Lorenz Institute for Evolution and Cognition Research, Austria, ³Collège de France, ⁴Department of Theoretical Biology, University of Vienna

Brain lateralization is commonly interpreted as crucial for human brain function and cognition. However, little is known about which aspects of morphological brain asymmetry are really uniquely human, how the magnitude and spatial pattern of asymmetry vary during postnatal ontogeny, and how these ontogenetic changes contribute to adult differences in humans and non-human apes. Here we used endocranial casts

that provide information on the asymmetry of the outer brain surface. These data are available for larger samples than MRI scans of brains and therefore make it possible to broaden the comparative framework. Our cross-sectional ontogenetic sample comprised 130 humans, 110 chimpanzees, 75 gorillas, and 75 orangutans from infants to adults. For each individual, we generated a digital endocast based on computed tomographic scans and measured 935 endocranial landmarks and semilandmarks. The semilandmarks were allowed to slide to a symmetric template so as gain point-to-point correspondence and to remove asymmetry resulting solely from an asymmetric placing of semilandmarks. To quantify endocranial asymmetry, we used a Procrustes approach among the measured landmark configurations and their relabeled reflections. We found that apes show a similar pattern of directional asymmetry like humans, including a left occipital petalia, a right frontal petalia, a right cerebellar petalia and a more projecting right temporal pole. However, humans were much more variable than apes. We discuss how postnatal ontogenetic changes contribute to the variation in adults.

This work is supported by the Max Planck Society and the Austrian Science Fund (FWF P29397).

Development of a maternal stress measure associated with low birthweight

LISA NEVELL¹, CHRISTOPHER J. CLUKAY¹, CHU HSIAO¹, EDWARD QUINN¹, FELICIAN M. MAISHA¹ and CONNIE J. MULLIGAN^{1,2}

¹Anthropology, University of Florida, ²Genetics Institute, University of Florida

Maternal stress has been shown to increase the risk of infant mortality and a host of adverse health outcomes throughout the offspring's life. The risk of adverse health effects is highest in babies born below 2.5 kg, the WHO definition of low birthweight (LBW). This study sought to develop a maternal stress measure associated with LBW by identifying maternal stress exposures that distinguish between mothers of LBW babies and mothers of larger babies. Mothers in the study (n=146) delivered singleton infants at HEAL Africa hospital in Goma, Democratic Republic of Congo. The questions that significantly distinguished mothers of LBW infants included, in decreasing order of significance: fear for one's life during the pregnancy, being unmarried, pregnancy was the result of rape, raped before age of 18, being ashamed to cry in front of husband or partner during pregnancy, and being a war refugee alone/without family in the past. The LBW-associated maternal stress measure was generated as an unweighted count of mothers' exposures to the six identified stressors. This measure of maternal stress was positively associated with LBW risk ($\beta=0.84$; $p=0.005$), doubled the adjusted relative risk of LBW (aRR = 2.29; 95% CI 1.59, 2.99), and explained 28% of the variation

in LBW, after controlling for maternal age and BMI. This maternal stress measure focused on the range of birthweights known to carry the highest disease risk, in the hope that this measure may provide clarity on the relationship between maternal stressors and the fetal environment among these study participants.

This research was supported by NSF grants BCS-1231264, BCS-1540372, BCS-1719866, DGE-1315138, UF Clinical and Translational Science Institute, UF College of Liberal Arts and Sciences, UF Research Opportunity Seed Fund.

Comparing genetic variation among Latin American migrants: implications for forensic casework in the Texas- and Arizona-México Borderlands

BRIANA T. NEW¹, BRIDGET F.B. ALGEE-HEWITT², KATE SPRADLEY³, LARS FEHREN-SCHMITZ⁴, CRIS HUGHES⁵, BRUCE ANDERSON⁶, MAREK E. JASINSKI⁷, JOANNA ARCISZEWSKA⁸, GRAŻYNA ZIELIŃSKA⁸, MARIA SZARGUT⁹ and ANDRZEJ OSSOWSKI⁸

¹SNA International, Defense POW/MIA Accounting Agency, ²Center for Comparative Studies in Race and Ethnicity, Stanford University, ³Anthropology, Texas State University, ⁴Anthropology, University of California, Santa Cruz, ⁵Anthropology, University of Illinois, Urbana-Champaign, ⁶Pima County Office of the Medical Examiner, Tucson, AZ, ⁷Historical Studies, NTNU Norwegian University of Science and Technology, ⁸Forensic Genetics, Pomeranian Medical University

Research on Arizona-Mexico border migrants highlights regions of origin, typically within Mexico, that are linked to migration routes, economic disadvantage, structural violence, and variance in admixture ratios. As migration trends continue to shift, with more migrants crossing and dying along the Texas-Mexico border, it is important to understand and contextualize the bio-geographic and socio-structural differences between migrants crossing in each region. A comprehensive comparative analysis of both groups from a genetic perspective was conducted using 15 standard forensic (CODIS) markers from unidentified and identified migrants. Population relationships were assessed between migrants and 27 Latin American groups from allele frequencies, calculating F_{ST} , and plotting spatial relationships. Genetic admixture proportions were inferred for a reduced sample using unsupervised model-based clustering.

Analyses of allele frequencies indicate that Texas migrants have the strongest correlation (>80%) with populations from Belize, Colombia, Costa Rica, El Salvador, Guatemala, Honduras, and Nicaragua. Arizona migrants have the strongest correlation (>80%) with populations from El Salvador, Guatemala, Eastern Mexico, Central Mexico, and an indigenous group from Southern Mexico. The admixture model, $k=4$, captures a small African contribution and clinal distributions

ABSTRACTS

in the quantity of indigenous ancestry, where levels of admixture are linked to geography. Texas migrants align best with higher European ancestry populations while Arizona migrants align best with higher Indigenous ancestry populations. These findings agree with prior genetics, population history, and migrant pathway studies. Results emphasize the different contexts these migrants originate from and the different migration routes they use, which has important implications for identification and advocacy strategies.

A tale of two towns: exploring the impact of the osteological paradox on interpretations of bioarchaeological data within the DOHaD framework

SOPHIE L. NEWMAN

Department of Archaeology, University of Sheffield

The Developmental Origins of Health and Disease (DOHaD) hypothesis has become a focus of intense research interest. However, methodologies investigating DOHaD in past populations often come with their own implicit biases, and interpretations are potentially further complicated when viewed through the lens of the osteological paradox. Integrating non-adult morbidity and mortality data with concepts from the osteological paradox enables a discussion concerning prediction of health risks following early life adversity for survivors into adulthood.

171 non-adults from two 18th/19th century cemeteries in North-East England were assessed for age-at-death, dental enamel hypoplasia, vitamin D deficiency, and growth parameters. A clear dichotomy exists in the results, with Coach Lane (North Shields, n=81) exhibiting greater evidence of 'stress' than Coronation Street (South Shields, n=90). However, significant growth deficiencies reveal that Coronation Street non-adults were not necessarily 'healthier', perhaps instead succumbing to acute stressors (e.g. infectious disease). Considering social context, non-conformists (Coach Lane) possibly received greater intra-community care than those reliant on parish poor relief, with prevalent pathology alternatively reflecting longer survival, and better resilience.

These three scenarios generate an equally varied discussion of consequences for 'survivors'. Should we expect an adaptive response to stress, increased frailty, or heightened mortality selecting out those experiencing childhood privation? Are the cumulative effects of living in notoriously poor environments a greater determinant of adult longevity? A simple comparative study can produce numerous narratives regarding health throughout the life-course. Only through multiple lines of evidence, and systematic consideration of the osteological paradox, can the strongest inferences be made.

Single mothers: no evidence for paternal care in wild, eastern chimpanzees

NICHOLAS E. NEWTON-FISHER and ADRIANA E. LOWE

School of Anthropology & Conservation, University of Kent

Paternal care is any fitness-enhancing behaviour directed by males selectively towards their own, rather than unrelated, infants. While such care is more common in monogamous species, where higher paternity certainty reduces the likelihood that investment will be misdirected, several promiscuously-mating primates reportedly exhibit some form of paternal care. This includes chimpanzees (*Pan troglodytes*), with evidence reported from two communities. To further investigate this issue, we used data on association patterns and aggression from a third community, from the Budongo Forest, Uganda, which demonstrated the highest reported rates for wild chimpanzees of within-community infanticide and yielded evidence that infanticidal attacks could be prevented by behavioural intervention. Thus, there were clear opportunities for males of this community to demonstrate significant direct paternal care by defending their offspring from infanticide. However, while we found that males directed less aggression towards mothers than towards non-mothers, they did not distinguish between mothers of their own and others' infants. We found no evidence of preferential association within mother-infant-father triads compared to mother-infant-non-father triads, and no evidence that fathers intervened to prevent infanticidal attacks. Our results contradict claims previously made for chimpanzees, and we suggest that mother-male association in this species is likely to be underpinned by maternal, rather than paternal, infant care strategies.

AEL was supported by a University of Kent Vice Chancellor's Scholarship. Data collection was funded by a grant to NNF from the Harry Frank Guggenheim Foundation.

Whose Bodies? Whose Data? Whose Responsibility? Ethical Concerns and Outcomes Regarding the Study of Indigenous Ancestral Remains

GEORGE NICHOLAS and LAURE SPAKE
Archaeology, Simon Fraser University

The question of "Who owns the past?" has loomed large in recent decades regarding tensions between archaeologists and descendant communities relating to who has rights to, benefits from, and control over archaeological and other sources of information about the past. Prominent here are concerns raised regarding ancestral remains, as manifested in deliberations about repatriation and reburial, the implications of DNA and aDNA-based research, lack of clarity in research ethics, intellectual property claims, and

the inequalities that exist in the protection (or lack thereof) of Indigenous heritage. Our presentation focuses on ethical considerations and concerns regarding indigenous ancestral remains, including both skeletal and genetic materials. We identify how information derived from these sources sometimes threatens, sometimes strengthens individual or group sense of identity, history, and wellbeing. We cite examples from North America, Australia, and elsewhere of both productive and problematic engagements, and lessons learned from collaborative projects that provide insights into responsible research practices that respect and benefit Indigenous people's relations with their ancestors.

NA

Grammatical traits track the peopling of the Americas

JOHANNA NICHOLS

Slavic Languages, University of California, Berkeley, Linguistic Convergence Laboratory, Higher School of Economics, Moscow, General Linguistics, University of Helsinki

As people began entering the Americas from the northwest the human frontier expanded southward and eastward. Distributions of grammatical structures shed light on how that process proceeded. Contra implicit received view, language movement was most likely non-gradual, non-unidirectional, and patch-based: early entrants seized the best nearby patches and later ones leapfrogged, skirted, or took second-choice patches. Thus conspicuously good patches hosted well-entrenched linguistic descendents of earliest immigrants. As populations and competition increased, the process repeated. Millennia later, structural features of early entrant languages may still cluster detectably around the earliest-settled patches and in the northwest more generally. Here I survey four likely early good patches and several structural features that are good criteria because they differ from the type (head-marking, often polysynthetic, minimally configurational) that has spread widely in expansions of major language families (all of which greatly postdate the earliest colonization episodes).

The patches are: the Klamath estuary (the first major estuary south of the ice sheets); the eastern Columbia Plateau-northeastern Sierra Nevada (now dry, but a rich riverine/lacustrine system in late glacial to mid postglacial times); the Lower Mississippi Valley (a known secondary staging area for spread of domestication); the central Andean highlands (continuously inhabited since remarkably early). Eight grammatical features, minority traits in the Americas and therefore visible diagnostics (pronoun consonantism, configurational syntax, dependent marking, non-possessible nouns, flexible lexical class,

ABSTRACTS

others) do indeed prove to cluster in the vicinity of these patches. This raises the further hypothesis that gene distributions roughly follow the linguistic distributions.

DFG Center for Advanced Studies "Words Bones Genes Tools", Eberhard Karls Universität Tübingen, Germany

Cold adaptations in the tropics? Evidence for undertaking a study on BAT activity in Polynesian samples.

ALEXANDRA NICLOU and CARA OCOBOCK
Anthropology, University of Notre Dame

The non-shivering thermogenic capacity of brown adipose tissue (BAT) indicates a possible evolutionary function in human cold adaptation. Previous studies demonstrated the significant metabolic activity of BAT in cold-adapted populations. However, no studies have looked at BAT activity in a tropical sample. Polynesian morphology defies traditional eco-geographical rules, which has spurred many evolutionary theories to explain this phenotype. Measuring BAT in a Polynesian sample will elucidate the range of BAT activity and address the cold-adapted Polynesian morphology paradox. In this study we assessed the metabolic activity of BAT in a temperate-climate sample in hopes of extrapolating the likely presence of and variation in BAT activity in a tropical population. In our study we inferred seasonal patterns of BAT activity by combining metabolic rate (MR) measurements and thermal imaging of the suprascapular region under room temperature (RT) and mild cold exposure (CE) in upstate New York (n=75, female n=46, ages: 18-63). Independent of the season, suprascapular skin temperature significantly decreased ($p < 0.001$) and MR significantly increased ($p < 0.05$) after cooling. Comparing winter and summer measurements, MR increases were not significant, while suprascapular skin temperatures were significantly higher in the winter ($p < 0.001$). These results indicate seasonal patterns of BAT activity in a temperate-climate sample, even in summer. This suggests an increased likelihood of detecting BAT activity in a tropical sample, promoting the need to analyze BAT activity in a Polynesian sample. Such a study will determine BAT variation in warmer climates and infer the role of physiological adaptations in the peopling of Polynesia.

Unique Beringian architectures found in extant Native Americans structure genomic differences in melanoma etiology

SARA D. NIEDEBALSKI¹, JEFFREY C. LONG¹,
MARIANNE BERWICK² and ANDREY S. DOBROFF²
¹Anthropology, University of New Mexico,
²Department of Internal Medicine, University of
New Mexico School of Medicine

Early humans entered the Beringian corridor during the Last Glacial Maximum, where they persisted, isolated from gene flow, for upwards of 20,000 years. The ancestral Native American population encountered extreme climates and distinct dietary resources in Beringia. These environmental and demographic pressures provided the opportunity to evolve novel genomic architectures with phenotypic consequences. In this study, we analyzed whole-genome sequences of Native American origin in mixed populations in the Thousand Genomes project. We report, for the first time, a cluster of 62 tightly linked single nucleotide variants found in a gene encoding a long non-coding RNA gene, Melanoma Associated Transcript-6 (MEAT6). The MEAT6 is a candidate gene for melanoma vulnerability.

Our principal hypothesis is that the 62 substitutions we have found dampen the function of MEAT6 and provide resistance to Melanoma. It is noteworthy that Native Americans and Hispanic Americans have lower melanoma prevalence than do European Americans. To investigate this, we measured cell proliferation and gene expression in *in vitro* cultured melanoma cell lines. Our experiments included transient silencing of MEAT6, which significantly reduced melanoma cell viability by 30%. Ongoing functional analyses of CRISPR mediated mutations in mice and computational modeling of RNA-secondary structures will further characterize the effect of Beringian-specific variants on melanoma outcomes. Together these findings describe genomic consequences of the Beringian Migration for contemporary Native Americans and provide a novel biological target for translational medicine. This work emphasizes the value of using an evolutionary approach to understand population-level disparities in health and disease etiology.

Genomic and anthropological perspectives on the Afro-Caribbean diaspora in the Lesser Antilles

MARIA A. NIEVES-COLÓN^{1,2}, DANIELA OROZCO-PÉREZ^{3,4}, JADA BENN TORRES⁵, ANDRÉS MORENO-ESTRADA⁴ and ANNE C. STONE²

¹Astrea Forensics, Claret Bioscience LLC, ²School of Human Evolution and Social Change, Arizona State University, ³Undergraduate Program in Genome Sciences, Center for Genome Sciences, Universidad Nacional Autónoma de México, ⁴National Laboratory of Genomics for Biodiversity (UGA-LANGEBIO), CINVESTAV, ⁵Department of Anthropology, Vanderbilt University

Over 7 million African peoples were forcibly transported to the Caribbean during the Transatlantic Slave Trade. However, research into the biohistories of Caribbean afro descendant peoples is still lacking. Here we use genomics as part of an integrative toolkit, which also draws upon anthropological and historical sources, to investigate the African diasporic experience in the Lesser

Antilles. We examine nuclear SNP genotypes from 73 individuals sampled in self-identified Afro-Caribbean communities from five Lesser Antilles: St. Kitts, St. Lucia, St. Vincent, Grenada, and Trinidad. We found the sampled individuals carry diverse ancestries with varying contributions from African, European, Native American, South and East Asian ancestors. These patterns differ among island groups and are highly sex-biased. To characterize sub-continental ancestries further, we used ancestry-specific PCA (ASPCA), a technique for comparing masked genomes from admixed populations with continental reference panels. Our preliminary findings suggest that African ancestry in the Afro-Caribbean sample is most similar to that of present-day peoples living in Lower Guinea, a region that includes Ivory Coast, Togo, Benin and Ghana. Using the same technique, we found that the South Asian ancestry component is most similar to populations living in present-day South India. Research into other sub-continental ancestries is currently ongoing. Our findings are consistent with the historical record of forced labor migrations to the Caribbean both during and after the colonial period. This work also underscores the complexity of the African diasporic experience in the Americas and increases understanding of the biocultural variation of historically marginalized Caribbean peoples.

This work was funded by the Arizona State University Center for Evolution and Medicine and the School of Human Evolution and Social Change.

Let's go digital! First steps towards setting up a digital bioarchaeological reference collection for the Eastern Mediterranean

EFTHYMIA NIKITA
STARC, The Cyprus Institute

In most Eastern Mediterranean countries, there is no formal legal framework specifically for the acquisition, curation and study of human skeletal remains. Until a few decades ago human bones were not even acknowledged as archaeological material and they were reburied once the excavation was complete. Nowadays, the importance of bioarchaeological data is not questioned; however, human skeletons are treated in the same way as any archaeological material. This approach simplifies the excavation and study of skeletal remains; however, it often impacts their long-term curation. Even though bioarchaeologists working in the region are largely familiar with ethical issues pertaining to their work, no dialogue has been initiated with the aim of formalising ethical standards. This presentation will briefly outline the current legislation under which the acquisition, curation and study of human skeletal remains falls with a geographical focus on Greece and Cyprus. Subsequently, it will make reference to a number of anecdotal evidence which illustrates current practices. Finally, it will outline current efforts at

ABSTRACTS

the Science and Technology in Archaeology and Culture Research Centre of the Cyprus Institute to establish a digital bioarchaeological reference collection. This collection encompasses both three-dimensional bone models as well as different types of dental calculus microdebris. Our efforts are still at an early stage; however, they are progressing systematically and their prospects and limitations will be discussed.

Functional morphology and physiology of phonation in gibbons

TAKESHI NISHIMURA¹, ISAO TOKUDA², RYOSUKE GOTO³, CHRISTIAN T. HERBST⁴ and YOSHIHIKO NAKANO³

¹Primate Research Institute, Kyoto University,

²Department of Science and Engineering, Ritsumeikan University, ³Graduate School of Human Science, Osaka University, ⁴Department of Cognitive Biology, Vienna University

Hylobatids are lesser apes inhabiting the canopy of the tropical forest in Southeast Asia. They produce a sequence of loud and pure-tone-like voices changing melodiously in fundamental frequency (f₀), which are referred to as "songs". Their song voices are produced by a technique similar to that of human sopranos, but little empirical data are available on the vibration mechanism of the vocal folds in gibbons. Here, we examined vibration patterns of the vocal folds *in vivo* with electroglottography (EGG) and recording acoustic signals of song calls in a female adult White-handed gibbon (*Hylobates lar*). We were successful in triggering song vocalizations and non-invasively monitoring vocal fold vibration by sensing the electrical conductance between two electrodes of EGG placed on the neck of this subject. The data showed that the voices are produced with vibration patterns that are different from that in normal speech and rather are comparable to those in singing for humans. We examined the glottal anatomy from the hylobatids, including this species, by the histological sections and the high-resolution imaging of the embalmed specimens of extracted larynges, to show that they have the features that are suggested to induce and regulate easily such vibrations. Such a view was supported by acoustic simulation implementing a glottal model representing the anatomical features in gibbons.

Supported by JSPS KAKENHI (#19H01002, TN) and OEAW APART (HCT).

Nitrogen Isotopes of Serially Sampled Nails From Chimpanzees and Baboons at Gombe National Park, Tanzania

REBECCA S. NOCKERTS¹, MICHAEL L. WILSON^{1,2}, DAVID L. FOX³, ROBERT C. O'MALLEY⁴, D.

ANTHONY COLLINS⁵, IAN C. GILBY⁶ and ANNE E. PUSEY⁷

¹Anthropology, University of Minnesota, ²Ecology, Evolution, and Behavior, University of Minnesota, ³Earth Sciences, University of Minnesota, ⁴, The American Association for the Advancement of Science, ⁵, Jane Goodall Institute, ⁶School of Human Evolution and Social Change, Arizona State University, ⁷Evolutionary Anthropology, Duke University

Nitrogen isotopes enable researchers to reconstruct trophic level, both in modern and historical populations. We present a preliminary analysis of nitrogen composition in serially sampled nail keratin from chimpanzees (*Pan troglodytes schweinfurthii*) and baboons (*Papio anubis*) of Gombe National Park, Tanzania.

Compared to baboons, the chimpanzees had nails significantly depleted in ¹⁵N (chimpanzees: $\delta^{15}\text{N}$ of $4.2 \pm 0.4\%$; baboons: $5.8 \pm 0.8\%$; $t=15.5$, $df=141$, $p<0.0001$) suggesting that baboons consumed substantially more animal protein. This apparent trophic difference is in fact partly driven by the ¹⁵N enrichment of some of the baboons' most common plant and prey foods compared to the chimpanzees' dietary resources.

$\delta^{15}\text{N}$ values for both species imply only minor consumption of meat or arthropods, contrary to observational data. However, we found that average plant $\delta^{15}\text{N}$ at Gombe is lower than any previously characterized African primate habitat: $1.2 \pm 2.1\%$, $n=613$. We therefore infer that the low $\delta^{15}\text{N}$ values result from the isotopic signature of plant foods, rather than minimal consumption of animal foods.

We also found ¹⁵N enrichment in chimpanzee nail samples reflected observed temporal variation in protein consumption. Peaks coincided with high consumption of social insects in February/March and increased hunting success in September/October.

Our results illustrate the importance of knowing the underlying floral $\delta^{15}\text{N}$ baseline when interpreting relative protein consumption. This has ramifications for the use of modern analogs for historical populations, as well as interpreting the diets of unhabituated primates, as trophic level can be substantially over or under-estimated.

Funding and logistical support were generously provided by The Leakey Foundation, The Wenner-Gren Foundation, The University of Minnesota, a GWU/SI Opportunity Research Grant, and The Jane Goodall Institute.

Longitudinal epigenome-wide association study of immigrant-related stress and resilience in children of Latinx immigrants in the US

AMY L. NON¹, ELIZABETH S. CLAUSING¹ and ALEXANDRA M. BINDER²

¹Anthropology, University of California, San Diego, ²Epidemiology, University of California, Los Angeles

Latinx children are the fastest growing group of youth in the US, and are increasingly born to mothers under heavy burdens of stress. Our aim is to investigate how immigrant-related stressors and resilience factors associate with epigenomic patterns over time in children of Latinx immigrants from childhood to adolescence. This question is particularly pressing in the context of rising hostile rhetoric and hate crimes directed towards Latinx immigrants since the last presidential election. We conducted a longitudinal epigenome wide association study (EWAS) of the embodiment of stress among these children in Nashville, TN, before and after the election of President Trump (2015-2018). Saliva and survey data were collected when children were aged 5-13 ($n=77$), and again two years later ($n=36$) for exploratory epigenomic analysis in relation to stressors over time. The EWAS revealed one CpG site associated with maternal discrimination experience (*SCN3B*) after FDR-adjustment (adj. p -value=0.08), and suggestive trends at various sites with other social variables (e.g. child worry over parent deportation, legal status, marital status, adj- p values ≤ 0.15). The rate of methylation change/month at various CpG sites was associated with child reports of discrimination and maternal social support post-election. Epigenetic age, age acceleration, and rate change in epigenetic age were associated with a range of social factors, including discrimination, worry over parent deportation, child's optimism, and parental social support (most p -values ≤ 0.05). These results suggest that immigrant-related stress and resilience factors may have measurable impacts on Latinx children's epigenomes, potentially contributing to intergenerational patterns of health inequalities.

Young Scholars Program at Foundation for Children's Health, Hellman Award (UCSD), and Chancellors Research in Excellence Scholars at UCSD (Application # 4-G021)

Developing Effective Strategies for Primate Conservation Education for Local and International Museums, Zoos, and Wildlife Centers

ALEXANDRA L. NORWOOD

Anthropology, University of Michigan

Cultivating positive attitudes toward primate conservation both in local communities who interact with primates and in the global population is critical to securing primates' future. Museums, zoos, and wildlife centers around the world endeavor to teach visitors better daily practices that have fewer negative environmental impacts and to encourage them to fund conservation efforts. Understanding how the strategies they use can be employed with maximum efficacy in different settings to improve public attitudes toward primate conservation is an important step toward reducing the extinction risk facing many primate species. Here I investigate the

ABSTRACTS

methodological underpinnings of conservation education and how different methods of conservation education have been applied in different educational and geographical settings. I then look at several case studies in primate conservation efforts by museum, zoos, and wildlife centers in both Africa and the United States in order to evaluate how well they are communicating with their respective publics, with the ultimate goal of beginning to synthesize a strategy that can be used by both researchers and museum professionals seeking to promote primate conservation to understand which educational methods will be most effective in their context.

Life and death of a Croatian noblewoman: a (bio)archaeological approach

MARIO NOVAK¹, IVOR JANKOVIC², TAJANA PLESE³ and FABIO CAVALLI⁴

¹Center for Applied Bioanthropology, Institute for Anthropological Research, ²Center for Applied Bioanthropology, Institute for Anthropological Research, ³Croatian Conservation Institute, ⁴General Hospital Trieste

The poster presents the results of multidisciplinary study of the skeleton recovered during the excavation of the Pauline monastery of the Blessed Virgin Mary in Moslavačka Gora, Croatia. The skeleton was retrieved from a monumental tomb located in the church apse. The monastery was one of the most important ecclesiastical centers in continental Croatia during the 14th/15th century and was abandoned between 1520 and 1544 due to Ottoman attacks. The inscription and coat of arms on the tombstone as well as archival records indicate that the skeleton belongs to Sophia Kaštelančić, a member of Croatian high nobility.

We conducted conventional bioarchaeological study, carbon and nitrogen stable isotopes analysis, CT scanning and 3D facial reconstruction. The skeleton belongs to a middle-aged woman with an estimated height of about 159 cm. Numerous small lesions such as ATML, caries, abscess, linear enamel hypoplasia, and osteophytosis were observed during the analysis; the most notable pathology is the fracture of right distal tibia and fibula that was also confirmed by CT scanning. C and N isotopes values are consistent with a terrestrial diet based on C3 plants with no marine input, and the consumption of large quantities of animal-based proteins. 3D facial reconstruction revealed her physical appearance which allows us to compare it with facial characteristics of other members of her family.

The presented results confirm the assumption that the skeleton belongs to Sophia Kaštelančić, thus making her the first historic individual with known name from that period in Croatia identified by using (bio)archaeological approach.

Cultural Inheritance Through Bead Manufacture: An Argument from Grassridge Rockshelter, South Africa.

APRIL NOWELL¹, BENJAMIN COLLINS^{2,3} and CHRISTOPHER J. H. AMES^{1,4,5}

¹Department of Anthropology, University of Victoria, ²Department of Anthropology, University of Manitoba, ³Department of Archaeology, University of Cape Town, ⁴Centre for Archaeological Science, University of Wollongong, ⁵School of Earth and Environmental Sciences, University of Wollongong

As paleoanthropologists, we are aware on a theoretical level of the recursive relationship that exists between the choices made by hominins, the activities in which they engaged, and the niches to which they were adapted. Identifying these relationships in the archaeological record is, however, a fundamental challenge that we face. We present an example of a social mechanism for cultural inheritance based on our analysis of ostrich eggshell (OES) beads from Grassridge Rockshelter, an early to mid-Holocene site in South Africa. OES beads are considered a proxy for identity construction, and for the establishment and maintenance of social networks from at least the Late Pleistocene onwards. Identity and sociality are key components for hominin cultural adaptations to the diverse global environments they encountered and they can be identified in the archaeological record through personal ornaments, such as beads made out of OES and other materials. More difficult to identify, however, is the importance of the social context in which OES beads were made. Thus, we also consider the benefits of having multiple generations engaging in craft production together. Through communities of practice, people reinforce common values, and pass on cultural, technical, and social knowledge—all essential elements to survival. In this respect, not only may the products of OES bead manufacture have contributed to past hominin cultural adaptations, but the practice of bead manufacture would also have presented opportunities to disseminate knowledge both vertically, between generations, and horizontally, across generations that would have positively contributed to socially constructed cultural niches.

The socioecology of parasite infection in wild Bornean orangutans (*Pongo pygmaeus wurmbii*) in Gunung Palung National Park, West Kalimantan, Indonesia

CAITLIN A. O'CONNELL^{1,2}, NATALIE ROBINSON³, ISHMA FATIHA KARIMAH⁴, TRI WAHYU SUSANTO⁵, IVONA FOITOVA⁶ and CHERYL D. KNOTT^{1,3,7}

¹Department of Anthropology, Boston University, ²Human and Evolutionary Biology, University of Southern California, ³Gunung Palung Orangutan Conservation Program, ⁴Department of Biology, State Islamic University Syarif Hidayatullah Jakarta, ⁵Department of Biology, National University, Jakarta, Indonesia, ⁶Department of Botany and

Zoology, Masaryk University, ⁷Department of Biology, Boston University

The socioecological model predicts that food availability and risk of parasite transmission influence sociality in primates. As a semi-solitary ape inhabiting the masting forests of Southeast Asia, orangutans provide a unique opportunity to compare social and non-social periods and highly variable foraging conditions within one population. This study compared two data collection periods when fruit availability differed markedly to determine whether sociality and parasite prevalence decrease as expected during periods of fruit scarcity. Fecal samples were analyzed using direct smear and fecal concentration techniques on-site at Cabang Panti Research Station from 2013-2014 and 2018-2019. From the high fruit period to the low fruit period, sociality decreased from 54% of focal follows containing a social event to 29%, while overall parasite prevalence remained the same at 100%. Interesting differences arose for certain parasite species, however. *Enterobius* sp. prevalence decreased during the low fruit period for both sexes but even more so for males (50% to 29% for females; 56% to 0 for males). Prevalence of *Trichuris* sp. increased for females during the low fruit period (5% to 43%) while prevalence among males remained the same. These results lend support to the prediction that social contact influences transmission risk for some parasite species, while other parasites may be more responsive to factors such as changes in reproductive state. These findings suggest that differences in the behavioral strategies of the sexes and the differential energetic demands of life history stages have an influence on parasitic infection patterns.

NSF (BCS-1638823, BCS-0936199); National Geographic Society; US Fish/Wildlife (F18AP00898, F15AP00812, F12AP00369); Leakey Foundation; Disney Conservation Fund; Wenner-Gren Foundation; Nacey-Maggioncalda Foundation; Conservation-Food-Health Foundation; Woodland Park Zoo; BOS-Canada, Primate Conservation Inc.

Relative enamel thickness, cuspal enamel thickness, and lateral wall enamel thickness in maxillary premolars and molars of apes and hominins

MACKIE C. O'HARA¹, PATRICK MAHONEY², GARY T. SCHWARTZ³, MATTHEW M. SKINNER^{2,4,5} and DEBBIE GUATELLI-STEINBERG^{1,2}

¹Department Anthropology, The Ohio State University, ²Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, ³School of Human Evolution and Social Change, Institute of Human Origins, Arizona State University, ⁴Max Planck Institute for Evolutionary Anthropology, Max Planck Institute, ⁵Evolutionary Studies Institute, University of Witwatersrand

ABSTRACTS

High relative enamel thickness (RET), thick cuspal, and thick lateral enamel are hypothesized to protect teeth from fracturing during hard object feeding (durophagy). However, it is unclear whether each trait is exclusive to durophagous species or if they co-occur.

RET, average enamel thickness (AET), cuspal, and lateral enamel thickness were recorded from mesial sections of maxillary premolars and molars. *Pan troglodytes* (n=8), *Gorilla gorilla* (n=6), and *Homo neanderthalensis* (n=8) are less likely to be durophagous; *Pongo* (n=10) and *Paranthropus robustus* (n=13) are more likely durophagous. *Australopithecus africanus* (n=10), *Homo naledi* (n=9), and *Homo sapiens* (n=20) provide additional comparisons. Cuspal and lateral enamel thickness was compared to AET within species.

H. neanderthalensis, *P. troglodytes*, and *G. gorilla* had low average RET (16.81, 11.30, 9.70, respectively) and none had particularly thick cuspal enamel. The lingual lateral walls of *P. troglodytes* (UM2) and *H. neanderthalensis* (UP4) had significantly thicker enamel compared to AET. Average RET of the other hominins was 20 or more. *H. naledi* (UP4/UM2), *H. sapiens* (UP4/UM2), and *P. robustus* (UM2) had significantly thicker enamel over lingual cuspal tips than AET. *H. naledi* (UP4/UM2), *H. sapiens* (UP4/UM2), *A. africanus* (UP4/UM2), and *P. robustus* (UP4/UM2) had significantly thicker lingual lateral walls than AET.

Significant thickening along lingual lateral walls is not exclusively found in durophagous species. The "durophagous" traits co-occur in *H. sapiens* and *P. robustus*, but *Pongo* has only slightly thickened lingual lateral enamel and RET (17.89). Together, results suggest the predicted durophagous enamel distribution may be present in non-durophagous species.

This research was supported by the Wenner-Gren Foundation, NSF GRFP DGE-1343012 to Mackie O'Hara, the European Research Council (ERC) under the European Union's Horizon 2020 (ERC-2018-COG-819960), and Max Planck Society.

Geometric motion analysis: A development of Slice's original invention

PAUL O'HIGGINS^{1,2,3} and ANTONIO PROFICO¹

¹PalaeoHub, Department of Archaeology, University of York, ²Hull York Medical School, University of York, ³Centre for Forensic Anthropology, The University of Western Australia

Geometric motion analysis as first described by Dennis Slice takes motion sequences represented by point markers and splits them into equal numbers of sequential frames. Each represents a posture within the whole motion cycle as a configuration of landmarks. The entire sequence represents the entire motion. Slice then carried out generalised Procrustes analysis (GPA) on

the set of frames and statistical analysis on the resulting shape variables. These analyses might compare sequential frames or the trajectory of all frames in the shape space.

This elegant approach allows motions to be understood and compared, either within or between individuals. It suffers however from some significant issues. Thus, GPA removes location orientation and scale differences between successive frames and this therefore undermines attempts to visualise and reconstruct whole motion sequences. For subsequent biomechanical analyses or modelling this is a problem. Further, during motion very large shape differences may arise among frames. These may span large distances in Kendall's shape space and so standard statistical approaches relying on tangent projection are inadequate.

Here we propose an alternative analysis of whole motion sequences in which location, orientation, and scale are preserved between frames. This eliminates the issues arising with Slice's standard method. We demonstrate the applicability of this approach using sit and squat motion data and show that this approach is highly effective in discriminating different motions and in assessing how motion covaries with interesting factors such as height, sex or body proportions, while preserving information relevant to subsequent biomechanical analyses.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 835571

Modular Control of Walking in Humans and Bipedal Chimpanzees

MATTHEW C. O'NEILL¹, RUSSELL T. JOHNSON², JACK T. STERN, JR.³, SUSAN G. LARSON³ and BRIAN R. UMBERGER⁴

¹Department of Anatomy, Midwestern University, ²Division of Biokinesiology and Physical Therapy, University of Southern California, ³Department of Anatomical Sciences, Stony Brook University, ⁴School of Kinesiology, University of Michigan

The evolution of hominin walking involved significant changes to the musculoskeletal system. However, it is unclear what changes in muscle control are required to transition from abducted, flexed-limb walking to extended-limb walking. It has been hypothesized that the control of walking is regulated through the activation of muscles in modules or functional groups called 'muscle synergies'. These synergies are thought to reduce the complexity of motor control, but how these compare between facultative and habitual bipeds is unclear. Here, we use model-predicted muscle activations for all major hind/lower limb muscles to estimate the muscle synergies of human and bipedal chimpanzee walking.

Marker and force platform data from humans (N=3) and bipedal chimpanzees (N=3) walking at matched dimensionless speeds were integrated with three-dimensional musculoskeletal models to calculate individual muscle forces and activations via static optimization. Predicted muscle activations exhibited broad agreement with electromyographic (EMG) data. Non-negative matrix factorization was used to decompose the predicted muscle activations into a set of motor primitives and muscle modules. Mean muscle synergies per species were compared using zero-lag cross-correlations (r).

Initial results suggest that the motor primitives in bipedal chimpanzee and human walking are similar, with $r=0.81-0.98$ across six muscle synergies. However, differences exist in the individual muscle modules associated with a given motor primitive, with bipedal chimpanzee synergies exhibiting a reduced emphasis on ankle plantar flexion and an increased emphasis on hip adduction and rotation. These results provide new insight into the likely shifts in neuromuscular control of walking during hominin evolution.

NSF BCS-0935321 and BCS-0935327

From hamadryas to humans: evolution and variation in catarrhine craniodental morphology

NATALIE O'SHEA^{1,2,3}, DAGMAWIT ABEBE GETAHUN^{1,2,3}, ERIC MAZELIS^{1,2,3,4} and CLAUDIA ASTORINO^{1,2,5,6}

¹PhD Program in Anthropology, The Graduate Center, City University of New York, ²New York Consortium in Evolutionary Primatology, ³Department of Anthropology, Lehman College, City University of New York, ⁴Museum für Naturkunde, Leibniz-Institut für Evolutions- und Biodiversitätsforschung, ⁵Department of Integrative Biology, University of California at Berkeley, ⁶Human Evolution Research Center, University of California at Berkeley

Understanding patterns of morphological variation and the forces that generate them has important implications for reconstructing the evolution and ecology of many fossil taxa. Exploring patterns of morphological variation at different taxonomic levels in several catarrhine taxa, we highlight the ways in which shape data can be used to shed light on the evolution of our species and our closest relatives. The relationship between genomic and morphological variation in two monkey genera highlights the importance a population-level perspective. Consistent with previous work on hominoids, overall skull shape among both baboon and vervet populations appears to be strongly influenced by neutral evolutionary processes, such as gene flow and genetic drift. These results support the use of morphological variation as a proxy for past population history in extinct species. Additional work suggests that craniodental morphology can also be used to

ABSTRACTS

identify separately evolving lineages in the fossil record. When investigating molar shape variation across the family Cercopithecidae, about 85% of specimens are correctly identified at the genus-level. Looking more closely at a single genus, cranial shape data alone are able to distinguish various species and subspecies of *Theropithecus*, extinct and extant. Finally, sexual dimorphism may also play a major role in shaping patterns of variation in the fossil record. Levels of sexual dimorphism within several human populations are found to be greater in young adults (21-55 yr) than old age adults (≥ 56 yr) for most craniometric variables, suggesting a greater role for age-related change throughout adulthood than has been previously recognized.

Research reported here was supported (in part) by NSF 0966166 (NYCEP IGERT).

It's all downhill: Stride length differences during slope walking

MIGUEL OCHOA¹, HANNAH ZAEHRINGER¹ and PATRICIA A. KRAMER^{1,2}

¹Anthropology, University of Washington, ²Orthopaedics and Sports Medicine, University of Washington

The human lineage has exploited mountainous environments for refuge and other resources for millennia, and our ability to ably traverse those rugged environments has been key. Many modern human populations still walk in steeply inclined environments and yet most gait studies focus on walking on level surfaces. Stride length—that is, the distance between ipsilateral heel strikes—is an important gait characteristic with implications for such evolutionarily important constraints as energy expenditure. This study examines stride length differences when walking with and without a burden to better understand the influence of incline on spatiotemporal gait parameters.

Anthropometric and kinematic data were collected from 10 healthy subjects (6F/4M, 27.77yr \pm 6.24yr) using a six-camera motion capture system (Qualisys, Gothenburg, Sweden). Participants walked up and down a ramp with a 20° incline at a self-selected comfortable walking pace in two conditions: unburdened and wearing a 10 kg backpack. Stride lengths for the left and right sides were calculated for each trial using a custom MatLab script (Mathworks, Nantucket, MA). Linear regression was used to explore the relationship between stride length, walking direction, and burden condition.

The results indicate that downhill strides were significantly shorter than uphill strides ($p < 0.001$), but burden is not a significant predictor ($p = 0.26$). Mass, stature, and leg length did not improve the fit of the model. People take shorter steps when walking downhill, but the cause of this is not fully known. More research should be conducted to further understand movement on slopes surfaces.

Evidence for brown adipose tissue activation among male and female reindeer herders from sub-arctic Finland

CARA OCOBOCK¹, PAIVI SOPPELA^{2,3}, MINNA TURUNEN^{2,3}, VILLE STENBÄCK⁴ and KARL-HEINZ HERZIG⁴

¹Anthropology, University of Notre Dame, ²Biology, University of Lapland, ³Biology, Arctic Centre, ⁴Physiology and Internal Medicine, University of Oulu

Brown adipose tissue (BAT) has received renewed interest from anthropologists in recent years. A better understanding of BAT activity variation among modern humans allows us to assess the potential evolutionary importance of this heat producing tissue for cold climate survival. To deepen our knowledge about existing variation, we measured BAT activity, inferred through metabolic rate and thermal imaging of the suprascapular region, among 20 reindeer herders (5 females and 15 males) from seven herding districts surrounding the Arctic Circle of Finland in January 2019. Room temperature resting metabolic rates were 1798 \pm 216 kcal/day for females and 1753 \pm 503 kcal/day for males. Participants underwent a 30-minute controlled cold exposure ($\sim 12^\circ\text{C}$)—cool enough to induce BAT activity but not shivering. During this time there was a significant 8.7% increase in metabolic rate ($p = 0.002$). The mean metabolic rate for women was 1967 \pm 245 kcal/day and 1870 \pm 487 kcal/day for men. Women had a slightly higher increase (9.5%) compared to men (8.2%), but this did not rise to the level of significance. However, 15% of the participants, all men, experienced a drop in metabolic rate in response to the cold exposure, a phenomenon that has been previously documented among the Yakut of Siberia. The results of this study demonstrate the presence of BAT activity in a cold climate population who regularly spend long periods of time exposed to the elements while also taking part in rigorous physical activity. The evolutionary implications for these findings, particularly among Neanderthals, will be discussed.

Funding for this project was provided by the National Science Foundation High Risk Research in Biological Anthropology and Archaeology. Grant Award: 1724819

Competing siblings and invested first time mothers: Weaning patterns in wild bonobos (*Pan paniscus*) revealed by stable isotope analysis

VICKY M. OELZE¹, GOTTFRIED HOHMANN², ISABALLA O'NEAL^{1,4}, SEAN LEE³ and BARBARA FRUTH^{4,5}

¹Anthropology, University of California Santa Cruz, ²Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ³Center for the Advanced Study of Human Paleobiology, George Washington University, ⁴Faculty of Science, Liverpool John Moores University, ⁵Centre for Research & Conservation, Royal Zoological Society

Weaning, the cessation of breast milk in infant diets, is extremely difficult to monitor and quantify in wild primates as mothers commonly allow nipple contact while the offspring is transitioning to solid foods. Here, we analyzed the stable isotopes of carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) to monitor weaning of wild infant bonobos. We analyzed a total of 130 fecal samples from 10 habituated mothers and their 18 infants (female=14, male=4) collected over a five year period at the LuiKotale Bonobo Project in DRC. Over 90% of all samples of mother-infant dyads were collected within the same 48 hours. We found differences between mother and infant fecal $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values being significantly predicted by infant age. The smallest average difference in $\delta^{15}\text{N}$ values was at the age of ~ 4 years (50 months), suggesting infants were largely weaned by this age. Infant fecal $\delta^{13}\text{C}$ values were more variable and dropped below those of their mothers after the age of 5 years (60 months) on average. With respect to weaning age, our results are similar to what was reported for the Ngogo chimpanzees (*Pan troglodytes schweinfurthii*). While we could not test for sex bias in female investment, we found that the number of maternal siblings had a significant effect on the weaning pattern, ranging from highest $\delta^{15}\text{N}$ values reflecting more dietary milk in infants of primiparous females to lowest $\delta^{15}\text{N}$ values in infants with three siblings. We discuss bonobo female life-history strategies as well as developmental and behavioral changes during early ontogeny.

Funding for this project was provided by the University of California at Santa Cruz, the Centre for Research & Conservation (CRC/KMDA) and the Leakey Foundation.

Dental status of the population from the Roman site of Nad Klepečkom-Viminacium

BAILEY A. OETTEL¹, ILIJA MIKIĆ² and EMILY E. HAMMERL³

¹Department of Anthropology, University of Nebraska-Lincoln, ²Institute of Archaeology, Belgrade, Serbia, ³Department of Anthropology, University of Nebraska-Lincoln

The effect that sex has on the presence of several different dental pathologies has been well documented in the literature. However, there have been no publications related to the dental health of the site of Nad Klepečkom (AD 100-200) in Serbia. Here, caries and calculus were examined from the teeth of 24 individuals out of the 94 inhumations identified at the site. The effect that sex had on each of these dental pathologies was calculated using Chi square analysis. The number of teeth with caries was found to be significantly affected by sex ($P = .012$), while the number of teeth with calculus was not significantly affected ($P = .066$). In regard to the side of the tooth in which carious lesions and calculus accumulations were found on, the side of the tooth in which carious

ABSTRACTS

lesions formed was highest for the interproximal surfaces, with 35.42% of the teeth with caries having them on those surfaces. For calculus, the lingual side of the tooth had the highest amount of calculus, with 54.76% of the teeth with calculus exhibiting it on that side. Also, females exhibited nearly double the amount of calculus on the lingual side, in comparison to males. These results are in agreement with previous studies that have found frequency of caries to be significantly different between the sexes. Additionally, the side of the tooth on which calculus accumulates may differ between the sexes in this population and warrants further study.

Detecting Vitamin D deficiency in an adult bedouin population from Hisban, Jordan using dental radiographic and histological examination

COURTNEY OLAH¹, MEGAN PERRY¹, AKACIA PROPST² and BONNIE KAHN²

¹Anthropology, East Carolina University,

²Anthropology, McMaster University

Recent skeletal analysis of bedouin skeletal remains from 19th century Hisban, Jordan identified a notable frequency of children dying with vitamin D deficiency. In this commingled sample of a minimum of 29 children, 55% of lower limb bones and 50% of all limb bones displayed abnormal curvature and metaphyseal flaring, respectively, two primary diagnostic signs of rickets. Such a high frequency of childhood vitamin D deficiency is surprising in an agropastoral community residing in a UV-rich region. Genetic conditions exist that inhibit bone mineral absorption and mimic skeletal rickets, many of which result in high infant mortality. Thus, identifying cases of surviving childhood rickets in the adults at Hisban (MNI=33), including sex-linked variation, could not only point to a genetic cause but may identify sex-related childhood behaviors as a factor. This study identifies patterns of childhood vitamin D deficiency in adults through radiographic and histological examination of dentition that can identify repeated periods of vitamin D deficiency during childhood dental development. Abnormal pulp chamber morphology revealed through radiographs and histological observation of interglobular dentine (IGD) have identified that approximately 55% of adults buried in Hisban had at least one episode of vitamin D deficiency during childhood. There is no clear difference between men and women in regard to the severity and timing of vitamin D deficiency episodes. These data contribute to identifying mortality differences within the group and understanding the prevalence of vitamin D deficiency in an area of moderate UV exposure.

Archaeological evidence for the Cooking Hypothesis in the Okote Member at site FxJj20 AB

GEORGIA OPPENHEIM¹, CHLOE DANIEL-HOLDEN², OUMEYMA BEN BRAHIM³, RUSSELL CUTTS⁴, DAN PALCU⁵, KEVIN UNO⁶, CAITLIN CRAIG⁷, JEANWON KIM⁸, DEANNA MAYBEE⁹, TERESIAH THUKU¹⁰, TAMARA CAPPS¹¹, AMANDA STRICKLAN¹², DAVID R. BRAUN¹³ and SARAH HLUBIK¹³

¹Anthropology, Wellesley College, ²Cognitive Science Program, Anthropology, Indiana University, ³Quaternary and Prehistory, Muséum National d'Histoire Naturelle, ⁴Anthropology, University of Georgia, ⁵Instituto Oceanográfico, University of São Paulo, ⁶Lamont-Doherty Earth Observatory, Columbia University, ⁷Anthropology, University of Victoria, ⁸Anthropology, New York University, ⁹Biomedical Anthropology, SUNY Binghamton, ¹⁰Anthropology, University of Nairobi, ¹¹Anthropology, University of North Carolina - Wilmington, ¹²Intelligence and Space Research, Los Alamos National Laboratory, ¹³Center for the Advanced Study of Human Paleobiology, The George Washington University

The Cooking Hypothesis proposes that morphological changes in early *Homo erectus* fossils indicate a dietary shift most parsimoniously explained by higher dietary returns from consuming cooked foods. Despite these theoretical expectations, the archaeological record has not provided solid evidence for this behavioral transition at the time when it is expected. In the Koobi Fora Formation, Kenya, consolidated reddened sediment patches were recovered in the 1970s at archaeological sites in association with other evidence of hominin behavior (FxJj20 East and Main). This evidence has been used to suggest Early Pleistocene hominins had some control over combustion processes. Early Pleistocene hominins would have encountered wildfire regularly on the East African savannah landscape, which may have facilitated habituation to fire, and further enhanced the adoption of fire using behaviors. Here, we present evidence of the intersection of combustion features and hominin behavior at the FxJj20 Site complex (FxJj20 East, Main, and AB), dated to 1.6 Ma. We provide data on site formation processes, as well as evidence of burning. We discuss spatial associations of burned materials. We combine Fourier Transform Infrared spectrometry; phytolith analysis; magnetic susceptibility data; polycyclic aromatic hydrocarbons, and thermally altered lithics (potlids, thermal curved fragments) as evidence of combustion. We describe ongoing work investigating the association of hominin behavior and fire and suggest future directions of research on this topic.

This research funded in part by the NSF Archaeology program #1624398 and a supplemental REU #1930719.

Testing Claims for Neanderthal Cannibalism at Krapina: A quantitative analysis of bone surface modifications on associated faunal remains

EMILY R. ORLIKOFF¹, MICHELLE M. GLANTZ², DAVORKA RADOVČIĆ³ and MICHAEL C. PANTE²

¹Anthropology, University of Michigan,

²Anthropology and Geography, Colorado State University, ³Hrvatski prirodoslovni muzej, Croatian Natural History Museum

The Krapina site in Croatia represents the richest Neanderthal deposit in the world. Yet, it is the evidence for cannibalism in the form of cut-marked, burnt, and highly fragmentary bone intermixed with faunal remains that makes this site so intriguing. However, recent inspection of the assemblage has led to contention over this interpretation, with suggestions of other agents potentially involved in the observed pattern, such as trampling or carnivore tooth marks.

Therefore, molds were taken of 10 suspected cut marks from the Krapina faunal remains and subsequently scanned with a white-light confocal profilometer to create high-resolution 3-D models of each mark. Measurements were then taken for 12 variables that include both volumetric and profile dimensions. The data obtained from each mark were then compared to a large experimental database of stone tool cut marks, carnivore tooth marks, trampling marks, and percussion marks. A Quadratic Discriminant Analysis (QDA) was performed for agent identification of each archaeological mark.

The results of the QDA indicate a mixture of agents at the site, with five marks classifying as trampling marks, three as cut marks, and one as a tooth mark. These results suggest potentially more trampling at the site than previously considered and may offer an alternative explanation for the high-level of bone fragmentation. Future research will investigate bone surface marks discovered on the Neanderthal remains to determine if there is a similar mixture of agents responsible for the bone surface modifications as found with the fauna.

Comparison of wrist mechanics between pronograde monkeys and orthograde apes

CALEY M. ORR

Department of Cell and Developmental Biology, University of Colorado School of Medicine, Department of Anthropology, University of Colorado Denver

The extant climbing and/or suspensory apes are characterized by a suite of wrist morphological features differentiating them from pronograde quadrupedal monkeys. Key features include reduction of the ulnar styloid process with retraction from the proximal carpal row, simplification of the triquetrum with distal migration of the pisiform, globular lunate, and an ulnarly-deviated distal radius with a deeply concave radiocarpal

ABSTRACTS

joint surface. It is accepted that triquetropisiform characters contribute to a complex permitting full forearm supination via the radioulnar joints, but other functional consequences of these derived features of the ape wrist remain poorly understood. A three-dimensional computed-tomography-based system of studying carpal kinematics permits detailed analysis of carpal joint mechanics in cadaveric specimens. Resulting data show that contrary to prior assumptions, shared derived features of ulnar-side wrist in apes do not increase ulnar-deviation mobility. Ulnar-deviation mechanics in chimpanzees follow a generalized, monkey-like pattern, but orangutans exhibit unique wrist-adduction kinematics. However, relative to monkeys, both apes are derived in having a high degree of mobility of the scapholunate and lunotriquetral joints, possibly related to restructuring the proximal carpal row as a quasi-deformable meniscus to allow effective load transfer in a more wrist positions than available to quadrupedal monkeys. Such a mobile proximal row likely requires dynamic stabilization when the hand is loaded in a semi-extended position (e.g., in knuckle-walking or digitigrady). Scaphoid-centrale fusion and a midcarpal screw-clamp mechanism might be further derived means of stabilizing the midcarpal complex and intercarpal joints of the proximal row in African apes and humans.

National Science Foundation (BCS-622515 and BCS-1539741), Wenner-Gren Foundation (Gr. 7484 and 8318).

Oral Health in the Inka Heartland: A Tale of Two Sites

MACIE L. ORRAND and BETHANY L. TURNER
Anthropology, Georgia State University

This study presents the results of a comparative dental anthropological analysis of two sites in the Inka imperial heartland. During the Late Horizon (1450-1532 CE), the Inka moved subject populations around the empire in a variety of ways, often linked to economic roles and social classes. Reconstructing the life histories of different servant groups is therefore critical to understanding Inka statecraft and the lived experiences of Inka subjects. Here, oral pathological conditions—caries, abscesses, antemortem tooth loss, and occlusal wear—are compared among human remains from two contemporaneous sites (N=37, N=64, respectively) to infer diet-related and/or activity-related stress. The first site, Salapunku, is roughly 15km southeast of Machu Picchu along the Urubamba River and was likely an administrative outpost. The second site, Saqsahuaman, overlooks the imperial capital of Cusco and likely functioned as a ceremonial center. Results identify heavy antemortem tooth loss and edentulism among the individuals from Salapunku compared to those from Saqsahuaman. In addition, Salapunku exhibits heavy wear patterning that

suggests a variety of habitual activity and may reflect different subsistence or economic backgrounds prior to living at the site. In comparison, individuals from Saqsahuaman exhibit higher frequencies of caries and abscesses, which may indicate differentiating diets or, paradoxically, less severe oral pathology. Overall, the results presented here point to varied diets and activity patterns between the two sites that may reflect their differing functions; future isotopic analysis will address these interpretations. This study therefore joins a growing body of work reconstructing Inka life from the “bottom up.”

Geographic patterns of dental morphological variation in the New World: A view from ancient Mexico and Central and South America

ALEJANDRA ORTIZ^{1,2} and SHARA E. BAILEY^{1,2}

¹Department of Anthropology, New York University,
²New York Consortium in Evolutionary Primatology

The detailed anatomical features of the dentition have long been used to track human population history. Although dental morphology provided the foundation for the Sundadont/Sinodont dichotomy and early models on the peopling of New World, a paucity of research on the topic in the past two decades has led to a characterization of Native American dental morphology largely relying on samples from the American Arctic and the United States Southwest. Less is known about the dental phenotypes of the ancient peoples of Mexico and Central and South America. Here we document patterns of dental morphological variation in a geographically diverse sample of pre-Hispanic Americans and test the hypothesis that Native Americans are a dentally homogeneous group. We examined 22 dental morphological traits in 798 individuals from 14 populations from Mexico, Central America (Belize, Guatemala, and Honduras), and South America (Bolivia, Chile, Peru, and Venezuela) using the Arizona State University Dental Anthropology System. The mean measure of divergence and Bray-Curtis indices were used to quantify dissimilarity among samples. Our results indicate greater dental diversity in this part of the Americas than previously identified. We found that populations from high-altitude regions cluster together and tend to exhibit a Sundadont dental complex, whereas those from the lowlands are more similar to each other and tend to show a Sinodont dentition. This variability agrees with recent cranial morphometric evidence, and prompts us to revisit the assumption that all Native Americans follow a strict Sinodont dental pattern.

Is relative enthesal length indicative of locomotor repertoire?

ANTONIO R. OTERO and ADAM D. GORDON
Anthropology, SUNY University at Albany

Various traits are used to infer locomotor repertoire from the skeleton. This study considers relative length of entheses – muscle and tendon attachment sites – in *Ateles geoffroyi*, *Colobus guereza*, *Hylobates lar*, and *Macaca mulatta*. Since different locomotor types require varying degrees of usage for separate muscles, we hypothesize that relative enthesal length will differ among species with different locomotor repertoires. This study aims to determine whether relative enthesal length can separate species into locomotor categories: brachiator (*H. lar*, n=72), intermediate/eclectic (*A. geoffroyi*, n=9), and quadrupedal (*C. guereza*, n=27, and *M. mulatta*, n=42). Specimens are adult and a mixture of captive and wild caught. Relative enthesal lengths were calculated as $ln[\text{enthesal length}/\text{bone length}]$ for seven entheses (pectoralis major, teres major, deltoid, biceps brachii, brachialis, supinator, gluteus maximus) across four long bones (humerus, radius, ulna, femur). Univariate ANOVA and *post hoc* Tukey test results show that relative enthesal length does not separate locomotor repertoire as expected, with 0 out of 7 ratio results matching the predicted group separations. However, a linear discriminant function analysis of all seven ratios predicts both locomotor category (97.8% correct classification with leave-one-out cross-validation) and species (95.0% correct classification with cross-validation), driven primarily by relatively short biceps brachii insertions and relatively long deltoid and brachialis insertions in brachiators compared to other locomotor categories. These results suggest that individual relative enthesal lengths may not be accurate indicators of general locomotor signal, but the relationship among relative enthesal lengths across the post-cranium may be good predictors of locomotor categories.

Metagenomic analysis of human dental calculus in the Mesolithic and Early Neolithic central Balkans

CLAUDIO OTTONI¹, RON PINHASI², DUŠAN BORIČIĆ³ and EMANUELA CRITIANI¹

¹Department of Oral and Maxillo Facial Sciences, Sapienza University of Rome, ²Department of Evolutionary Anthropology, University of Vienna, ³The Italian Academy for Advanced Studies in America, Columbia University

Dental calculus – plaque mineralized on the surfaces of teeth during life – is composed of calcium phosphate salts mixed with the remnants of previously viable microorganisms and a variety of plant and animal tissues. This mineral matrix preserves ancient DNA molecules that may be used to reconstruct oral microbiomes of ancient humans, and may potentially inform on dietary behavior. Recent studies suggested that the transition from foraging to farming subsistence that occurred during the Neolithic changed the human oral microbiome. However, no clear

ABSTRACTS

characterization of past oral microbiomes associated with foraging activities has been possible so far due to the limited number of samples analyzed and the lack of complementary multidisciplinary datasets.

This study aims at reconstructing the oral microbiome of ancient humans associated with forager lifeways before the advent of the Neolithic in Europe, and track potential dietary sources. We conducted shotgun metagenomics, the untargeted sequencing of all DNA content of a sample, on dental calculus samples of Mesolithic and Early Neolithic humans from the Danube Gorges, in the central Balkans (Southeast Europe).

We reconstructed the oral microbiota of 27 individuals, and compared them with those of other ancient and modern humans. By integrating stable isotope and microfossil evidence in dental calculus, we demonstrate that foraging lifestyles are associated with distinctive oral microbiota. Our study sheds new light on the dynamics characterizing ancient foraging subsistence, and offers new insights into the understating of cultural and biological changes in human evolution associated with the introduction of food-producing economies.

The European Research Council (ERC Starting Grant Project HIDDEN FOODS, G.A. 639286)

Lessons from the past: 13,000-years of climate change effects on diet, foraging risk, and demography of Great Plains foragers and farmers

ERIK R. OTÁROLA-CASTILLO¹, MELISSA G. TORQUATO¹, JOHN B. RAPES¹, BENJAMIN SCHIERI^{1,2} and MATTHEW E. HILL³

¹Anthropology, Purdue University, ²Mathematics, Purdue University, ³Anthropology, University of Iowa

Introduction: Food security and risk management are prominent 21st century challenges, with ~795 million people estimated to be undernourished worldwide. Climate change is projected to affect the availability and stability of food sources, exacerbating global malnutrition. However, this is not a novel human challenge. Food security risk management in the face of climate change was crucial to survival of ancestral foragers and farmers throughout human evolution. Still, little is known about the effects of climate change on foraging-risk management-strategies of small-scale societies.

Methods: We apply the concept of "Dietary Portfolios," an optimization technique that models resource diversity utilization as a bet-hedging strategy to manage foraging-risk. We investigated the effect of climate change and foraging-risk on dietary portfolios of ~3,000 archaeological components from the North American Great Plains and adjacent regions.

Results: Dietary-portfolio risk analyses show variation in foraging-risk over time on the Great Plains, with a notable increase between ~8,500-6,000 years cal BP ($t=2.53$, $p=0.012$). This coincides with the Holocene Climate Optimum and indicates there was resource scarcity on the Great Plains at that time. Bayesian main effects models show that dietary portfolio diversity was affected by foraging risk, annual temperature and precipitation, and temperature seasonality. Interaction effects show that Great Plains peoples fluctuated between generalist-specialist strategies in response to variations in foraging risk and climate change.

Conclusion: Preliminary results of observed-to-expected portfolio comparisons across space and time track variations in foraging and resource risk, providing insight into climate change-related impacts on human-environment interactions over the past 13,000 years.

Funding provided to Otárola-Castillo through the Exploratory research in the Social Sciences grant by Purdue College of Liberal Arts.

Comparing activity budgets in female white-faced capuchin monkeys (*Cebus capucinus*) with and without infants in the edge and interior of a fragmented forest in Costa Rica

JENNA L. OWENS^{1,2}, LAURA M. BOLT^{2,3} and AMY L. SCHREIER^{2,4}

¹Department of Sociology and Anthropology, James Madison University, ²La Suerte Biological Research Station, Maderas Rainforest Conservancy, ³Department of Anthropology, University of Waterloo, ⁴Department of Biology, Regis University

Habitat loss results in isolated fragments of tropical rainforest, and threatens forest-living species. In this study, we examined the influence of anthropogenic edge effects on female white-faced capuchin monkeys (*Cebus capucinus*) with and without infants to determine whether proximity to forest edge influences activity budget. We conducted this study in a fragmented rainforest at La Suerte Biological Research Station (LSBRS), Costa Rica in summer 2019, and collected instantaneous scan samples on individual female capuchins every 2 minutes. We predicted that females would not show significant differences in activity budget across edge and interior habitat zones. We also expected that females with infants would rest more and travel less than females without infants, as carrying infants and lactating are energetically costly behaviors. Based on previous findings, we further predicted that females with and without infants would feed for equal amounts of time. As expected, females showed no overall differences in activity budget between forest edge and interior. Females with and without infants showed significant differences in activity budgets, but not in the ways anticipated.

Throughout the site, females with infants fed less and rested more than females without infants. Our results are in line with published literature suggesting that female capuchins adjust their activity patterns to compensate for the energetic demands of infant care. Our results also support previous findings from LSBRS indicating capuchins do not show preference for forest edge or interior, further suggesting that proximity to forest edge has a neutral effect on female capuchin activity budgets.

Scent marking and reproductive competition in male woolly monkeys (*Lagothrix lagotricha poeppigii*)

EVELYN PAIN¹, ANDREAS KOENIG^{1,2}, AMY LU^{1,2} and ANTHONY DI FIORE³

¹Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, ²Department of Anthropology, Stony Brook University, ³Department of Anthropology, University of Texas at Austin

Scent marking is widespread throughout the primate order, but field studies on this behavior are rare. Several functions have been proposed for scent marking, with attracting/competing for mates receiving the most empirical support. We examined scent marking by male woolly monkeys (*Lagothrix lagotricha poeppigii*) to evaluate whether this behavior plays a role in reproductive competition. Data were collected at Tiputini, Ecuador, on 4 groups ($N=21$ males) over 10 months. We hypothesized that scent marking serves as a form of intra-sexual competition or inter-sexual advertisement within and between groups. We predicted that the timing of scent marking and sexual behavior would be correlated, that scent marking would be more frequent following intergroup encounters (IGEs), and that male size would be positively correlated with scent marking rates. We tested all predictions using GLMMs. We found a tendency for scent marking to occur more on days when sexual behavior was observed ($0.05 < p < 0.10$, 60.9% of days with sexual behavior versus 47.4% without), and for males to engage in sexual behaviors more frequently during focal samples when they scent marked ($0.05 < p < 0.10$, 26.1% of focal samples with scent marking versus 17.2% without). We found a relationship between male size and scent marking rates; however, contrary to our prediction, larger males scent marked less frequently than smaller males ($p < 0.01$). There was no effect of IGEs on scent marking ($p > 0.10$). Our results

ABSTRACTS

suggest that scent marking by males plays a role in within-group reproductive competition and may comprise part of an alternative reproductive tactic employed by smaller males.

Data collection was supported by the Leakey Foundation, Nacey Maggioncalda Foundation, National Science Foundation [BCS 1540403; BCS 1638822; BCS 1732326], Tinker Foundation, Stony Brook University, and University of Texas Austin

Gelada (*Theropithecus gelada*) contact calls vary by caller identity and behavioral state

MELISSA C. PAINTER¹, MORGAN L. GUSTISON², ELIZABETH TINSLEY JOHNSON³, ALIZA LE ROUX⁴ and THORE J. BERGMAN^{1,5}

¹Department of Psychology, University of Michigan, ²Department of Integrative Biology, University of Texas at Austin, ³Department of Integrative Biology, Michigan State University, ⁴Department of Zoology & Entomology, University of the Free State, ⁵Department of Ecology and Evolutionary Biology, University of Michigan

Close-range vocalizations, also referred to as contact calls, are some of the most frequently uttered nonhuman primate vocalizations. The acoustic structure of these calls can vary substantially, suggesting they may convey information. Here, we analyze two potential sources of acoustic variation in gelada (*Theropithecus gelada*) contact calls: caller identity and behavioral context in which the call is uttered. Analyses were based on seven measures of acoustic and temporal call parameters, and male and female calls were analyzed separately. Calls were significantly discriminable by caller in both females and males, according to discriminant function analyses and subsequent MANOVAs on the first two linear discriminants (females: $F(22, 142) = 5.764, p < .001$; males: $F(20, 130) = 6.363, p < .001$). Fundamental frequency measures were weighted heavily in the first discriminants, contributing to variation across individuals. To account for the identity signal in the subsequent analysis, call parameters were averaged for each individual in each behavioral context (foraging, moving, and socializing). These averages were significantly discriminable by context in both females and males (females: $F(4, 40) = 5.073, p = .002$; males: $F(4, 28) = 4.350, p = .007$). Peak frequency measures were weighted heavily in the first discriminants, contributing to variation across contexts. Results suggest gelada contact calls have the potential to convey information about caller identity and behavioral state, as previously shown for baboon contact calls. While geladas have an expanded vocal repertoire compared to baboons, their derived calls do not seem to come at the expense of meaningful variability in contact call structure.

Investigating Mortuary Patterns and Community Organization at the Late Iron Age site of Ban Pong Manao, Central Thailand

GINA PALEFSKY¹, CHIN-HSIN LIU² and KAEWSIRI DEVANWAROPAKORN³

¹Department of Anthropology and Heritage Studies, University of California, Merced, ²Department of Anthropology, California State University, Northridge, ³Faculty of Archaeology, Silpakorn University

This study investigates how mortuary practices may reflect aspects of skeletally embodied lived experiences at the late Iron Age site of Ban Pong Manao in central Thailand (c. 300-500 CE). Archaeological research in this region has identified changes in sociopolitical organization and social stratification thought, in part, to have resulted from an influx of non-local peoples, goods, and ideas fostered through intensified trade-related contact. These developments coincide with observed changes in mortuary traditions and associated grave good assemblages. It remains unclear whether these changes reflect the introduction of non-local peoples and/or burial traditions or are evidence of emergent social stratification.

We use paired radiogenic strontium and stable carbon and nitrogen isotope data of human tooth and bone from a subset of the mortuary sample ($n=12$) to ask whether differences in mortuary contexts (e.g., grave goods) reflect differences in day-to-day experiences during life. Despite variability in grave goods, all individuals analyzed in this study were locals with relatively homogenous radiogenic strontium isotope values (average $^{87}\text{Sr}/^{86}\text{Sr} = 0.70811 \pm 0.00014$). These individuals consumed diets that were similar to one another (average $\delta^{13}\text{C}_{\text{bone collagen}} = -12.81 \pm 2.16\text{‰}$; average $\delta^{15}\text{N}_{\text{bone collagen}} = 9.62 \pm 0.62\text{‰}$). We interpret these preliminary results as evidence that differences between mortuary contexts at Ban Pong Manao may not correspond with an individual's region of origin or dietary practices, but rather may reflect one or more aspects of lived experiences and/or social identity that will be explored in the context of ecological variability and trade.

Funded by the UC Merced Center for the Humanities, Arizona State University Center for Bioarchaeological Research, ACLS/Henry Luce Foundation Dissertation Fellowship, and the University of Florida Gibson Dissertation Writing Fellowship.

New data on the Plio-Pleistocene colobine fauna from the Shungura Formation (Omo Group deposits, Lower Omo Valley, Ethiopia): insights from the postcranial anatomy

LAURENT T.J. PALLAS¹, GUILLAUME DAVER¹, GILDAS MERCERON¹, LESLEA J. HLUSKO² and JEAN-RENAUD BOISSERIE^{1,3}

¹PALEVOPRIM: Laboratoire Paléontologie, Évolution, Paléoécosystèmes, Paléoprimatologie - UMR 7262, Université de Poitiers, ²Department of Integrative Biology, University of California, Berkeley, ³CFEE: Centre Français des Études Éthiopiennes - USR CNRS 3137, Ministère français de l'Europe et des Affaires étrangères (MEAE)

By recording a continuous, well calibrated temporal framework spanning roughly 2.9 million years, the Shungura Formation provides us with a unique window into the evolutionary history of vertebrates in eastern Africa. Particularly, it documents an abundant cercopithecoid fauna with a marked colobine taxic diversity. Yet, despite the high locomotor diversity documented hitherto for African Plio-Pleistocene colobines, no colobine postcranial material from Shungura has been published to date, leaving us with a paleoecological picture far from being complete.

We report here new postcranial materials ($n=36$) from small-, medium- and large-sized colobines. Using traditional morphometrics, we investigate the positional behaviors and locomotor substrate preferences of early colobines stemming from Shungura. We explore their niche partitioning and ecological dynamics based on two ecological proxies: body mass and locomotion. Within our fossil sample, we provide evidences for locomotor diversity based on joint morphologies consistent with arboreal-, mixed- and terrestrial locomotor substrate preferences. Our results also support leaping, climbing and suspensory behaviors as part of their locomotor positional repertoire. Distinct locomotor substrate preferences, positional behaviors and body masses are evidenced among synchronous early colobines specimens from members C, E & G, highlighting clear cases of niche partitioning. Our study hints at a drop in diversity between members G and L, with, in the latter member, a predominance of small specimens displaying arboreal locomotor substrate preferences only.

Our insights of the ecological dynamic of fossil colobines over a major period of climatic deterioration appears valuable in light of the current global warming and climatic deterioration.

ABSTRACTS

Evidence for multiple human lineages in China during the Middle Pleistocene: a premolar endostructural perspective

LEI PAN¹, JEAN DUMONCEL², ARNAUD MAZURIER³ and CLÉMENT ZANOLLI⁴

¹Paleoanthropology, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences, ²Laboratory AMIS, UMR 5288 CNRS, Université Toulouse III, ³UMR 7285 CNRS, Institut de Chimie des Milieux et Matériaux, Université de Poitiers, ⁴Laboratory PACEA, UMR 5199 CNRS, University of Bordeaux

With the incorporation of more fossil evidence, the co-existence of archaic ("*Homo erectus*-like") and derived ("modern-like") dental morphological patterns were highlighted in East Asian specimens spanning from the mid-Middle to early Late Pleistocene. The possible presence of multiple human lineages was suggested but not fully understood.

Using micro-CT techniques and a landmark-free geometric morphometric approach, we investigated premolar root structural organization and morphological variation of enamel-dentine junction (EDJ) of Chinese Middle Pleistocene hominins, and compared our results with a number of fossil and modern human groups.

Our analyses highlighted an evolutionary trend of premolar structure from the early Middle Pleistocene to recent times. For the root structure, we found an evolutionary trend of shape simplification along the *Homo* lineage examined here, and detected *erectus*-like signals in one late Middle Pleistocene specimen from China. For the EDJ morphology, we found a trend toward crown base reduction, symmetric occlusal EDJ outline and higher EDJ topography, but also observed different evolutionary trajectories of the EDJ shape in Asian fossil hominins. Moreover, this study brings insights into the taxonomy/phylogeny of a few late Middle Pleistocene specimens (generally categorized as "archaic *H. sapiens*") whose evolutionary placement was in debate. Considering the substantial differences, the morphological deviation between these samples cannot be simply interpreted as biogeographical variation of a single lineage. A scenario of geographical isolation, persistence of archaic lineages and possible admixture among populations during the late Middle Pleistocene is discussed.

Strategic Priority Research Program of CAS (XDB26000000), the National Natural Science Foundation of China (41702026, 41872030), the French Centre National de la Recherche Scientifique (CNRS).

History of being breastfed predicts decreased maternal-origin microchimerism in young women

TIFFANY D. PAN^{1,2}, SAMI B. KANAAN³, NANETTE R. LEE^{4,5}, JOSEPHINE L. AVILA^{4,6}, J LEE. NELSON^{3,7} and DAN TA. EISENBERG^{1,2}

¹Department of Anthropology, University of Washington, ²Center for Studies in Demography and Ecology, University of Washington, ³Clinical Research Division, Fred Hutchinson Cancer Research Center, ⁴USC-Office of Population Studies Foundation, Inc., ⁵Department of Sociology, Anthropology & History, University of San Carlos, ⁶Department of Architecture, University of San Carlos, ⁷Department of Medicine, University of Washington

Microchimerism (Mc) is the presence of a small quantity of cells or DNA from a genetically distinct individual. This phenomenon occurs naturally with bidirectional maternal-fetal exchange during pregnancy, and Mc can persist for decades after delivery. Biomedical researchers have found associations between Mc and both positive and negative immunological outcomes of clinical importance, such as autoimmune disorders, infectious diseases, tissue transplantation outcomes, and reproduction. However, little is known about why Mc is detectable at varying levels in different individuals. We examined potential determinants of maternal-origin Mc (MMc) in young adult women in the Philippines: gestational age at participant's delivery (in utero exposure to MMc), history of being breastfed or not (post-partum exposure to MMc), maternal telomere length (maternal cells' ability to replicate and persist in the study participant), and participant's parity (fetal-origin Mc's effect on microchimeric milieu). Bivariate negative binomial regression models evaluating each predictor separately suggest that MMc decreases with increased gestation duration, among breastfed participants, and with increased maternal telomere length. When we included all predictors in a multivariate model, only history of being breastfed remained a significant predictor of decreased MMc (detection rate ratio=0.15, p=0.007). Our results diverge from experimental findings in mice of breastmilk-derived MMc and human organ transplantation studies that showed increased immune tolerance of maternal grafts with history of being breastfed. MMc persistence or detectability may also fluctuate throughout life or differ by cell type and function.

This research is partially supported by the National Institute of Health [R01HL117737, P2CHD042828, T32HD007543], the National Science Foundation [BA-DDRIG1751388, BCS-DDIG0962282, BCS1519110], and the Wenner-Gren Foundation [Dissertation Fieldwork Grants 9662, 8111].

Bioarchaeology of violence and medieval monasteries in Central Europe

ANNA PANKOWSKÁ¹, PATRIK GALETA¹, PETRA UHLÁK SPĚVÁČKOVÁ² and KAREL NOVÁČEK³

¹Department of Anthropology, University of West Bohemia in Pilsen, ²Department of Dentistry, University Hospital and Faculty of Medicine in Pilsen, Charles University in Prague, ³Department of History, Palacký University Olomouc

Violence in European medieval monasteries has been poorly investigated by bioarchaeologists. A sample of 30 human skeletons from Teplá monastery (Czech Republic) dated to the High Middle Ages offers a unique possibility to study direct evidence of violence through the analysis of trauma. The aim of this study is to investigate the defensive function of medieval monasteries. We studied skeletal markers of violence to identify the group of individuals who might have been involved in the monastery defense. To differentiate trauma caused by interpersonal violence from trauma resulting from accidents, we adapted the criteria outlined in the Istanbul Protocol and its form modified for bioarchaeological investigation. The results of the analysis reveal that 69% (13 out of 30) of the individuals were confidently confronted with violence and all of them were males. The majority of injuries were classified as sharp force trauma. There were more individuals with ante-mortem than perimortem injuries. The true prevalence of ante-mortem injuries confidently associated with violence was 20% which indicates that some of those males had previous combat experience and were successfully treated. All individuals were buried with dignity and respect in front of the western gate of the Abbey Church. The most probable explanation of our findings is that the analyzed individuals were a group of clients who were tasked with the defense of Teplá monastery.

The occurrence of 'pelvic patterns' in female skeletons with parity information

DORIS PANY-KUCERA^{1,2}, MICHAELA SPANNAGL-STEINER^{1,2} and KATHARINA REBAY-SALISBURY¹

¹OREA, Austrian Academy of Sciences, ²Department of Anthropology, Natural History Museum Vienna, Austria

Aiming to link reproductive and social status of women in prehistoric times, we recorded a set of pelvic features that may arise from the context of past pregnancies and births. A combination of two or more pronounced feature expressions is termed a 'pelvic pattern'. Classic features such as the preauricular sulcus, margo auricularis groove, dorsal pubic pitting, and ventral pubic lesions were assessed in combination with the newly described sacral preauricular extension (SPE), sacral preauricular notch (SPN) and corresponding facets at the ilium.

ABSTRACTS

We developed a summary formula which calculates a value from the weighting for each single assessed feature (w_i) the assessability (a_i) and the ratio of the single expression degree (x_i) to the maximal possible expression degree (y_i). The formula was now tested on a subsample of female skeletons from the Simon collection (Geneva) with parity information ($n = 28$, 10 nullipara, 18 uni- or multipara, for which all features were assessable).

Nulli- and unipara do not show combinations of more than two marked features. The number of combinations of pronounced pelvic features increases in female individuals who had two or more children. The highest values correlate with a parity record of two or more children, and were found in women with feature combinations including the SPE or SPN. Based on this, the presence of a pelvic pattern may indicate past parity, especially when SPE or SPN are present. This study was undertaken in the framework of the ERC-funded project 'The value of mothers to society'.

This project has received funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme under grant agreement No 676828.

A genetic analysis of male reproductive skew among ring-tailed lemurs (*Lemur catta*) from Bezà Mahafaly, Madagascar

JOYCE A. PARGA¹, MICHELLE L. SAUTHER², FRANK P. CUOZZO³, RICHARD R. LAWLER⁴, LISA GOULD⁵ and JENNIFER PASTORINI^{6,7}

¹Anthropology, California State University, Los Angeles, ²Anthropology, University of Colorado, Boulder, ³Lajuma Research Centre, South Africa, ⁴Sociology and Anthropology, James Madison University, ⁵Anthropology, University of Victoria, Canada, ⁶Anthropologisches Institut, Universität Zürich, Switzerland, ⁷Centre for Conservation and Research, Sri Lanka

In many species, males attempt to monopolize matings, and if monopolization is successful, male reproductive skew may be high. Conversely, if many males mate, low reproductive skew (multiple sires) may result. In the ring-tailed lemur, estrous females mate with several males, which is suggestive of low paternity skew; however, our previous analysis of ring-tailed lemurs from Bezà Mahafaly, Madagascar (Parga et al., 2016) found a wide range of skew indices in different lemur groups. Here we present a broader analysis to determine whether high or low male reproductive skew is more common in this population, and we investigate how male age is related to reproduction. We analyzed genotypic data on an additional 44 infants from this population using a panel of 8 microsatellite loci. Parentage was determined with 80-95% confidence, and Nonacs' B skew index was calculated per group. Results showed that for most groups, low skew was the norm. Moreover, male reproductive skew at the

population level was low ($B=0.018$, $p=0.01$). Lastly, older males showed decreased reproductive success. Only 14% of old males reproduced, while 29% of prime-aged males produced infants. Five males remained in the population long enough to progress into old age; although one male never reproduced, 4 males who produced infants in their prime years sired no infants as old males. Our results demonstrate that many males share reproduction in this species both within groups and at the population level. Our data also add to the growing literature on the decreased reproductive potential of senescent individuals.

Funded by the National Science Foundation (BCS 0922465), Leakey Foundation, National Geographic Society, Wenner-Gren Foundation, NSERC, Swiss National Science Foundation, Vontobel Foundation, Julius Klaus Foundation, and A.H. Schultz Foundation.

Changing Femoral Robusticity Between Medieval and Early Modern Denmark

KAELA PARKER

Anthropology, University of Manitoba

The aim of this poster is to explore the transition in femoral strength and rigidity in medieval and early modern Denmark. Using two samples, the cemetery of Tirup (1150-1350 CE) and the Black Friars cemetery (1240-1607 CE), the cross-sectional geometric properties of the right femora were examined. Cortical areas (measures of compressive and tensile rigidity and strength), second moments of area (measures of maximum and minimum bending rigidity), polar second moments of area (measures of torsional rigidity), section moduli (measures of maximum and minimum bending strength), and polar section moduli (measures of torsional strength) were calculated from 212 CT scans. The geometric properties of the femora were examined at five locations along the femoral shaft (20%, 35%, 50%, 65%, and 80%) as well as at Ward's triangle in the femoral neck in order to compare bone strength and rigidity between the medieval and early modern periods. Results indicate that male robusticity remained relatively consistent through time (although strength and rigidity increased significantly in the femoral neck). For females, a significant temporal increase in strength and rigidity ($p<0.05$) was noted along the femoral shaft and neck. In fact, when male and female robusticity was compared the distinction seen in the medieval period is obscured and female femoral strength and rigidity is nearly equivalent to that seen among the males in the early modern period. Results are discussed in the context of changing socio-economic conditions which worsened in the early modern period in Denmark.

This research was supported by SSHRC - SSHRC Doctoral Fellowship (K. Parker - #752-2018-2041) and SSHRC Insight Grant (R. Hoppa - #435-2017-729).

The Impact of Forensic Anthropology in Undergraduate Anthropology Programs

NICHOLAS V. PASSALACQUA¹, SEAN MULLHOLLAND², MARIN A. PILLOUD³ and ALEXANDRA KLALES⁴

¹Anthropology and Sociology, Western Carolina University, ²Department of Economics, Management, and Project Management, Western Carolina University, ³Anthropology Department, University of Nevada, Reno, ⁴Forensic Anthropology Program, Washburn University

Anecdotally, it has been suggested that undergraduate anthropology students are more interested in forensic anthropology than any other specialty, but that forensic anthropologists are less-desired as colleagues in academia due to the nature of their work. The goal of this project was to examine these two related questions: (1) does having a forensic anthropologist, or an undergraduate concentration in forensic anthropology, increase the number of majors in anthropology programs? And (2) are forensic anthropologists less likely to be hired for relevant biological anthropology academic positions? To address these questions, the following data were analyzed: number of degrees in anthropology, by U.S. institutions (from the National Center for Education Statistics); number of forensic anthropology and anthropology majors at institutions with forensic anthropology concentrations; number of forensic anthropology job postings per year (from the Bioanth job wiki pages); and number of forensic anthropologists hired for those jobs.

Results found that programs with a forensic anthropology concentration saw large increases in the overall number of anthropology majors, contrary to the national trend of declining anthropology degrees. Programs that hired a forensic anthropologist also saw increases in the overall number of anthropology majors; however, to a smaller and varied extent. For academic jobs specifically desiring a forensic anthropologist, forensic anthropologists were hired in only 58% of postings (no failed searches were included). This study shows a reluctance to hire forensic anthropologists in academia, despite their positive impact on the growth of anthropology programs; it also has implications for the education of future forensic anthropologists.

Morphological and experimental evidence for the functional differentiation between the hands and feet in primates: predicted and unexpected findings

BIREN A. PATEL

Integrative Anatomical Sciences, University of Southern California, Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California

Force plate studies investigating primate quadrupedal mechanics consistently demonstrate that most taxa experience lower peak vertical forces

ABSTRACTS

on their forelimbs than on their hindlimbs. This functional differentiation in habitual limb loading is reflected in the structural properties of the mid-diaphysis of the humerus and femur, with the latter tending to be more robust. These findings support the hypothesis that long bone diaphyses respond to their habitual external loading history. The current study tests this hypothesis further by investigating robusticity differences between metacarpals (Mc) and metatarsals (Mt) of anthropoids with published quadrupedal force plate data: *Pan*, *Pongo*, *Miopithecus*, *Chlorocebus*, *Erythrocebus*, *Macaca*, *Papio*, *Ateles*, *Sapajus*, *Cebus*, *Aotus*, *Saimiri*, *Callithrix*. From μ CT scans, polar second moment of area was measured in the Mc2-5s and Mt2-5s. As predicted, monkey Mt2-5s are more robust than their Mc2-5s, supporting the hypothesis that there is a relationship between bone strength and habitual loads between limb pairs during quadrupedalism. In *Pan* and *Pongo*, however, Mc2-5s are either equal in strength or stronger than their Mt2-5s. *Pongo* may need relatively stronger metacarpals because of their greater emphasis on below-branch behaviors. *Pan* may also need relatively stronger metacarpals because of forelimb suspension, but also because their weight is supported by smaller surface areas when using a knuckle-walking posture. The latter could result in greater stresses in the hand than the foot, despite absolute magnitudes of forces being higher in the latter during quadrupedalism. Thus, relative strength properties of primate metapodials are a result of both an animal's kinetics and kinematics.

Funded by the National Science Foundation (BCS-1317047; BCS-1317029; BCS-1539741).

Effects of early life adversity and novel foraging circumstances on maternal behavior

SAM K. PATTERSON¹, SHIRLEY C. STRUM^{2,3} and JOAN B. SILK¹

¹School of Human Evolution and Social Change, Arizona State University, ²Department of Anthropology, University of California, San Diego, ³Uaso Ngiri Baboon Project, Kenya

Baboon mothers' early life experiences exert important effects on their development, longevity, sociability, and survivability of their offspring. It is unknown how early life experiences influence maternal behaviors. We investigate this in 46 mother-infant pairs of olive baboons from Laikipia, Kenya. We examined nursing rates, carrying rates, count of approaches to infant, and count of nipple rejections. Using long-term data from the Uaso Ngiri Baboon Project, we constructed an adversity index based on the sum of five binary measures from mothers' early life: droughts, intense mobbing, early loss of mother, birth of a competing sibling, and group size. *Opuntia stricta* is an invasive cactus that has been spreading through the study area and its fruit has become

an important component of the baboons' diet. We scored mothers based on whether this novel fruit was present at their birth. Using mixed MCMC models, we found that mothers with greater adversity carried their infants at higher rates than mothers with less adversity. For nursing rates, there was an interaction between *O. stricta*, adversity, and age. Without access to *O. stricta*, greater adversity was associated with higher nursing rates. Presence of *O. stricta* at birth was associated with higher nursing rates. Mothers with greater adversity approached their infants less than other mothers. No substantial differences were found for maternal nipple rejections. These results suggest early life experiences can have lasting consequences on maternal behavior and these behaviors may function as one proximate mechanism for intergenerational effects of maternal experience.

Funding provided by the National Science Foundation, the Leakey Foundation, the National Science Foundation Graduate Research Fellowship, and SHESC and IHO at Arizona State University.

Incorporating insights from dental quantitative genetics into studies of past biological variation in the Americas

KATHLEEN S. PAUL¹, CHRISTOPHER M. STOJANOWSKI² and G. RICHARD SCOTT³

¹Department of Anthropology, University of Arkansas, ²School of Human Evolution and Social Change, Arizona State University, ³Department of Anthropology, University of Nevada Reno

Dental morphology has long provided insight into human population histories and global-scale migrations. In these efforts, expression frequencies are assumed to approximate population-level genetic variation. Recent quantitative genetic studies have provided theoretical ground-truthing for this approach and have referenced narrow-sense heritability estimates to prescribe analytical "best practices" for dental biodistance research (Stojanowski et al., 2018, 2019). We apply these insights to a study of past biological variation in the Americas using bioarchaeological crown and root data amassed by the late Christy Turner II. These 15 composite datasets represent regional populations across North, Central, and South America. Data were subjected to multiple proximity (Bray-Curtis) and agglomerative hierarchical clustering (unweighted pair-group mean) analyses to assess biological structure across the Americas. Each analysis altered sample composition to accommodate insights from quantitative genetics related to: a) use of crown versus root traits, b) designation of presence/absence breakpoints for sample frequency calculation, and c) trait weighting based on narrow-sense heritability estimates. Preliminary results based on "best fit" truncation indicate anywhere from three to six major bioregional clusters, with the number varying based on data treatment. Consistent to all

simulations was the primary branching of Bering Strait and Aleutian Islands/Alaskan Peninsula samples on cluster dendrograms, with one exception: the analysis using heritability-weighted crown traits. Results indicate robusticity of several population relationships but also highlight the sensitivity of dental morphology data to analytical treatment. Further quantitative genetic work with representative samples may increase the resolution of dental biodistance research in the Americas and globally.

NSF BCS-1063942, NSF BCS-1750089; IRB ASU Exemption 45CFR46 (4)

Using 3D Modelling to Tell Individual Stories from the American Civil War

KRISTEN E. PEARLSTEIN¹, TERRIE SIMMONS-EHRHARDT², BERNARD K. MEANS³, BRIAN F. SPATOLA¹, ANGI M. CHRISTENSEN⁴, RICHARD M. THOMAS² and MARY R. MANI⁴

¹Anatomical Division, National Museum of Health and Medicine, ²Forensic Science, Virginia Commonwealth University, ³Anthropology, Virginia Commonwealth University, ⁴Laboratory, Federal Bureau of Investigation

The Anatomical collections at the National Museum of Health and Medicine (NMHM) contain skeletal specimens that highlight the history of military and civilian medicine dating from the American Civil War and the founding of the museum in 1862. NMHM curates over 2,000 skeletal specimens from the Civil War consisting primarily of single bone elements that display a variety of pathological conditions including battlefield trauma, bacterial infection, and amputation. The NMHM is collaborating with Virginia Commonwealth University and the Federal Bureau of Investigation Laboratory to digitize and disseminate high-quality 3D models via online portals, enabling scholars and educators to manipulate, analyze, and 3D print the models from anywhere in the world. Manipulation of the digital models allows researchers the opportunity to study aspects of bone healing and response to disease in submillimeter detail. Micro-computed tomography (micro-CT) scanning and digital model manipulation of elements from the Civil War has revealed skeletal responses that are not macroscopically visible. The ability of micro-CT analysis to reveal the internal bone structures has aided in the interpretation of experiences of individual soldiers. For example, bullet debris, hair-line fractures, and punctured neural canals which were not previously observed can now be visualized. This project presents a number of Civil War cases where micro-CT analysis revealed internal data that were not externally visible, but may have contributed to soldiers' documented post-trauma

ABSTRACTS

(post-surgical) experiences. The sharing of these military medical assets improves historical knowledge and diagnostic capabilities in the fields of medicine and anthropology.

Modern human sulcal pattern variation and asymmetry on the external surface of the temporal lobe

ALANNAH PEARSON¹, P. DAVID POLLY² and EMILIANO BRUNER³

¹School of Archaeology and Anthropology, Australian National University, ²Department of Earth and Atmospheric Sciences, Indiana University, Bloomington, ³Paleoneurobiology of Hominins, Centro Nacional de Investigación sobre la Evolución Humana

Cerebral folding patterns include sulci and gyri visible on the external surface of the brain. Although paleoneurologists rely on sulcal imprints preserved on the endocranial surface for inferences in fossil species, the specific mechanisms behind sulcal formation remain unknown, but axonal-neuronal tensioning, genetic factors and biomechanical pressures of cerebral constraint-expansion have been proposed. Temporal lobe sulcal variation in extant *Homo sapiens* is considered high but quantification is lacking. We used a sample of 21 adult individuals (male = 10, female = 11) from T1-weighted *in vivo* Magnetic Resonance Imaging (MRI) of the brain, to generate 3D virtual mesh and identify lateral sulcal variants for the posterior rami of the Sylvian fissure and two segments of the superior temporal sulcus on the external surface of the left (L) and right (R) temporal lobes. The posterior ascending ramus of the Sylvian fissure had a higher prevalence of sulcal variants in the left than right lobes (L = 7: R = 4), with the posterior descending ramus of the Sylvian fissure having equal variants (L = 4: R = 4). The ascending segment of the superior temporal sulcus had higher prevalence of variants in left rather than right lobe (L = 6: R = 5), while the posterior segment of the superior temporal sulcus had more variants in the right than left lobes (L = 5: R = 6). These findings indicate external temporal lobe sulcal patterns in extant *Homo sapiens* are asymmetric with high variation relevant for inferences in fossil *Homo*.

A.P. was funded by the Australian Government Research Training Program Scholarship and E.B. funded by the Spanish Government (#PGC2018-093925-B-C31).

Teasing apart function and phylogeny in the human upper limb

OSBJORN M. PEARSON and ETHAN C. HILL
Department of Anthropology, University of New Mexico

A generally tacit assumption of functional studies of hominin limb bones is that phylogeny plays a minor, if any, role in functional adaptations. Thus, diaphyseal shapes and sizes serve as pure

reflections of function, allowing patterns of activity to be read without complication. However, bones are complex. Many physiological factors, including genotype or differences in methylation, potentially affect responsiveness of bone to mechanical stimuli. In this study, we seek an approximate answer for how strongly phylogeny confounds such interpretations in Neandertals and recent humans. To assess this problem, we collected data on midshaft shape and external robusticity (maximum + minimum diameters divided by length) for the humerus, radius, and ulna of the skeletons of 29 groups, split by sex, and including Neandertals, Skhul-Qafzeh, and Gravettians (total $n = 444$). A canonical variates analysis (CVA) on the data showed variation in robusticity drives the main pattern, contrasting robust populations, generally from high latitudes, against less robust populations from warmer areas. Midshaft shapes exert less influence. Neandertals and other Pleistocene foragers generally fall among ecogeographically similar recent samples on axis 1 (40.5% of the variance) but low on axis 2 (33.2% of the variance), reflecting the fact that they have a robust humerus relative to their forearm bones. These patterns are largely unaffected by phylogenetic similarity. Divisions of the data by lifestyle, climate, and sample explain 9.2%, 27.0%, and 43.2% of the overall variance, respectively.

Supported by the Wenner-Gren Foundation, a National Science Foundation Graduate Fellowship, the Boise Foundation, and the University of New Mexico.

A Closer Look at the Spatial Distribution of Hominin Fossils at Pin 8, Hill Antechamber, Rising Star Cave

BECCA PEIXOTTO^{1,2}, MARINA C. ELLIOTT², JOHN HAWKS^{2,3} and LEE R. BERGER²

¹Center for the Exploration of the Human Journey, Perot Museum of Nature and Science, ²Evolutionary Studies Institute, University of the Witwatersrand, ³Department of Anthropology, University of Wisconsin-Madison

Following the initial 2013 discovery of hominin fossils in the Rising Star Cave system in Cradle of Humankind, South Africa, excavations focused on an area within a ~5 x 8 m chamber subsequently named Dinaledi Chamber. While the majority of fossil material recovered in 2013 was from this chamber, scattered skeletal remains were collected from the surface approximately 12 m away in an area identified in field notes as "Pin 8". Now considered part of the Hill Antechamber, recent excavations near Pin 8 have recovered additional hominin material. Some advanced mapping technologies are not feasible within the confined spaces in of the cave system. All specimens are piece-plotted on an arbitrary grid established in the Dinaledi Subsystem, and other mapping approaches are applied in specific contexts. Here, we evaluate the efficacy of using open source GIS, including QGIS and tools within

that package, to map the fossils in 3 dimensions within this spatially distinct area of the Dinaledi Subsystem. This offers an expedient method for initial visualization of the spatial relationship of specimens and for communicating those results with other members of the research team who cannot access the space themselves.

National Geographic Society, Lyda Hill Foundation, University of the Witwatersrand, South African Centre of Excellence in the Palaeosciences, and the South African National Research Foundation

Biological Distance Analysis of Medieval Hungarian Populations: The Influence of the Migration and Hungarian Conquest Periods on Dental Morphology

ROSE L. PERASH¹, SÁNDOR ÉVINGER², TAMÁS HAJDU³, TAMÁS SZENICZEY³ and G. RICHARD SCOTT¹

¹Anthropology, University of Nevada, Reno, ²Anthropology, Hungarian Natural History Museum, ³Biological Anthropology, Eötvös Loránd University

In comparison to surrounding Central European populations, the Medieval Period in the Carpathian Basin has been marked by successive major peopling events from Eurasian steppe populations. The Avar (568-822 AD), Magyar (895-970 AD), and árpád (1000-1301 AD) periods represent phases of united rule in this region, but are underrepresented in systematic bioarchaeological analyses. This study asks what kind of biological heterogeneity can be revealed across these samples and to what extent these migratory events are represented by dental morphology. Tooth crown and root traits were scored using the Turner-Scott system for Avar ($n = 83$), Magyar ($n = 29$), and árpád ($n = 226$) era samples. Missing values were estimated using K nearest-neighbor imputation, and correlated or underrepresented variables were removed. Pooled temporal analysis using Mahalanobis D^2 revealed close biological affinities, demonstrating that these cultural phases do not easily map onto distinct biological groupings. While Medieval Hungary is traditionally portrayed as a dynamic period of mass population changes, preliminary analysis of the dental anthropological record suggests otherwise. Biological continuity may be underrepresented in current literature and dental morphology can elucidate this population history when used in collaboration with cranial and genetic evidence. Future studies will explore the connection between these biological markers, as well as the impact of local populations in the Carpathian Basin through a combined spatial-temporal analysis.

ABSTRACTS

Predicting descent locomotion in early primates based on morphology and behavioral observations of extant taxa

BERNADETTE A. PERCHALSKI^{1,2}, MADISON BRADLEY² and DOUG M. BOYER²

¹Basic Medical Sciences, University of Arizona College of Medicine Phoenix, ²Evolutionary Anthropology, Duke University

Headfirst progression allows animals to anticipate discontinuous paths and adjust navigation while maintaining visual contact with target resources. During their evolution, primates may have lost the ability to descend tree trunks headfirst via interlocking due to claw loss. To assess the link between morphology and locomotion, we constructed a Bayesian Model using extant behavioral observations collected in an experimental setting from nine strepsirrhine species moving on narrow supports oriented between horizontal and vertical in fifteen-degree increments. Descent style (headfirst or not) was recorded for 3139 bouts and modeled as a Bernoulli-distributed outcome of a series of multilevel models that incorporated effects of experimental support orientation and diameter, intermembral index (IMI), intrinsic foot and ankle proportions, mass and age. The best-fit model describing descent patterns in the experimental sample was used to predict narrow branch descent behavior in extant and extinct euarchontans. The treeshrew *Ptilocercus* was predicted as more likely to use headfirst descent than *Tupaia*, probably due to longer metatarsals, shorter hallux, and shorter phalanges in the latter. The basal haplorrhine *Archicebus* was predicted to use headfirst descent less frequently than living tarsiers, probably also due to longer metatarsals, shorter phalanges and low IMI. Larger adaptations *Darwinius* and *Notharctus* were similar in predicted locomotion to extant *Eulemur* species, which were experimentally observed to abandon headfirst descent on supports of 60° and steeper. The timing of claw loss during primate evolution would likely have had different impact on the ability to descend headfirst in a *Ptilocercus*-like ancestor compared to a *Archicebus*-like ancestor.

Funding for this research was provided by the Duke Lemur Center Director's Fund and the National Science Foundation (NSF BSC 1751686).

Seasonal variation in energy balance in wild male geladas

RACHEL F. PERLMAN¹, JACINTA C. BEEHNER^{2,3}, ANDREAS KOENIG^{1,4} and AMY LU^{1,4}

¹Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, ²Department of Psychology, University of Michigan, ³Department of Anthropology, University of Michigan, ⁴Department of Anthropology, Stony Brook University

The effects of food availability and environmental stress on reproduction are well-known for primate females but remain remarkably understudied in

males. However, males face comparable energetic challenges that may ultimately influence reproductive success. Here, we examined how seasonal changes in rainfall and temperature were associated with energy balance (measured via urinary C-Peptide) in 39 wild male geladas (*Theropithecus gelada*) from the Simien Mountains National Park, Ethiopia, across a 13-month period. The gelada social system comprises dominant leader males with reproductive units (N=20) and bachelor males that cannot mate until they take over a unit (N=19). Using rainfall as a proxy for food availability and low temperatures as a proxy for thermoregulatory demands, we predicted that rainfall and temperature would be positively associated with energy balance. First, contrary to expectations, low rainfall and low temperatures were followed by *higher* energy balance for all males (P<0.001). High energy balance during the driest and coldest months of the year is associated with a dietary switch from aboveground grass to underground plant parts, potentially indicating a nutritional advantage to such foods. Second, leaders exhibited lower energy balance than bachelors during the annual 'takeover season', which coincides with the driest months (P<0.001), and perhaps explains why bachelors are successful at takeovers during this time of the year. Future work investigating food nutritional composition and seasonal variation in above- vs. below-ground foraging should help clarify these patterns and elucidate how bachelors maintain relatively better energy balance during the 'takeover season'.

Support was provided by the National Science Foundation (DDRIG BCS-1732231; BCS-1723228; BCS-0715179; IOS-1255974), National Geographic Society (8100-06; 8989-11), Leakey Foundation, International Primatological Society, Nacey Maggioncalda Foundation, and Sigma Xi.

Surprising direction of evolutionary changes associated with hunter-gatherer and agriculturalist immunological differences

GEORGE PERRY¹, GENELLE HARRISON^{2,3}, JOAQUIN SANZ^{3,4}, JONATHAN BOULAIS^{3,4}, MICHAEL MINA^{5,6}, JEAN-CHRISTOPHE GRENIER³, YUMEI LENG⁵, ANNE DUMAINE³, VANIA YOTOVA³, CHRISTINA BERGEY¹, SAMUEL NSOBYA⁷, STEPHEN ELLEDGE⁸, ERWIN SCHURR², LLUIS QUINTANA-MURCI⁸ and LUIS BARREIRO⁹

¹Departments of Anthropology and Biology, Penn State University, ²Department of Human Genetics, McGill University, ³Department of Human Genetics, CHU Sainte-Justine Research Center, ⁴Department of Biochemistry, University of Montreal, ⁵Department of Pathology, Brigham & Women's Hospital, ⁶Department of Genetics, Harvard Medical School, ⁷Department of Pathology, Makerere University, ⁸Unit of Human Evolutionary Genetics, Institut Pasteur, ⁹Department of Medicine, University of Chicago

The shift from a hunter-gatherer to an agricultural mode of subsistence is believed to have been associated with profound changes in the burden and diversity of pathogens across human populations. Yet, the extent to which the advent of agriculture affected the evolution of the human immune system remains unknown. Here we present a comparative study of variation in the transcriptional responses of peripheral blood mononuclear cells to bacterial and viral stimuli between Batwa rainforest hunter-gatherers and Bakiga agriculturalists from Uganda. We observed increased divergence between hunter-gatherers and agriculturalists in the early transcriptional response to viruses compared with that for bacterial stimuli. We demonstrate that a significant fraction of these transcriptional differences are under genetic control and we show that positive natural selection has helped to shape population differences in immune regulation. Across the set of genetic variants underlying inter-population immune-response differences, however, the signatures of positive selection were disproportionately observed in the rainforest hunter-gatherers. This result is counter to expectations on the basis of the popularized notion that shifts in pathogen exposure due to the advent of agriculture imposed radically heightened selective pressures in agriculturalist populations. Specifically, the theorized agriculture-associated increases in pathogen load and commensurate immune system adaptation – if they did occur – were not so great (at least for these populations) to have overwhelmed a longer-term pattern of stronger positive selection on these traits in hunter-gatherers.

NIH grant R01-GM115656 (to G.P. and L.B.)

Incremental Dental Collagen Isotope Analysis and Reconstructing Childhood Diet at an 18th-19th Century Land-Owning Family in North Carolina

MEGAN A. PERRY¹, CORRINE TAYLOR¹ and ROBERT H. TYKOT²

¹Department of Anthropology, East Carolina University, ²Department of Anthropology, University of South Florida

Breastfeeding and weaning practices can impact a child's immune system development and nutritional status and cause long-term health effects. Here we explore the potential relationship between the weaning process and childhood frailty in a late 18th and early 19th century land-owning family in coastal North Carolina. The 10 individuals recovered from the Gause family cemetery in 2017 and 2018 includes 6 children under the age of 8. Incremental $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of dentin collagen of 13 teeth along with 10 bone samples provide a record of dietary and trophic level shifts that occurred during the weaning and post-weaning periods. The incremental dentin indicated that the weaning process ceased by 2 years of age, and breastmilk

ABSTRACTS

was supplemented by C₄ sources, likely maize products, while adult diets had a stronger signature from marine and C₃ sources. Comparing the timing of weaning in addition to the composition of solid foods used to supplement breastmilk between subadult and adult individuals found only slight differences in their childhood diets and weaning practices, indicating these factors are not linked to childhood mortality in this sample. However, an offset between co-forming bone and dentin δ¹⁵N in those dying as children were suffering from physiological stress. Overall, this evidence will identify the weaning practices and dietary supplementation of “elite” land-owning families in the Lower Cape Fear region and their potential impact on population frailty.

Life histories of white-faced capuchin monkeys (*Cebus capucinus*) at Lomas Barbudal Biological Reserve, Costa Rica: Aspects relevant to the evolution of learning strategies

SUSAN E. PERRY^{1,2} and IRENE GODOY³

¹Anthropology, University of California-Los Angeles, ²Behavior, Evolution and Culture Program, University of California-Los Angeles, ³Animal Behaviour, Universität Bielefeld

The life histories of white-faced capuchins are particularly interesting due to evolutionary convergences between capuchins and humans regarding encephalization, longevity, length of the juvenile phase, alloparenting, and social learning propensities. Here we describe some of the features of capuchin demography relevant to an evolved relationship between life history and learning strategies. For humans, it has been hypothesized that grandparents are special repositories of knowledge, enabling social transmission of rarely used or difficult skills. Many capuchins co-reside with grandparents: In a sample of 202 genotyped 2-year-olds, 48% co-resided with a maternal grandmother, 15% with a maternal grandfather, 6% with a paternal grandmother, and 1.5% with a paternal grandfather. Alloparenting may offer sex-differentiated social learning opportunities. At age 5-8 months, when alloparents are of peak importance, males spent 12.5% of their time dorsal on male alloparents and 5.2% on female alloparents, whereas same-aged females spent 1.8% of time on male alloparents and 10.5% of their time on female alloparents. Co-residence with fathers and grandfathers may indirectly influence the stability of the group (defending it from potentially infanticidal immigrant males), thereby increasing the number of models from which developing individuals could learn. Among 5-year-olds, individuals co-residing with a father or grandfather lived in groups that were larger and contained more immatures, compared to

individuals not co-residing with a father or grandfather (group size: mean=26.7±0.7 vs. 22.6±0.7, t=-4.1, P=0.0001; immatures: 12.9±0.3 vs. 10.7±0.4, t=-4.3, P<0.0001).

NSF (1638428, 0613226, 848360, 1232371, 9633991, 9870429), NGS (6 grants), Leakey (9 grants), Templeton World Charity Foundation (1 grant), Wenner-Gren (2 grants), ISHE, Wild Capuchin Foundation, MPI-EVAN, UCLA, Univ. Michigan

Bounding Middle Period cemetery use in San Pedro de Atacama, Chile

WILLIAM J. PESTLE¹, MARK HUBBE^{2,3} and CHRISTINA TORRES-ROUFF^{3,4}

¹Anthropology, University of Miami, ²Anthropology, The Ohio State University, ³Instituto de Arqueología y Antropología, Universidad Católica del Norte, San Pedro de Atacama, Chile, ⁴Anthropology and Heritage Studies, University of California, Merced

The San Pedro de Atacama oases, located in northern Chile's hyperarid Atacama Desert, have been occupied for over 2500 years. Since the initial settlements, local social developments have been influenced by engagement in regional systems of exchange and periods of intense interaction with complex polities, both of which have affected local patterns of diet and health. Here, we examine cemetery use in the oases across time, with emphasis on cemeteries active during the Middle Period (ca. AD 400-1000), a time associated with the establishment of formalized social inequality. We explore cemetery use and burial practices through analysis of a large corpus (n=248) of direct (human bone collagen) AMS assays, which form part of a larger bioarchaeological dataset being used to assess patterns and experiences of social inequality on an individual scale during the Middle Period.

At the extremes of their calibrated 95% confidence intervals, the dated burials were found to span nearly fifteen centuries, from 80-1420 calAD. The three oases that form the core of the putatively Middle Period sample (Coyo, Qitor, and Solcor; n=187) attest to a concentration of cemetery activity in the second half of the Middle Period, from roughly 650-1000 calAD, as well as continued cemetery use in the subsequent Late Intermediate Period. These data permit us to propose a later initiation of the most pronounced activities associated with the Middle Period in the Atacama oases, allowing us to better contextualize discussions of diet, health, and violence between cemeteries and within this population during this dynamic period.

This material is based upon work supported by the National Science Foundation under Grants Nos. BCS-1358753 and BCS-1359644.

Strategies for presenting human origins science for middle- and high-school students and teachers

AMY L. PETERSON^{1,2}, IRENE E. SMAIL^{1,2}, E. SUSANNE DALY^{1,2}, ALEJANDRA ORTIZ³ and HALLIE EDMONDS⁴

¹Institute of Human Origins, Arizona State University, ²School of Human Evolution and Social Change, Arizona State University, ³Department of Anthropology, New York University, ⁴Center for Evolution and Medicine, Arizona State University

In recent decades the quality of K-12 science education, and how it applies to human origins, has deteriorated. A major barrier to improving this educational quality is the lack of sufficient teaching resources for young learners (middle- and high-school age). For over 35 years, the Institute of Human Origins (IHO) at Arizona State University has engaged in public education about our origins and has continued this legacy by creating AskAnAnthropologist.asu.edu to provide human origins teaching materials appropriate for middle- and high-school aged students.

In recent years, our goal has been to increase viewership to AskAnAnthropologist.asu.edu and further engage with diverse communities of learners. To do so, we focused on building a social media presence, and last year we created the Dr. Anthropology Facebook page to share AskAnAnthropologist content and promote science articles that interest young learners. Our first month's average reach was 504 users, and our subscribers have increased fourfold within a year of active posting.

To appeal to diverse audiences we offer translations to Spanish, interactive activities, and links to the Next Generation Science Standard (NGSS). Our AskAnAnthropologist.asu.edu viewership now includes a global audience with 8% viewership from Canada, 6.5% from Great Britain, and 1% each from Australia and Spain. Our goals to expand the website's impact include increasing our offerings of Spanish-language content and increasing our hands-on activity offerings. AskAnAnthropologist.asu.edu's mission is to construct an online human origins science education repository that serves a global community of science and social studies educators and young learners.

Funding provided by The John Templeton Foundation and Institute of Human Origins, Arizona State University

"I Would Not Feel So All Alone, Everybody Must Get Stone[s]": Social Stone Handling Facilitates Bonding Among Subadult Male Long-Tailed Macaques in Bali

JEFFREY V. PETERSON and AGUSTIN FUENTES
Department of Anthropology, University of Notre Dame

ABSTRACTS

This study investigates the degree to which stone handling, a unique form of object manipulation, may facilitate social bonding between individuals. Stone handling has been classified as a cultural behavior through work with Japanese macaques (*Macaca fuscata*), and has recently been studied among long-tailed macaques (*Macaca fascicularis*) in Bali, Indonesia. In lieu of adaptive explanations, stone handling is considered a non-functional or pseudo-foraging behavior that persists because decreased foraging time due to provisioning allow for "free time" unavailable to non-provisioned populations. We collected 210.75 hours of observation on 14 subadult male long-tailed macaques from two groups at the Padangtegal Monkey Forest in Bali. Here, we present in-depth analysis of 63 bouts of stone handling lasting 190 minutes. All focal animals exhibited stone handling, though there was substantial variation in overall stone handling time between individuals. Of total stone handling time (1816 seconds), 56% occurred with at least one neighbor in close (3 meters) proximity, which we call social stone handling. During social stone handling bouts, at least one neighbor was stone handling simultaneously 66% of the time. We constructed a multilevel social network, with each level representing a different affiliative context (e.g., grooming, proximity, and affiliative gesture exchange) and found that individuals with strong relations in the social stone handling network do not have correspondingly strong relations in their multilevel network ranking (via Borda Count) or any of its individual layers. We therefore argue that stone handling at Padangtegal may function as a key social bonding context for subadult males.

This research is funded by a National Geographic Society Waitt Grant (WW-082R-17) and a University of Notre Dame Graduate Student Research Award

Ancient DNA; Twitter and other disasters. A contribution on scientific innovation and ethical communication in bioarchaeology.

EMMANUELE PETITI and JULIA GRESKY

Natural Sciences, German Archaeological Institute

While studies on ancient human skeletons are received with increasing enthusiasm in public arenas, these new research experiences do not always convey innovative solutions to tackle the major ethical issues outlined by the most recent developments in bioarchaeology.

The authors will compare the language used by several relevant scientific publications (e.g. palaeogenetics and others) with that used by their audience in social media and blogs. The conceptual structures bridging these two communication pathways will be tested against three key points, which are crucial to bioarchaeologists today: gender, social inequality and race. These are social constructs, their features are shaped by historical settings and they play a key

role in defining identities. Yet, the study of archaeological human bones might be perceived as enforcing only one of many possible identities, on both a historical and biological base. This failure in delivering a meaningful separation between cultural and biological is often intrinsic to the aims of the research projects. The most immediate consequence of such miscommunication is that scientific data become a political tool to legitimate contemporary social segregation. Stepping from "mainstream" to "awarestream", the authors intend to stress the ethical responsibilities of all specialists working on human remains in formulating research aims and a language aware of the major global issues as well as in acknowledging the freedom of press and media as best litmus test for the ethical conduct of research groups.

Postnatal vertical transmission is associated with maternal parity and offspring growth in captive vervet monkeys (*Chlorocebus aethiops sabaeus*)

LAUREN PETRULLO¹, MATTHEW JORGENSEN², NOAH SNYDER-MACKLER^{3,4,5} and AMY LU⁶

¹Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, ²Department of Pathology, Section on Comparative Medicine, Wake Forest School of Medicine, ³Department of Psychology, University of Washington, ⁴Center for Studies in Demography & Ecology, University of Washington, ⁵Washington National Primate Research Center, University of Washington, ⁶Department of Anthropology, Stony Brook University

The assembly of the gut microbiome during early life has been linked to the pace of offspring growth. Yet, our understanding of how maternal vertical transmission mediates this relationship has been limited to experimental studies on the perinatal transfer of vaginal microbiota. Further, the influence of maternal traits on transmission is largely unknown. Recent research shows that the milk microbiome is taxonomically diverse, dynamic, and continuously transferred to offspring across lactation, potentially modifying the offspring gut microbiome during postnatal life. Here, we used matched maternal milk and offspring fecal samples to investigate the relationship between maternal traits, vertical transmission of milk microbiota, and early postnatal growth in captive vervet monkey mother-offspring dyads (N=15). Controlling for sex and neonatal body mass, we found that low parity females had offspring that grew faster ($p > 0.001$) and were larger than their counterparts by 6 months of age ($p < 0.01$), despite producing lower volumes of milk than high parity females ($p < 0.05$). In low parity dyads, the proportion of microbial strains shared by females (milk) and offspring (fecal) (e.g. a proxy for the strength of vertical transmission) was also greater than in high parity dyads ($p < 0.001$). Furthermore, infants that shared more microbial strains with their mothers grew more quickly (p

< 0.05). Taken together, these data suggest that enhanced vertical transmission of milk microbiota may be a strategy by which low parity females can compensate for reduced milk volume and promote infant growth.

Covariance among the zygomatic bone, the frontal bone, and the zygomaticotemporal space

ALESHA PETTIT

Anthropology, University of Nevada Las Vegas

This study analyzes the zygomatic shape, eye orbit shape, zygomaticotemporal space, and frontal bone of multiple primate species. Integration of these morphological regions has implications for evolutionary changes and constraints among primates. Specifically, this study analyzes the association of brain size, vision, mastication, and evolutionary morphological changes to the upper face among primates and explores what this might signify regarding evolutionary constraints due to functional relationships of vision, mastication, and neurocranium form. CT scans of primate skulls were analyzed using the software AnalyzePro, yielding 3 dimensional coordinates. This study used 37 gorilla, 35 chimp, 40 human, and 10 hominin skull CT scans. Morphometric and statistical analyses from Morphologika, MorphoJ, and Excel were used to determine the statistical significance among the different species. Specific hypotheses include 1) the zygomatic bone shape covaries with frontal bone shape, 2) frontal bone shape covaries with eye orbit shape, and 3) frontal bone shape covaries with the zygomaticotemporal space. Previous studies have shown a relationship between the zygomatic bone and the eye orbit, but this study expands on this idea to include the entire shape of the frontal bone, capturing relationships between the brain, vision, and mastication. Results indicate that there are multiple influences on the form of the zygomatic, reflected in the covariance in form among the zygomatic bone, the frontal bone, and the zygomaticotemporal space. More broadly, this may imply that much of the variation in the zygomatic reflects functional constraints with, and selection on, surrounding anatomy.

Who were the people of the Fourth Cataract of the Nile? What their teeth tells us about human migration patterns through the Sahara

EMMA LW. PHILLIPS^{1,2}, JOEL D. IRISH¹ and DANIEL ANTOINE²

¹School of Biological and Environmental Sciences, Liverpool John Moores University, ²Egypt and Sudan, The British Museum

Nubia is often regarded as the 'corridor' between sub-Saharan Africa in the south, and Egypt in the north. Its unique geographical position provides an opportunity to examine patterns of human

ABSTRACTS

migration through the middle Nile valley via the analysis of the dental remains. Nubia's relationship with Egypt has been the subject of much research, but investigations into its ties with sub-Saharan Africa have been less extensive. Using skeletal collections curated at the British Museum, this project explores the biological affinities of the inhabitants of the Fourth Cataract region of Upper Nubian. Results are contextualised using data from Lower Nubia and sub-Saharan Africa. Non-metric dental traits are used to assess inter-group affinities, following the ASUDAS system. The Mean Measure of Divergence was applied to quantify the data and multi-dimensional scaling used to illustrate inter-sample affinities. Dating from the Kerma (2000 BC) to Medieval periods (AD 1500), the Nubian assemblages provide a deep-time perspective of their biological relationship with sub-Saharan Africa. The inclusion of both Upper and Lower Nubian samples also tests how geographical distance affects relatedness among groups. Results from 600 individuals, comprising of eight groups, indicate that the sub-Saharan African groups have greater phenetic affinity to Fourth Cataract assemblages (MMD=0.06-0.10, $p \leq 0.05$) than to the Lower Nubia samples (MMD=0.09-0.13, $p \leq 0.05$). Temporal shifts were also observed, with the biological affinity between sub-Saharan sites and the Fourth Cataract assemblages lessening over time. This change may be indicative of greater genetic admixture and potentially increased migration from the North.

Support from the Wellcome Trust (British Museum grant 097365/Z/11/Z), Liverpool John Moores University (Matched-Funded PhD Scholarship), and the National Science Foundation (BNS-9013942, BNS-0104731).

Little evidence of C₄ plant consumption in mound building *Macrotermes* termites from six savanna woodland chimpanzee sites across Africa

SETH PHILLIPS¹, RUDOLF SCHEFFRAHN², ALEX K. PIEL³, FIONA STEWART³, ANTHONY AGBAR⁴, ALEXANDER TICKLE⁴, VOLKER SOMMER⁵, HJALMAR KÜHL⁴, CHRISTOPHE BOESCH⁴ and VICKY M. OELZE¹

¹Anthropology, University of California, Santa Cruz, ²Fort Lauderdale Research & Education Center, University of Florida, ³School of Biological and Environmental Sciences, Liverpool John Moores University, ⁴Department of Primatology, Max Planck Institute for Evolutionary Anthropology, ⁵Department of Anthropology, University College London

It has been proposed that the consumption of C₄ plant feeding termites may have led to the relatively high carbon isotope signatures observed in many fossil hominins. Previous analysis of carbon stable isotopes in termites from Kruger National Park found that an average of 35% of termite diets were comprised of C₄ plants. However, given the diversity of termite ecology across genera and

localities, those results are unlikely to be representative of the isotope ecology of all termites that could have been exploited by hominins. In the present study, we analyzed the carbon and nitrogen stable isotope ratios of 79 termite samples within the genus *Macrotermes* located at six savanna woodland sites inhabited by chimpanzees and utilized stable isotope mixing models to determine the input of C₄ plants within these samples. Additionally, we tested the effect of termite caste and habitat type in a subset of 47 samples from 12 mounds from the same field site. Our results suggest that C₄ plants comprised only 5-15% of *Macrotermes* diets across all six sites. Caste and habitat type had significant effects on carbon, but not nitrogen, isotope values in the subset we analyzed. The major soldier caste of *Macrotermes subhyalinus* had the most depleted carbon isotope signatures. These results call into question prior hypotheses of termite consumption by early African hominins as well as recent work on chimpanzee isotope ecology.

This project was funded by the Max Planck Society and the Krekeler Foundation as well as the University of California, Santa Cruz.

Strong dental trait correspondence between the outer enamel surface (OES) and the enamel-dentine junction (EDJ) in the Great Ape Dental Scoring System

VARSHA PILBROW¹ and THOMAS MCGAIN²

¹Anatomy and Neuroscience, The University of Melbourne, ²Medical School, Australian National University

The EDJ provides an accurate morphological record of the fully formed tooth on the basement membrane. However, enamel deposition toward the end of tooth formation can obscure dental morphology at the OES. As non-metric dental traits at the OES play a key role in differentiating hominoid species and determining their phylogeny, we test the role of enamel deposition in the manifestation of dental traits by comparing the expression of dental traits at the OES and EDJ in the Great Ape Dental Scoring System. This is a newly devised set of reference plaques showing dental trait expression in extant great apes, with application for fossil hominoid systematics.

We micro-CT scanned 254 teeth from 11 gorillas and nine chimpanzees and segmented the enamel and dentine tissues to generate surface meshes. We scored 185 graded traits on incisors, canines, premolars, and molars. A trait with identical score at the OES and EDJ was marked as 'true' correspondence; a score deviating by one was recorded as 'graded' correspondence. Other trait correspondences were disregarded.

We found that 'true' correspondence in gorillas was 68%, but in chimpanzees was 66%, and explained this by the thinner enamel in gorilla dentition. Protrusions such as cingula, tubercles,

cones and crests had stronger true correspondence in gorillas. In chimpanzees, foveae, wrinkles and accessory ridges had stronger true correspondence, fitting with their crenulated dental morphology. In both taxa, 95% of the traits showed 'graded' correspondence. This clarifies the role of enamel deposition and validates the Great Ape Dental Scoring System.

Funded by the L.S.B Leakey Foundation

Perceptions of race and ancestry in biological anthropology: Teaching, research, and public engagement

MARIN A. PILLOUD and DONOVAN M. ADAMS

Department of Anthropology, University of Nevada, Reno

Research that evaluates phenotypic patterns among ancestry groups is often critiqued as reinforcing traditional concepts of race. Further complicating this problem is the misappropriation of anthropological research in the production of race science and by racial extremists in the justification of racial hierarchies. Therefore, it is critical for biological anthropologists to be aware of how their research is at risk of misuse and engage in dialogue regarding best practice. To address these concerns, an online survey approved by the Institutional Review Board of the University of Nevada, Reno was distributed online to student and professional biological anthropologists (n=257). Questions were asked related to three core areas: teaching, research, and public engagement.

Almost half of respondents do not teach concepts of ancestry and/or race during their courses. Of those that do, these concepts are generally discussed in terms of historic racism in anthropology, eugenics, and microevolutionary differences between populations. While the distinction between social race and biological ancestry is largely agreed upon, there is some disagreement as to whether ancestry is also a social construct. Most respondents argue that terminology used for ancestry groups should be based on geography rather than those based on society or nationality. Nearly half of respondents suggest political correctness is a problem in biological anthropology and that concerns over the ethical implications of aspects like photography, ancestry, and terminology result in the silencing of research. Overwhelmingly, anthropologists argue there is an obligation to address misappropriation of research.

ABSTRACTS

Geometric morphometric analysis of postcranial sexual dimorphism in Cercopithecoids

ERIN F. E. PINKSTON¹, KATIE M. ALLEN² and NOREEN VON CRAMON-TAUBADEL¹

¹Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, ²Anthropology, University at Buffalo

When estimating sex in human and non-human primates, both the os coxae and the skull are consistently identified as the most accurate skeletal elements when relying on metric and nonmetric analyses. However, it is less well understood to what extent the scapula, which has a corresponding locomotor function in the pectoral girdle as the os coxae in the pelvic girdle, mirrors the patterns of sexual dimorphism observed in the os coxa. While the scapula and os coxa are homologous postcranial elements, it is expected that the os coxa present higher levels of sexual dimorphism than the scapula given that the sexually dimorphic effects of parturition affect the pelvic, but not the pectoral, girdle. This was tested by employing geometric morphometric analysis of three-dimensional landmark data collected from scapulae and ossa coxae of adult males and females of three taxa: *Chlorocebus pygerythrus* (vervet monkey), *Macaca fascicularis* (crab-eating macaque), and *Macaca mulatta* (rhesus macaque). Mahalanobis and Procrustes distances between the mean shapes for each sex were quantified and Discriminant Functions Analysis was used to assess rates of sex misclassification for each skeletal element. Results indicated statistically significant differences in shape between sexes for each element. Misclassification rates were broadly similar for the os coxa and scapula in macaques, while in vervets the scapula displayed slightly lower misclassification rates for the scapula than the os coxa. Hence, the results show that, for the purposes of sex estimation in these cercopithecoid taxa, the os coxa is not inherently better than the scapula.

This research is supported by the UB Research Foundation

Decomposing climate variability to predict risk-management strategies

ANNE C. PISOR

Anthropology, Washington State University

Members of the genus *Homo* have faced some very specific resource constraints, including those due to their high energy throughputs and their reliance on rare nutrients and minerals. Shortfalls in these resources can strike entire communities, and these shortfalls are not infrequently caused by changes in climate. Biological anthropologists, archaeologists, and cultural anthropologists have proposed menus of risk-management options for human individuals facing community-wide shortfalls; however, the question of whether specific

risk-management options are usually used for managing shortfalls with specific characteristics is largely relegated to verbal models. Can we decompose climate variability to specific features of shortfalls, such as their frequency and rate of onset, and assess whether these features predict which risk-management strategy individuals use? Here, I draw on data and theoretical predictions from across the anthropological literature to explicitly model the relationship between risk-management strategies – e.g., mobility, raiding, and trade – and the features of shortfalls – e.g., frequency, duration, rate of onset – for sedentary and non-sedentary populations. I find that these strategies are not mutually exclusive but may be used in tandem in response to shortfalls with specific features. These findings demonstrate how we can marshal existing anthropological data to better predict how vulnerable populations will respond to climate change-related shortfalls and figure out how we can better support them as they respond. I outline how this synthesis fits into a larger effort to increase the engagement of evolutionary-leaning anthropologists with contemporary climate change, from data collection to policymaking.

Religious fasting: an adaptive response to resource scarcity or pathogen threat?

CAITLYN PLACEK

Anthropology, Ball State University

Deliberate fasting, the intentional change in nutrient condition of an individual that results from the abstention of food and liquids, is widespread across human societies occupying diverse ecological settings. Existing models predict that fasting is an adaptive response to either resource scarcity or increased pathogen risk. Formal tests of these hypotheses, however, are scant, with existing studies primarily focusing on Western biomedical, adult populations. The aim of this biocultural investigation was to therefore test these models of religious fasting in a non-Western population who vary in access to resources and pathogen risk.

Research took place among rural and peri-urban participants in Mysore, Karnataka, India. A quantitative investigation was conducted to explore differences in fasting across age, gender, and location, and to test the *a priori* hypotheses (N=465). Logistic regression and negative binomial regression were used to assess the presence/absence and frequency of religious fasting, respectively.

Logistic regression analyses revealed that peri-urban, adult male participants had greater odds of religious fasting. A significant interaction in the demographic model suggests that rural participants fast more frequently as age increases, whereas peri-urban participants fast in similar frequency across adolescence and adulthood.

Tests of the two *a priori* hypotheses revealed that resource scarcity best predicted both the odds and frequency of fasting. The pathogen avoidance model was not supported.

In summary, this study found support for the resource scarcity model of fasting, with variation in fasting frequency across age, gender, and location. Results are discussed in the context of life history theory.

NIH Fogarty International, Grant/Award Number: R25 TW009338

Diet-Breadth Analysis in the Southwest: Comparison of Metabarcoding and Shotgun Sequencing Methods with Coprolites

PAIGE N. PLATTNER¹, MERADETH SNOW¹, ALEKSANDAR KOSTI² and MARSHA WIBOWO²

¹Anthropology, University of Montana, ²Joslin Diabetes Center, Harvard Medical School

The ability to capture diet-breadth from past populations using the archaeological record can be potentially biased due to lack of preservation. Several new techniques have been developed to study this further through genomic analysis of human coprolites. Samples from sites across the American Southwest have been analyzed with two different techniques in order to aid in establishing a better baseline for the molecular approaches available for the reconstruction of past diets. This research quantifies and compares the results of the economical metabarcoding (PCR-based NGS sequencing) and deep HiSeq shotgun sequencing methods for future inquiries regarding the agricultural integration process in past populations. Maize was a dietary staple in the Southwest, but the full breadth and extent to which the population was dependent on crop yield has remained unclear across time and space. The sites selected for analysis contained coprolites preserved in dry caves. These sites allowed for a cross-cut of time and region in order to better estimate the timing and extent of the introduction of maize and other components to the diet in the Basketmaker/Pueblo periods. The results of metabarcoding were limited to plants and vertebrate animals consumed, due to the nature of the PCR-primers that targeted these species. Alternatively, the broad range and deep data of shotgun sequencing has yielded higher quality results with more coverage and confidence. This research concluded that the choice of aDNA techniques ought to be considered with a cost-value comparison for the needs of individual projects.

Funding for the MiSeq sequencing fees were obtained through the University of Montana Genomics Core voucher program.

ABSTRACTS

Males, females, canines and body size: inferring the pattern of change in hominin dimorphism

J. MICHAEL PLAVCAN

Anthropology, University of Arkansas, Fayetteville

Sexual dimorphism in canine tooth size and body size are correlated across primates. However, within hominins there is a unique dissociation between size and canine dimorphism. Reduced canine dimorphism is a basal hominin trait, while most studies suggests that early hominins showed strong size dimorphism. This presents a conundrum for inferring behavior. Identifying the phylogenetic valance of changes in male and female trait values and dimorphism can highlight how dimorphism changes as a consequence of changes in male and female traits. Data for canine tooth size, skull size and body mass were gathered for 90 species of primates, as well as estimates for early hominins. Phylogenetic analyses tracing character states using maximum parsimony (using the 10K Trees phylogeny in Mesquite) were used to trace relative changes for each trait in each sex, as well as dimorphism for each species. Simple bivariate comparisons show that changes in mass dimorphism are primarily a function of changes in male size, while changes in canine dimorphism are associated with changes in both male and female canine size. *A. afarensis* is unique in showing an extreme dissociation in canine and size dimorphism, with an apparent shift in female body size being the primary cause. The results suggest that a loss in canine dimorphism is primitive for hominins, and thus uninformative about social behavior. The results corroborate the hypothesis that changes in female size are responsible for the unusual pattern of hominin dimorphism seen in the fossil record.

Supported by NSF BNS 8814060, SBR 9616671

Primate paleoenvironments of the Homa Peninsula, southwestern Kenya

THOMAS W. PLUMMER¹, PETER W. DITCHFIELD², ELIZABETH WHITFIELD¹¹, SCOTT BLUMENTHAL³, EMILY G. EARLY⁴, FRITZ HERTEL⁵, RAQUEL LAMELA LOPEZ¹, JAMES S. OLIVER⁶, RICK POTTS^{7,8}, THOMAS VINCENT¹¹, STEPHEN FROST⁹ and LAURA C. BISHOP^{10,11}

¹New York Consortium in Evolutionary Primatology,

²Research Laboratory for Archaeology and the

History of Art, University of Oxford, ³Isotopic

Paleoecology Laboratory, University of Oregon,

⁴Arizona Museum of Natural History, ⁵Department

of Biology, California State University, Northridge,

⁶Earth and Mineral Science Museum, Penn State

University, ⁷Human Origins Program, National

Museum of Natural History, Smithsonian

Institution, ⁸Palaeontology Section, Earth Sciences

Department, National Museums of Kenya,

⁹Department of Anthropology, University of Oregon,

¹⁰The Sino-British College, University of Shanghai

for Science and Technology, ¹¹Research Centre

in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

This poster examines the palaeoenvironments of the diverse primate fauna of the Homa Peninsula in southwestern Kenya. The Homa Peninsula has numerous fossil and archaeological occurrences that have been discovered over the course of a century of fieldwork, presenting the opportunity to examine primate environments over a considerable time frame (early Pliocene through Pleistocene) within a relatively constrained geographical region. Early work on the peninsula focused particularly on the older, Mio-Pliocene sediments of the Kanam and Homa Formations (Fm), which have yielded extensive mammalian faunas along with geochemical evidence of paleoenvironmental context. Numerous localities have produced important mammalian type fossils and archeological evidence of hominin activity. There is an extensive record of cercopithecoid fossils from the Homa, Rawi, Kasibos and Kanjera Formations, including a partial cranium of *Cercopithecoides kimeui* from the Rawi Formation (Frost et al 1993), and an assemblage comprised of at least 18 *Theropithecus oswaldi* individuals from Kanjera North. We use a range of methods to reconstruct the environments in which these primates lived, often in association with evidence of hominin activities. Sedimentological studies provide a baseline for the depositional history of the localities, and reveal the local availability of water. Stable carbon isotopic studies of paleosols provide profiles of locality vegetation structure, whilst isotopic studies of the fauna themselves support dietary reconstructions. Studies of the co-occurring fossils also reveal faunal community structure discontinuously over 6 million years.

Funding from the National Science Foundation, The Leverhulme Trust and the Peter Buck Postdoctoral Fellowship, Smithsonian Institution supported this research.

Impacts of the Smithsonian Human Origins Program's expert-led public events

BRIANA POBINER, RICHARD POTTS and ELLA BEAUDOIN

Anthropology, Smithsonian Institution

The Smithsonian Human Origins Program's approach to public events includes a strong focus on interactions between experts and public audiences. Two examples of this are the twice monthly "Scientist is In" program in the Smithsonian's Hall of Human Origins, and programs in 19 U.S. public libraries in association with the traveling exhibit "Exploring Human Origins: What Does It Mean to Be Human?". What is the value and impact of scientists interacting with the public in these two examples? We present relevant data on the "Scientist is In" program for 2012 and programs connected with the traveling exhibit from 2015 to 2017. Smithsonian expert-led museum program participants rated their general science interest

high, stated that they "enjoy studying science" and would like "to be a scientist", and found topics in the Hall of Human Origins that relate to their personal lives more so than visitors who experienced only the museum exhibit. More participants in expert-led programs in the public libraries noted the importance of scientific research in their understanding of what it means to be human, viewed the topic of human evolution as personally relevant, and learned about perspectives different from their own compared to those who attended the exhibit only. They also indicated their increased interest in discussing human evolution topics in the future after attending the expert-led programs. We conclude that interacting with scientists and other experts can have a strong impact on visitor understanding, relevance, and perceptions of human evolution through informal public programs.

"Exploring Human Origins: What Does It Mean to Be Human?" was supported by a grant from the John Templeton Foundation, and the Peter Buck Human Origins Fund (Smithsonian).

Reconstructing the Ancestral Social Organization of Lorisiformes and Lemuriformes

STEPHANIE A. POINDEXTER^{1,3}, SIMON T. MADDOCK², ALICIA RICH¹, VINCENT NIJMAN³, K. A. I. NEKARIS³ and EVA C. GARRETT¹

¹Anthropology, Sensory Morphology and Genomic Anthropology Lab, Boston University,

²Faculty of Science and Engineering, University of Wolverhampton, ³Anthropology, Nocturnal Primate Research Group, Oxford Brookes University

Lorisiformes and Lemuriformes are thought to share primitive characteristics with extinct primate species from the Paleocene and the Eocene. When reconstructing the ancestral social organization of nonhuman primates, it is important to factor in the broad range of social organizations seen in extant loridid, galago and lemur species. Using recently updated data on social organizations in 81 species of Lorisiformes and Lemuriformes, published in *All the World's Primates* (2016), we used BEAST to estimate phylogenetic relationships and phytools to perform stochastic character mapping to infer ancestral states. We found that the ancestral social organization between Lorisiformes and Lemuriformes was most likely a neighborhood social system (>50%), characterized as frequent intra- and intersexual home range overlap. The last common ancestor (LCA) for all Lorisiformes and the LCA for all Lemuriformes present during the Eocene, likely displayed a neighborhood (>50-60%) social system as well. Given these estimations, the dispersed family, or pair-living social system seen in strepsirrhine species at the terminal nodes is likely a derived trait that evolved multiple times. Here we present data that could have implications for on-going discussions

ABSTRACTS

about the diel pattern in ancestral primates. The neighborhood social system in extant primates is most commonly associated with small-bodied nocturnal primates (e.g. galagos), which by proxy suggests that the LCA between Lorisiformes and Lemuriformes present during the late Paleocene (~60 MYA) was nocturnal.

A second dental morphology examination of biological affinities of northeastern Indian populations relative to other South Asians. The case of Chakhesang, Pochury and Rengma Nagas

TSIAPISA POJAR¹, BANRIDA LANGSTIEH¹ and BRIAN E. HEMPHILL²

¹Department of Anthropology, North Eastern Hill University, ²Department of Anthropology, University of Alaska, Fairbanks

The biological affinities of many Tibeto-Burman-speaking ethnic groups of northeastern India remain largely unknown due to cultural proscriptions regarding submission of bodily fluids for DNA analysis. Oral traditions claim little affinity between these ethnic groups and other ethnic groups of South Asia. This study employs 17 tooth-trait combinations of the Arizona State University Dental Morphology System among 753 individuals of three self-identified divisions of Nagas (Chakkesang, Pochury, Rengma), the largest ethnic group of Nagaland. These data were contrasted with 11 samples encompassing 1,908 living individuals of ethnic groups from south-eastern peninsular India, west-central peninsular India, and northern Pakistan based upon pairwise MMD values examined with correspondence analysis (CA) neighbor-joining cluster analysis (NJ) and multidimensional scaling (MDS).

CA indicates that, with the exception of *tuberculum dentale*, traits scored on separate teeth within dental fields yield unique biodistance information. Results are consistent across NJ and MDS as both identify a fundamental division between members of northeastern ethnic groups and all other South Asians. Secondary divisions distinguish Indic-speaking ethnic groups of west-central peninsular India from Dravidian-speaking ethnic groups of southeastern peninsular India. Ethnic groups of northern Pakistan show no affinities to peninsular Indians or to Tibeto-Burman-speaking ethnic groups of northeast India. Among the three Naga groups, affinities are closer between Pochuries and Rengmas than with Chakkesangs. These results not only confirm that northeastern Indians are recent émigrés to South Asia, but also corroborate oral traditions, which claim that Pochuries and Rengmas were once a single ethnic group that fissioned, while Chakkesangs were not.

This work was supported by a Fulbright Specialist Fellowship to BEH.

No Funding

Effect of Thermal and Chemical Treatments on Elastic Modulus and Anisotropy of Bone

TAYLOR A. POLVADORE, GRACE V. CALHOUN and DAVID J. DAEGLING

Anthropology, University of Florida

Chemical fixation and thermal sterilization of skeletal specimens are thought to alter bone material properties, but the magnitude of these effects as well as their impact on anisotropy are not well documented. We prepared radial sections of *Bos taurus* humeri subjected to three treatments: 1) 70% ethanol immersion, 2) 10% buffered formalin fixation, and 3) thermal sterilization in an autoclave set to 121°C for 30 minutes. Elastic moduli were determined through microindentation, which tests hardness of bone by loading prepared specimens under an indenter of known geometry for a precise interval of time. The subsequent plastic deformation of bone is measured for determining microhardness and elastic modulus via regression. We used a Knoop indenter to supply 50g of load for 10 seconds at 0, 30, 60 and 90 degrees to the longitudinal axis of the humerus. For each bone section, 9 indents were produced at each of the four angles, producing 36 indents per section. Sections from the same individuals were tested across the treatments and controls. A factorial 3-way ANOVA reveals significant interaction among main effects, with the exception of treatment vs. indenter angle interaction. Autoclaved specimens showed a significant decrease in elastic modulus compared to controls ($P < 0.001$), whereas formalin and ethanol storage did not significantly impact elastic modulus. Across all treatments and controls, patterns of anisotropy remained consistent, with the bone being stiffest longitudinally. Stiffness appears to be unchanged in bone preserved in ethanol or formalin as measured on a microstructural scale.

Supported by NSF BCS-1440532.

Extension and refinement of a landmark-free method for 3D shape analysis

BENJAMIN J. POMIDOR

Scientific Computing, Florida State University

Geometric morphometrics has traditionally relied on anatomical landmarks for the statistical analysis of shape, but widespread availability of 3D surface and volumetric scanning technology has driven the development of surface-based morphometric analysis tools. Generalized Procrustes Surface Analysis (GPSA) is one of these methods, developed by Pomidor, Makedonska, and Slice. GPSA uses a modified, symmetric version of the iterative closest point (ICP) algorithm within a generalized Procrustes framework to analyze shape using point clouds. Presented here is a combination of refinements to GPSA, including the reformulation of the shape distance metric and derived superimposition cost function to

operate on triangulated surface meshes instead of point clouds, the introduction of local shape descriptors and sample-to-mean correspondence for better homology estimation, and the addition of low-pass filtering using $\lambda\mu$ smoothing for better-conditioned calculated surface meshes. The refined method is also extended to enable resistant-fit superimposition using a correspondence quality metric together with the trimming step from trimmed ICP. Evaluation of the refined method using generated and real-world data shows only slightly better correlation with landmark data compared to GPSA, but significant improvement in the retention of highly variable features and general mesh quality. This improvement comes at the cost of sensitive smoothing parameterization that can be temperamental at very high resolutions. Comparison of the usual least-squares superimposition to the resistant-fit superimposition shows that large variation from a single feature is shared across the object in the least-squares case, while the resistant-fit superimposition successfully contains this variation in the originating feature.

Brain Morphology of the Taung Endocast Inferred from Comparative Great Ape and Human Evidence

MARCIA S. PONCE DE LEÓN, SILVANO ENGEL and CHRISTOPH P. E. ZOLLIKOFER

Dept. of Anthropology, University of Zurich

Since its discovery the "Taung child" (*Australopithecus africanus*) has been in the center of debates about the evolutionary course and timing of hominin brain reorganization. However, because cortical sulci and gyri are variable inter-individually, and variably expressed as endocranial imprints, the endocranial morphology even of well-preserved fossil specimens such as Taung continues to be discussed controversially. Here we use new geometric-morphometric data about spatial variation of great ape and human sulci/gyri to reassess key endocranial structures of the Taung endocast. Our quantitative approach indicates a primitive sulcal patterning in the frontal lobe of Taung, confirming earlier studies on *Au. africanus* frontal sulcal patterning. Furthermore, our comparative data provide no positive evidence for a derived (i.e. posterior) position of the lunate sulcus in Taung. When and how the transition from primitive (great-ape-like) to derived (human-like) external cortical morphologies occurred during hominin evolution thus still remains an open question.

Funded by Swiss NSF grant #31003A_135470 to C.P.E.Z.

ABSTRACTS

Defining the meaning of “population” in archaeological contexts: A study on modern interpretations of ancient cranial variation

SARAH A. PONIROS

Archaeology, University of Sheffield

Programs that predict ancestry from cranial metric variation, such as FORDISC or CRANID6, are frequently used in biological and forensic anthropology. However, there are considerable practical and ethical issues that stem from the way these programs work when applied to past populations, as many users interpret these groups as genetically homogenous, a product of colonialist interpretations in archaeology. The programs use a global database of cranial measurements from 74 populations, both modern and archaeological. These populations are defined by geographic parameters—where individuals died or were excavated—with limited information regarding their genetic ancestry. This is problematic as small samples of individuals of known geographic origin but undocumented ancestry are determining the parameters of ancestral variation in anthropological studies.

This project explores the cranial morphology in the Poundbury Roman cemetery, a population included in the CRANID6 database. The aim is to explore the variation at the site using K-means cluster analysis to evaluate the extent to which it represents a homogenous population. The Poundbury male sample contains six significant phenotypic outliers and one female suggesting several individuals did not conform to homogenous within-population diversity. Furthermore, the males have considerably more phenotypic variation than the females (WSS= 783 and 580, respectively), suggesting males are more phenotypically varied than females at Poundbury. Using this, and similar, populations as models of homogenous groups in ancestry assessment is incorrect and also hides important information about genetic diversity. This is questionable on ethical grounds as it creates invisibility of non-dominant ancestral groups in the past.

Thank you to the University of Sheffield Doctoral Academy for funding my Ph.D.

High energy apes on a hot planet: the challenge of fueling an increasingly energy hungry hominin

HERMAN PONTZER

Evolutionary Anthropology, Duke University, Duke Global Health Institute, Duke University

The global climate crisis is a product of increased energy demand to fuel industrialized economies and modern lifestyles. While anthropogenic climate change is a recent phenomenon, the human dependence on increasingly larger energy supply has ancient origins. Here I examine the

history of human energy use for insight into the present climate crisis. Beginning approximately 2 million years ago, hominin metabolic rates accelerated, increasing daily energy demand. Then, beginning between 1,000,000 and 500,000 years ago, hominins learned to control fire, providing an external (i.e., extra-somatic) energy source to use for human ends. Humans' reliance on external energy sources has grown exponentially since then, with the successive additions of animals, wind, water, and fossil fuels to our energy economy. Today, average global energy expenditure per capita is nearly 20-times that of our somatic (metabolic) energy expenditure. Total daily energy use (somatic plus external) varies regionally, from less than 2-times somatic expenditure for foraging populations, to ~5-times somatic expenditure in India and ~70-times somatic expenditure in the U.S. External energy is used primarily to enhance ranging, production and trade of goods, food acquisition, and somatic maintenance, but not reproduction. Assuming global population growth plateaus at 10 billion but global average expenditure grows to meet current U.S. levels, global energy demand will increase ~300%, leaving few feasible solutions to mitigate climate change. Reducing per capita growth in expenditure would require reversing a 1,000,000 year trend toward increasing external energy dependence. Developing non-fossil fuel sources of external energy is essential to our species future.

Reconstructing Diet from Tooth Wear: a New Quantitative Mesowear Approach

JOSHUA J. PORTER¹ and FRANCES L. FORREST²

¹Anthropology, The George Washington University, ²Sackler Educational Laboratory for Comparative Genomics and Human Origins, American Museum of Natural History

Despite the substantial research into mesowear and reconstructing paleodiet, we currently lack a resolved quantifiable understanding of mesowear. Traditionally, mesowear has been qualitatively scored into 4-6 groups. However, this approach limits the resolution of our paleodietary reconstructions by expressing information categorically and not continuously. Consequently, a quantifiable mesowear method is needed. In this study, we use a substantial sample ($n = 120$) of digitally measured modern Bovidae molars. We focus on taxa modernly classified as C⁴ grazers (i.e. *Alcelaphini*), C³-C⁴ mixed feeders (i.e. *Tragelaphini*), or C³ browsers (i.e. *Bovini*). We photographed these molars and then measured and quantified their occlusal relief and cusp shape in ImageJ. Preliminary findings on modern taxa suggest that there is a significant relationship between quantitative mesowear and diet. In addition, regional differences in food external mechanical properties could be driving some of the variation observed but without more samples from more regions, this

cannot be quantitatively supported. We will also apply this approach to fossil fauna at critical East African hominin localities such as Lake Turkana, Kenya. Further quantifiable mesowear studies on modern and fossil samples would provide a more nuanced understanding of the relationship between modern and paleoecology and heterogeneity within the broader ecosystem.

The genetic differentiation of early Americans

COSIMO POSTH

Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Institute for Archaeological Sciences, Archaeo- and Palaeogenetics, University of Tübingen

The early genetic diversification of Native American populations remained for a long time poorly understood because of the scarcity of ancient DNA data from the Americas. In 2018 six studies collectively reported genome-wide data of almost 170 ancient individuals spanning from Alaska to Patagonia and dated from around 11,000 to 200 years ago. Co-analysing this data revealed that ancient South Americans derived nearly all of their ancestry from just one of the two early branches that primarily contributed to non-arctic Native Americans. This ancestry resulted from an early dispersal and rapid star-like radiation, followed by genetic continuity in different regions for at least ~9,000 years. However, multiple gene flow events between North and South America were identified such as the one that provided new ancestry to the Andes by at least ~4,200 years ago and one that contributed to individuals older than 9,000 years from Chile and Brazil. Nevertheless, both groups derive from the same ancestral source as the vast majority of other Native Americans. These findings are evaluated in comparison to cranial morphological studies to investigate the biological transformations that took place when groups ancestral to present-day people established in each American region.

Population-level assessment of atlanto-occipital fusion and cranial modification across Peru (1300-1500 CE)

LAURA N. POTT¹, RITA M. AUSTIN^{1,2}, ANDREA R. ELLER² and SABRINA B. SHOLTS²

¹Department of Anthropology, University of Oklahoma, ²Department of Biological Anthropology, National Museum of Natural History, Smithsonian Institution

Atlanto-occipital fusion (AOF), a rare spinal anomaly characterized by the partial or complete fusion of the first cervical vertebra (atlas) to the occipital bone, can arise from congenital and environmental causes. The compression and restriction of movement associated with cranial modification, for example, may influence AOF by changing the way the atlas bears the weight of

ABSTRACTS

the skull. Cranial modification involves the use of boards, pads, or cloth wrappings to permanently alter the shape of infants' crania. AOF has been described in three regions of pre-Hispanic Peru where cranial modification was practiced, but the two conditions have not been directly linked. This study examines the distribution of AOF and its potential relationship to cranial modification in a sample of skeletal individuals from nine coastal and highland regions of Peru held at the Smithsonian's National Museum of Natural History (n=1407, 1300-1500 CE). Twenty cases of AOF were observed in four coastal regions—two of them previously unreported—at an overall frequency of 1.4%. AOF occurred at a significantly higher frequency of 6.9% in the southern region of Ica ($p=0.00$, $\chi^2=0.05$). There was not a correlation between cranial modification and the presence ($p=0.23$, $\chi^2=0.05$) or completeness ($p=0.17$, $\chi^2=0.05$) of AOF, suggesting cranial modification is not one of the environmental factors that influences AOF. Genetic or environmental conditions may be explored as factors shaping the coastal distribution of AOF, and further research covering additional highland and jungle regions would better characterize its geographical distribution across Peru.

Funding for this study was provided by the Natural History Research Experiences (NHRE) NSF REU site (OCE-1560088).

Pair-living as a stepping stone towards more complex societies in primate social evolution

LUCA POZZI¹ and PETER M. KAPPELER^{2,3}

¹Anthropology, UT San Antonio, ²Behavioral Ecology and Sociobiology Unit, German Primate Center, ³Sociobiology/Anthropology, University of Göttingen

Primates exhibit great diversity in social systems, including solitary, pair- and group-living species. Recent comparative analyses yielded conflicting results about the number and direction of evolutionary transitions among these three social systems as well as about the selective pressures favoring the evolution of pair-living, in particular. In this study, we examined evolutionary transitions in primate social evolution by systematically exploring the effects of using independent categorizations of sociality and different phylogenetic hypotheses with a vastly expanded data set. We included 362 species of primates and we used Bayesian phylogenetic comparative methods (BayesTraits and Stochastic mapping) to compare six alternative evolutionary models of social evolution. We found strong evidence for a solitary social organization at the root of the primate tree and consistently found the strongest support for a model that invokes frequent transitions between solitary ancestors and pair-living descendants, with the latter giving rise to species living in multi-male multi-female

groups (Bayes factor > 10). We also explored the influence of taxonomic sampling in our dataset by creating multiple subsets using different sampling schemes (from 95% to 50% of the taxa represented in the original dataset). Our analyses showed consistent support that pair living was a stepping-stone in the evolution of structurally more complex primate societies, a result that bolsters the role of kin selection in social evolution.

Ardipithecus ramidus hand provides support for an African ape-like ancestor of humans and chimpanzees

THOMAS C. PRANG¹, KRISTEN R. RAMIREZ^{2,3,4}, MARK GRABOWSKI⁵ and SCOTT A. WILLIAMS^{4,6}

¹Department of Anthropology, University at Albany, ²Department of Anthropology, The Graduate Center, City University of New York, ³Department of Cell Biology, Office of Medical Education, New York University School of Medicine, ⁴New York Consortium in Evolutionary Primatology, ⁵Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University, ⁶Center for the Study of Human Origins, Department of Anthropology, New York University

The locomotor behavior of the *Homo-Pan* last common ancestor (LCA) is critical for understanding the origin of bipedalism. The postcranial morphology of *Ardipithecus ramidus* suggests that the earliest hominins retained adaptations for arboreal locomotion. However, whether the LCA possessed a locomotor repertoire including below-branch suspension is currently a matter of debate. Here we use phylogenetic comparative methods and evolutionary modeling to test hypotheses about the morphometric affinities of the *Ar. ramidus* hand and its implications for patterns of hominin hand evolution. Our extant data include 26 linear measurements of metacarpals and phalanges representing 53 anthropoid taxa (N=416). Multivariate analyses show that our metric data separate anthropoid taxa according to locomotor behavior and phylogeny, and several variables distinguish extant hominoids from other anthropoids, including ulnar carpo-metacarpal joint metrics. The *Ar. ramidus* hand is most similar to chimpanzees, bonobos, and orangutans among the taxa sampled. In addition, the relative length and curvature of the *Ar. ramidus* manual phalanges fall exclusively within the ranges of variation of the most suspensory anthropoids (*Pan*, *Pongo*, hylobatids, atelines). Our evolutionary modeling analyses show that *Ar. ramidus* occupies the same selective regime as chimpanzees and bonobos despite having a relatively shorter fifth metacarpal. Accordingly, we identify an evolutionary shift between *Ar. ramidus* and all later hominins plausibly associated with increased manipulative capabilities. Our results, when interpreted within the context of recent analyses, suggest that the *Homo-Pan* LCA may have been a large bodied, semi-terrestrial quadruped with adaptations to below-branch suspension.

Reassessing the accumulated copying error model with an eye toward detecting high-fidelity cultural transmission during the Paleolithic

L. S. PREMO

Department of Anthropology, Washington State University, Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Paleoanthropologists do not yet have a good handle on when high-fidelity cultural transmission evolved in the hominin lineage. The accumulated copying error (ACE) model has been used to investigate the Paleolithic archaeological record for evidence of non-vertical cultural transmission. ACE provides two predictions for a vertically transmitted continuous trait: 1) its mean should remain constant through time and 2) its variance should increase exponentially through time. ACE makes two simplifying assumptions: 1) the population has infinitely many vertical transmission chains and 2) the value of the continuous trait of interest can become infinitely large. Although both assumptions are violated by all empirical cases, researchers have interpreted instances where archaeological assemblages yield lower-than-expected values as possible evidence of biased cultural transmission. Here, I use simulation to show that the mean and variance of a continuous trait passed via vertical cultural transmission in a finite population decrease through time at a rate proportional to population size due to the combined effect of proportional copying error and sampling bias. Next, I extend ACE to show that functional constraints limit continuous trait variation. Ignoring the roles that finite population size and functional constraints play in empirical cases increases the likelihood of incorrectly interpreting "lower-than-expected" continuous cultural variation as a sign of oblique transmission, perhaps even conformity. Even if a continuous attribute is acquired via individual learning, one should expect it to exhibit low variation whenever its functionally relevant values are constrained.

Examining sampling strategies for archaeological dental calculus through the exploration of the regional variation of bacteria in the oral microbiome

SAMANTHA DR. PRICE^{1,2}, TRACY L. PROWSE¹, JESPER L. BOLDSSEN³, MELANIE KUCH², ANA T. DUGGAN^{1,2}, KATHERINE EATON^{1,2}, JENNIFER KLUNK² and HENDRIK N. POINAR^{1,2}

¹Anthropology, McMaster University, ²McMaster Ancient DNA Centre, McMaster University, ³ADBOU, University of Southern Denmark

Archaeological dental calculus is a valuable reservoir of bacterial DNA that is used to examine the oral microbiome in the past. This study investigates variation in the bacterial community found in dental calculus from teeth in different regions of the mouth, and compares intra-individual variation to variability in bacterial communities

ABSTRACTS

between individuals. A shotgun sequencing approach was used to obtain DNA from the dental calculus of sixteen adult individuals from the Medieval cemetery of Tirup, Denmark (AD 12th to 14th centuries). Intra-individual variation was assessed using dental calculus from three to six teeth in different regions of the mouth from eight individuals. Inter-individual variability was explored through analysis of dental calculus from the right mandibular second premolar of eight additional individuals. The DNA profiles generated from the metagenomic analysis of the shotgun sequences indicates that samples from the same individual share similar bacterial community profiles and more closely resemble each other than the samples that came from the same tooth, but different individuals. Any variability between teeth from the same individual appear to be due to slight differences in abundances in the bacterial communities. These results suggest that the bacterial communities found in the dental calculus from different regions of the mouth within an individual are more alike in composition than that from the same tooth in separate individuals. The slight variation of the bacterial composition in different regions of the mouth need not constrain future studies to sampling a singular tooth type.

Topernawi Gorge: A New Fossil Catarrhine Site from the Oligo-Miocene of the Turkana Basin, Kenya

PATRICIA PRINCEHOUSE^{1,2} and EIPA EMMANUEL AORON^{2,3}

¹Institute for the Science of Origins, Case Western Reserve University, ²Paleoanthropology Department, Turkana Basin Institute, ³Program in Human Evolutionary Biology, Turkana University

The Oligocene-Miocene boundary in Africa offers one of the most dramatic transitions in all the Cenozoic, but East African sites are vanishingly rare. At this moment the Afro-Arabian continental plate made contact with the Eurasian plate, and faunal interchange, environmental shifts, and massive concomitant extinction took place that structured the faunal make up and ecology of the ensuing Neogene up to the present day. Many native African clades went extinct but Primates thrived and stem catarrhines split into hominoids and cercopithecoids and left Africa to colonize new territory throughout the old world. Depending on what diagnostic criteria are adopted to define superfamily Hominoidea, it appears to have originated in the mid to late Oligocene and exploded in a major evolutionary radiation in the earliest Miocene. This timing is also supported by molecular clock data. Here we report on Topernawi Gorge a rich new site spanning approximately 20-28mya, and in specific the results of analysis of the locality Phillip's Blue Hill, with 2 species of catarrhines squarely situated in a pre-contact native African paleoecological context rich in hyracoids, anthracotheres, embrithopods

and other distinctive Oligocene mammals. This locality allows examination of the ecological context in which hominoids emerged from stem catarrhines, and evidence that apes and old world monkeys diverged dynamically as part of a selection-driven character displacement event in which the two lineages co-created new niches.

morphomap: an R package for analysis of diaphyseal cortical thickness, shape and cross-sectional geometry

ANTONIO PROFICO¹, LUCA BONDIOLI², PAUL O'HIGGINS^{1,3,4} and DAMIANO MARCHI^{5,6}

¹Palaeohub, Department of Archaeology, University of York, ²Bioarchaeology Service, Museo delle Civiltà, ³Hull York Medical School, University of York, ⁴Centre for Forensic Anthropology, The University of Western Australia, ⁵Department of Biology, University of Pisa, ⁶Evolutionary Studies Institute and Centre for Excellence in Palaeosciences, University of the Witwatersrand

The cross-sectional geometry of long bones is commonly used to infer their biomechanical properties in investigations of past and present primate locomotion as well as to assess intensity and repetitiveness of physical activities, and to estimate body mass. While cross-sectional geometry has proved to be very useful for reconstructing bone loading patterns, a limitation of the technique has been that only a few cross sections along the diaphysis can be analyzed. The advent of virtual imaging and image processing offers the prospect of semi automating the sectioning and calculation of geometric properties at high resolution. We present the morphomap package, developed in the R environment, to extract cross sections from long bone meshes at specified intervals along the diaphysis and to calculate two and three dimensional morphometric maps, cross-sectional geometric parameters, and semilandmarks on the periosteal and endosteal contours of each cross section. We demonstrate the validity of this computational tool by showing that it obtains the same results as those from manual and other computational approaches. We then demonstrate the functionality of morphomap in a comparison of human and chimpanzee femora. The tool produces 61 cross sections along each diaphysis, at increments of 1% between 20% and 80% of their biomechanical length, automatically draws morphometric maps and calculates the parameters described above. The results illustrate the potential of morphomap in identifying differences in diaphyses that can be related to differences in locomotion and lifestyle in living and fossil primates.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 835571.

Investigating visual preferences for symmetry, faces, and behinds in brown spider monkeys (*Ateles hybridus*)

MICHAEL J. PROULX^{1,2}, EMMA HOWARD¹ and ALEXANDRA A. DE SOUSA³

¹Psychology, University of Bath, ²REVEAL Research Centre, University of Bath, ³Centre for Health and Cognition, Bath Spa University

Old World monkeys, apes, and humans have been studied extensively to discover visual preferences ranging from symmetry, colors, conspecific faces, and behinds (anogenital region). Whether such preferences extend to New World monkeys is unknown. Here we examined preferences in captive brown spider monkeys (*Ateles hybridus*). Given the use of socially significant stimuli, we also examined whether there were any sex differences. Visual preference was assessed by comparing combinations of symmetric versus asymmetric stimuli, naturalistic conspecific faces versus schematic patterns, and conspecific faces versus conspecific behinds. The preference was assessed by recording the viewing frequencies for the presented stimuli. We found higher viewing frequencies for symmetrical over asymmetrical naturalistic and schematic stimuli only in males. There was no difference in viewing frequencies for conspecific facial or anogenital stimuli. Through demonstrating a preference for facial and pattern symmetry, but no clear preference for conspecific faces, these findings imply preferences in humans for facial and pattern symmetry have an early origin shared with the New World monkeys studied here.

Subadult Human Sacrifice in Maya Caves: Reformulating the Emphasis of Maya Sacrificial Practices

MICHAEL G. PROUT

Anthropology, California State University, Los Angeles

Current models of Maya sacrifice view most victims as men. Investigations of Midnight Terror Cave, Belize between 2008 - 2010 found a human osteological assemblage of over 10,000 bones, the largest reported for a cave in the southern Maya lowlands. Analysis indicates that approximately a quarter of the bones belong to subadults, which make up 43% of the minimum number of individuals. Determination of age at death produced a mortality curve that differs significantly from a normal curve with the numbers peaking between 5 - 10 years of age, when mortality is generally low. These figures are similar to those produced from the Cenote of Sacrifice at Chichen Itza. The high quantity of bones in caves coming from children between 5 - 10 years of age indicates child sacrifice was much more central to Maya sacrificial

ABSTRACTS

practices than previously appreciated. Greater attention must be paid to this segment of societal ritual if we are to gain a comprehensive understanding of Maya sacrifice.

Risk of Lead Exposure on a Roman Imperial Estate at Vagnari, Italy (1st – 4th c. AD)

TRACY L. PROWSE¹, MAUREEN CARROLL², JANE EVANS³ and MICHAEL INSKIP⁴

¹Anthropology, McMaster University, ²Archaeology, University of Sheffield, ³National Environmental Isotope Facility, British Geological Survey, ⁴Radiation Sciences Graduate Program, McMaster University

The widespread use of lead in Roman Italy is inferred by the presence of lead artifacts on archaeological sites, regular references to its use in ancient written sources, and environmental evidence of lead accumulation in ice cores dating to the Graeco-Roman period (ca. 500 BCE – 300 CE). Evidence of metal working, lead scrap, and lead objects from the site of Vagnari suggests that lead was an abundant resource on this estate and used for a variety of purposes. Pb isotope analysis of lead manufacturing debris and artefacts (n=38) recovered in the *vicus* indicate that some of the ores were extracted from mines in Sardinia.

This study investigates whether the use of lead on this site is correlated with elevated lead levels in the teeth of its inhabitants and explores the possible health consequences of its use on the people working and living at Vagnari. LA-MC-ICP-MS analysis was performed on 5 deciduous and 15 permanent molars from the Vagnari skeletal sample. Each tooth was ablated 10 times from the enamel through the dentine following the growth orientation of dentine tubules, avoiding the circumpulpal area and external enamel. Our results show that 40% (n=8) of the sample had highly elevated lead levels (up to 37.7 ppm) - including men, women, and children - suggesting that individuals were exposed to high levels of lead during tooth development. This interdisciplinary study examines the relationship between lead production, lead exposure, and health risks for members of this rural Roman community.

Funded by the Social Sciences and Humanities Research Council of Canada (#430-2017-00291).

Sensitivity of ancestral state reconstruction to the phylogenetic positions of fossils: A test case using anthropoid primate facial skeletons

ALEXANDER D. PRUCHA

Center for the Advanced Study of Human Paleobiology, The George Washington University

Ancestral state reconstruction (ASR) allows evolutionary biologists to predict what the common plesiomorphic conditions for given traits might

have been within clades of interest. When used in conjunction with three-dimensional geometric morphometric (3DGM) data of skeletal material, ASR can produce precise visualizations of species' hypothetical last common ancestors (LCAs) as they are predicted by various applicable evolutionary models. However, the potential accuracy of ASR depends heavily on the inclusion of fossils in the analysis, as fossils are the only direct evidence of morphologies' evolutionary history.

Of course, the evolutionary relationships between fossil primates and extant primates cannot be confirmed to the extent that the relationships between modern taxa may be confirmed via molecular data. Thus, especially for Miocene hominoids whose mosaic morphologies do not definitively ascribe them to one crown ape clade or another, multiple hypotheses exist for phylogenetic placement relative to extant apes. Using 3DGM data for the hominoid facial skeleton, this project investigates the effect on ASR of modulating the phylogenetic placement of fossil taxa within an anthropoid tree. Preliminary results, conducting ASR on a phylogeny which includes a virtual reconstruction of the stem hominoid *Ekembo*, suggest that changing the exact phylogenetic position of this fossil can significantly affect ASR-based predictions of shape change in different crown ape lineages' subsequent evolution. This analytical approach may thus improve our ability to visualize what different hypotheses of Miocene ape phylogeny mean for hypotheses of more recent apes' form and evolution—for example, that of the *Pan-Homo* LCA and its contemporaries.

Funding provided by the Smithsonian 2.0 and Collections Care and Preservation Funds, and by The George Washington University.

Population survey and habitat preference of night monkeys (*Aotus azarae*) in Tambopata, Peru

MACKENZIE R. PRYOR and SHARON GURSKY
Anthropology, Texas A&M University

While extensive research has been conducted on Azara's night monkey (*Aotus azarae*) in the southernmost part of their distribution, few studies of this species have been conducted in the northernmost part of their distribution. This project compares the population density of night monkeys at three sites in the northernmost part of their range in Tambopata, Peru. Each site comprised a different forest stage. This study took place June to July 2019. Line transects were walked at a pace of ~3km/hr along the existing trails from 5:30pm – 7:30pm and 4:00am – 6:00am. Upon detecting a monkey, the time, the distance between the animal and the observer, the distance between the animal and the trail, the height in the canopy, and the size of the group were recorded. A total of 120.54 km was

walked in total, during which 57 monkeys were observed with an average group size of 2.3. 24 monkeys were observed in the early secondary, 22 monkeys in old secondary, and 11 monkeys in near primary forest. The new secondary forest site had a density of 25.1 monkeys/km, the old secondary forest site had a density of 30.5 monkeys/km, and the near primary forest site had a density of 15.0 monkeys/km. On average across all sites, the monkeys were seen in trees with a DBH of 29.9 and at a height of approximately 14.9 meters. While there was no significant difference between the three habitat types, there was a trend toward taller trees in the primary forest habitat.

Funding was provided by the MSC LT Jordan Institute and the Texas A&M Department of Anthropology.

Re-evaluation of the affinities of the ?*Dryopithecus wuduensis* mandible

KELSEY D. PUGH^{1,2}, M. KATHLEEN PITIRRI³, JULIA L. ARENSON^{1,2}, BRIAN M. SHEARER^{4,5}, CHRISTOPHER C. GILBERT^{1,2,6,7} and ERIC DELSON^{1,2,5,7,8,9}

¹PhD Program in Anthropology, Graduate Center of the City University of New York, ²New York Consortium in Evolutionary Primatology, (NYCEP), ³Department of Anthropology, Pennsylvania State University, ⁴Department of Cell Biology, New York University School of Medicine, ⁵Morphometrics Group, NYCEP, ⁶Department of Anthropology, Hunter College of the City University of New York, ⁷Department of Vertebrate Paleontology, American Museum of Natural History, ⁸Department of Anthropology, Lehman College of the City University of New York, ⁹Institut Català de Paleontologia Miquel Crusafont (ICP), Universitat Autònoma de Barcelona

A mandible of a catarrhine primate was discovered in the Late Miocene deposits of Wudu County, Gansu Province, China in 1948 and was published several decades later as the holotype of *Dryopithecus wuduensis*. The specimen's attribution to *Dryopithecus* was based on similarities to European apes in premolar proportions, enamel thickness, and size, which are also features that serve to distinguish it from Asian fossil apes, such as *Sivapithecus*. More recently, similarities to plio-pithecoids have been noted, but the affinities of the Wudu mandible to other catarrhines have yet to be examined quantitatively. This study analyzes the morphology of the Wudu mandible in the context of a broad catarrhine sample using linear indices of dental and mandibular proportions and 3D geometric morphometrics of the corpus. Results do not suggest clear affinities to any one non-cercopithecoid catarrhine taxon, but confirm that the short third premolar and elongate fourth premolar of the Wudu mandible differentiate it from most European apes, as well as from Asian fossil apes and extant great apes. An elongated third molar and narrow incisor row further distinguish it from European apes, as well as hylobatids. In many of the described features, the Wudu

ABSTRACTS

mandible is most similar to sampled stem hominoids (and, to a lesser degree, pliopithecoids). Thus, these results support the distinctiveness of *D. wuduensis* from Asian and some European apes, though an expanded fossil sample is necessary to better contextualize the phenetic affinities of this mandible and further explore its intriguing potential similarities to stem hominoids.

Funding was provided by the NSF (BA-DDRIG-1613434), Wenner-Gren Foundation (9297), and The Leakey Foundation.

Visualising mastoiditis with a potable X-ray system

SAMANTHA L. PURCHASE¹, ELIZABETH CRAIG-ATKINS¹, PIA NYSTROM¹ and JAYDIP RAY²

¹Archaeology, University of Sheffield,

²Neuroscience, University of Sheffield

This project aims to develop a new method of diagnosing mastoiditis in skeletal remains and to expand the understanding of the aetiology and epidemiology of mastoiditis. Mastoiditis is a common childhood infection and one of only a handful of processes that create permanent bony evidence of childhood physiological stress. Nonetheless, it is seldom studied archaeologically and the methods that exist are destructive or require access to large, stationary imaging equipment. We theorize that our method will produce radiographs diagnostic of both childhood mastoiditis (CM) and adult mastoiditis (AM); and the presence of mastoiditis in the sample will correlate with that of lesions indicative of chronic maxillary sinusitis (MS) and lower respiratory infection (LRI). A sample of 40 individuals from Black Gate cemetery, Newcastle-upon-Tyne, England (8th–12th century C.E.) were analysed. All individuals with at least one complete mastoid process had it/them imaged in three planes using a hand-held X-ray system. All individuals older than 16 years were examined for lesions indicative of MS and LRI. Almost half (13/27) of the sample had lesions indicative of CM and fifteen percent (6/40) had lesions indicative of AM. Of the individuals diagnosed with AM, 33.3% (2/6) and 16.7% (1/6) also had lesions indicative of MS and LRI, respectively. The method was successful at diagnosing both types of mastoiditis. That so many had lesions indicative of CM indicates that CM was common, but not always life threatening; the co-occurrence of AM, MS, and LRI suggests that broad environmental risk factors influenced the population's morbidity.

Elucidating *Paralouatta's* semi-terrestriality using the virtual morpho-functional toolbox

THOMAS A. PÜSCHEL¹, JORDI MARCÉ-NOGUÉ^{2,3}, JUSTIN GLADMAN⁴, BIREN A. PATEL⁵, SERGIO ALMÉCIJA^{3,6,7} and WILLIAM I. SELLERS⁸

¹Institute of Cognitive and Evolutionary Anthropology, University of Oxford, ²Department of Pathology and Anatomical Sciences, Jacobs School of Medicine and Biomedical Sciences, University at Buffalo, State University of New York, ³Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, ⁴Department of Engineering, Shared Materials Instrumentation Facility (SMIF), Duke University, ⁵Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ⁶Division of Anthropology, American Museum of Natural History, ⁷New York Consortium in Evolutionary Primatology, American Museum of Natural History, ⁸School of Earth and Environmental Sciences, University of Manchester

Currently, there are no extant platyrrhine primates living in the main Caribbean islands. However, the fossil record of this island region has provided spectacular findings of different platyrrhines that were part of a diverse radiation showing exceptionally unusual morphologies. Among these, the Cuban genus *Paralouatta* represents some of the most enigmatic primates ever discovered in the Greater Antilles. *Paralouatta's* post-cranium has been interpreted as showing signs of semi-terrestriality, a locomotor adaptation without known analog in platyrrhine evolutionary history. Nevertheless, whether or not the post-cranial traits of *Paralouatta* are truly indicative of semi-terrestriality is still uncertain. Using different virtual morpho-functional tools on a comparative sample of 3D talar models of diverse anthropoids representing diverse locomotor modes, this study aims to further assess if *Paralouatta* corresponds to a semi-terrestrial species. Specifically, finite-element analysis and geometric morphometrics were used to quantify biomechanical performance and shape, respectively, and then several machine-learning (ML) algorithms were trained using both the biomechanical and morphometric data to clarify the locomotor behavior of the fossil specimens. The ML algorithms categorized the *Paralouatta* fossils as arboreal quadrupeds. However, some of the obtained results are still suggestive of some level of terrestriality, hence all this information is discussed in terms of platyrrhine evolution. The proposed methodological approach can be certainly beneficial when elucidating the behaviors of other fossil species.

T.A.P.: Leverhulme Trust Early Career Fellowship, ECF-2018-264; SA: NSF-BCS 1316947, AEI/FEDER EU (CGL2017-82654-P), and the Generalitat de Catalunya (CERCA Programme); BAP: National Science Foundation (BCS-1317047; BCS-1317029; BCS-1539741); The Leakey Foundation.

Infancy at Altitude: Milk composition, infant growth, and high altitude adapted infant phenotypes

E A. QUINN

Anthropology, Washington University in St. Louis

Infancy is a critical period of selection for humans. Phenotypic changes during infancy may be important for survival and may have long term influences on adult phenotypes. This may be particularly important in challenging environments, such as high altitude. Reduced stature and prioritization of adipose tissue have long been heralded as part of a suite of genetic adaptations to high altitude; emerging evidence suggests that marginalization, nutrition, infectious disease, and chronic cold stress may be the primary drivers of reduced linear growth in infants and young children from high altitude adapted populations.

We review the growing body of evidence that some of this early regulation of infant growth may be associated with macronutrients, hormones, and immune factors in human milk. Hormonal signals in milk, especially those involved in metabolism, do not show strong associations with overall infant weight or length for age but do show associations with body fat patterning as measured by skinfold thicknesses. Such body fat patterning may be important in regulating cold and immunological stressors experienced by infants from high altitude populations.

Previously, we have reported that linear growth among ethnically Tibetan infants and young children from Nepal does not correlate with altitude but may be sensitive to pathogen exposure and nutritional stress. Beall (1981) hypothesized that infectious disease may be an important selective pressure on growth among high altitude populations; evidence from human milk and illness histories of children demonstrate that infectious disease exposures are key factors contributing to growth phenotypes in high altitude adapted populations.

This research was funded by the National Science Foundation BCS 1518013, the Wenner Gren Foundation, and the Leakey Foundation for

Biological Anthropology in Peru: A Contemporary Analysis of Its Education and Job Market

BREIDY IVAN. QUISPE VILCAHUAMAN

Anthropology, University of California Riverside

In Peru, the field of biological anthropology is dominated by Western scholars with little academic contribution from Peruvian bioanthropologists. This limitation is reflected in the lack of graduate programs, academic meetings, national peer-reviewed journals, and new generations of specialized Peruvian bioanthropologists. The nonexistent educational opportunities for biological anthropologists has led other career

ABSTRACTS

professionals to take the lead in research that should be examined from a biological anthropological perspective. Thus, this study has two aims: (1) to analyze the current state of academic training for undergraduate students who are trying to pursue a career in biological anthropology, and (2) to examine the job market for biological anthropologists in the national and private sectors. For this research, the curriculum of undergraduate programs from eleven anthropology departments nationwide were analyzed to identify courses offered that relate to biological anthropology. Additionally, informal interviews were conducted with Peruvian biological anthropologists working for different national institutions. The results indicated there is more academic opportunities in biological anthropology for undergraduate students in southern Peruvian universities, yet even this is limited. Additionally, this research shows that the biggest employers of bioanthropologists are national institutions with more demand in forensic anthropology. Therefore, this research demonstrates a first attempt to investigate the development of biological anthropology in Peru and its job market in national institutions.

Who cares? The “learning to mother” hypothesis and allomaternal care in *Colobus guereza*

DOMINIQUE L. RABOIN^{1,2}, ANDREA L. BADEN^{3,4} and JESSICA M. ROTHMAN^{3,4}

¹Anthropology, Rutgers University, ²Psychology, Hunter College, City University of New York, ³Anthropology, Hunter College, City University of New York, ⁴Anthropology, New York Consortium for Evolutionary Primatology

Allomaternal care (AMC), or infant care provided by individuals other than the infant's mother, allows mothers the opportunity to feed and rest while their infants are monitored by conspecifics. While AMC alleviates a mother's burden, it is costly to the individuals providing care because any AMC behavior is lost time for helpers to feed, rest, and invest in their own reproduction. Several hypotheses have been proposed to explain the potential adaptive function of AMC by conspecifics. The “learning to mother” hypothesis states that infant handling enhances maternal skills in juvenile and subadult females, thereby increasing their subsequent reproductive success. Here, we test the “learning to mother” hypothesis to explain helper behavior during AMC in a forest-living colobine. Research was conducted in Kibale National Park, Uganda, where seven mother-infant dyads in three groups of *Colobus guereza* were observed during six consecutive months. Females handled infants more often than males (Mann-Whitney U, $p < 0.01$), and non-adults handled infants more often than adults (Mann-Whitney U, $p < 0.01$). The infant's distance to mother and the infant's nearest neighbor's age and sex best predicted the occurrence of AMC (GLMM, $p < 0.001$). Juvenile females

were the nearest neighbor to infants significantly more often than were adult females (conditional average estimate=3.46, $|z| < 0.001$). These patterns fit the “learning to mother” hypothesis in that non-adult females care for conspecifics' infants to gain valuable parental experience, a hypothesis that is supported in species closely related to *C. guereza*.

ABC Grant for Thesis Research, Psychology Department, Hunter College, National Science Foundation, (1521528, J. Rothman)

Comparison Maba 1 (Guangdong, China) to eastern sample of European Neandertals – Krapina 3

DAVORKA RADOVČIĆ

Department of Geology and Paleontology, Croatian Natural History Museum

Maba 1 is a specimen found in 1958, first described in 1959 noticing similarities within this specimen with European Neandertals (Woo and Peng 1959, from Schwartz and Tattersall 2002). U-series dating done on rhino teeth give an estimate of about 170 to 130,000 BP for the Maba specimen (Yuan et al. 1986). More recent dating of the flowstone covering the layers thought to be the origin of the fossils found, date the Maba specimen to at least $230 \pm 5,000$ BP, with an older estimate dating it to $278,000 \pm 4,000$ BP. Given the approximate dating of the Maba 1 specimen, it makes sense to compare it to the most complete specimen from the Krapina site – Krapina 3, that preserves comparable areas of the cranium (Radovčić et al. 1988). Krapina 3 is dated to about 130,000 BP (Rink et al. 1995), thus possibly broadly penecontemporary to the Maba specimen. The two specimens are overall very similar. The differences are noticeable in morphological details of the frontal bone: more rounded frontal eminence, more protruding and thicker supraorbital torus with deeper sulcus in the Maba specimen. However, Maba is in these details similar to Krapina 6. Other differing morphological detail is ridge along the nasal bones in Maba, and nasion that is positioned posterior to the anterior face of the supraorbitals. While the overall similarity of Maba and Krapina specimens is not a definite evidence, it does indicate gene flow between the East Asian sample and eastern sample of European Neandertals.

An inverse kinematics solution to the problem of collecting 3-D motion data outside of the lab

ZACHARY R. RADWANSKI¹, CHARLES BRIMMER¹, NATHAN E. THOMPSON² and MATTHEW C. O'NEILL³

¹College of Osteopathic Medicine, Midwestern University, ²Department of Anatomy, New York Institute of Technology, College of Osteopathic

Medicine, ³Department of Anatomy, Midwestern University

Accurate quantification of three-dimensional (3-D) segment and joint motion (i.e. kinematics) is fundamental to determining the mechanics, energetics and control of locomotor tasks. There is longstanding interest in measuring kinematics in field and zoo-based studies, but to date this work has been limited due to an exclusive reliance on direct kinematic methods. Model-based inverse kinematics permits quantification of full 3-D segment and joint motion with limited marker sets and in the presence of marker position errors. Here, we evaluate the potential for using a model-based, inverse kinematic approach to collect 3-D motion data in field or zoo-based settings.

Three-dimensional motion of the pelvis and lower/hind limbs of humans (N=3) and bipedal chimpanzees (N=3) walking at matched dimensionless speeds in a controlled, lab-based setting were used to establish the baseline kinematic dataset. A model scaling perturbation and two marker perturbations were introduced to the baseline dataset to emulate issues encountered in typical field or zoo-based studies. The baseline and perturbation kinematics were then compared using root mean square error (RMSE).

Model scaling misspecifications led to RMSEs of less than 5° in human and chimpanzee kinematics, on average. Reducing the pelvis and limb marker number from >29 to 9 resulted in less than 5° RMSE in humans and chimpanzees, on average. Simulating markerless data collection increased the RMSE to $8 \pm 2^\circ$ in humans, but less in chimpanzees. These initial results suggest that an inverse kinematic approach holds significant potential for improving the quality of 3-D motion data collected in zoo or field-based settings.

NSF BCS-0935321

Coronal suture shape at bregma differentiates some primate clades

TODD C. C. RAE¹, SARAH CRUDGINGTON¹ and KELSEY PUGH²

¹Centre for Research in Evolutionary, Social & Inter-Disciplinary Anthropology, University of Roehampton, ²Graduate Center & New York Consortium in Evolutionary Primatology, CUNY

Skeletal features diagnosing clades are essential for determining the phylogenetic relationships of fossil taxa. Hominoids (extant and fossil) have been hypothesised to share a synapomorphy of a wide frontal at the coronal suture; alternatively, this condition has also been explained via allometry. These proposals are tested here via analysis of the angle of the coronal suture at bregma.

Coronal suture angle at bregma was measured from photographs of primate crania in norma superioris. Variation across higher taxa was determined via ANOVA and Tukey's Posthoc test.

ABSTRACTS

Allometry was tested at the level of genus, with mean angle correlated with body and brain weight, respectively. Character state reconstruction was achieved via homogeneous subset coding and traced across the extant primate topology.

Mean bregmatic angle for genera is not significantly correlated with body or brain weight. Significant variation is present between higher taxa, however, with Platyrrhini and Hylobatidae possessing a narrow frontal. Character state reconstruction by genus shows the narrow condition is derived within Primates; platyrrhines and hylobatids evolved the narrow condition convergently, although variation within Platyrrhini renders reconstruction of their last common ancestor equivocal.

The wide frontal in Hominoidea is thus the primitive condition for Catarrhini and does not indicate propinquity of descent, nor is it a passive consequence of size. The presence of the derived narrow condition in platyrrhines and hylobatids has implications for the interpretation of the fossil record.

The ontogeny of shape and integration in the hands and feet of catarrhine primates

ANNA J. RAGNI

Department of Anthropology, Smithsonian Institution, National Museum of Natural History, Department of Vertebrate Paleontology, Richard Gilder Graduate School, American Museum of Natural History, New York Consortium in Evolutionary Primatology

Extant primates differ in their locomotor ontogeny, which may impact the degree of bony shape change through development. Understanding how locomotor ontogeny relates to bony shape change is critical when using juveniles to reconstruct fossil hominin locomotion. This study implements a 3D geometric morphometrics approach to quantify bony shape changes through ontogeny in the capitate, third metacarpal, lateral cuneiform, and third metatarsal of five catarrhine primate taxa: *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Macaca mulatta*, and *Homo sapiens*. The hypothesis that only taxa with significant locomotor shifts through ontogeny would show significant bony shape change ($p < 0.05$) was not supported. Instead, all taxa except *Homo sapiens* showed significant changes in shape through ontogeny (quantified as change in In-Centroid size regressed against change in In-Procrustes distance, $p < 0.05$), though few pairwise differences were statistically significant between taxa in terms of this change. The hypothesis that *Homo* would show significantly less integration between the hand and foot in comparison to other taxa also was not supported ($p > 0.05$). These results show that behavioral locomotor shifts do not correlate significantly with degree of shape change any more than other

factors through ontogeny. *Homo* is not unique in its integration pattern between the hand and foot through ontogeny, and therefore patterns of bone development and integration between the hand and foot are likely conserved across this broad range of catarrhine taxa, particularly within the hominoids, supporting prior hypotheses of exaptation in the *Homo* hand.

Female mobility networks in Central Europe during the Middle Ages: implications on the spread of cultural relationships through migration

COREY S. RAGSDALE¹, JOHNATHAN JUSTICE¹ and PETR VELEMÁNSKÝ²

¹Department of Anthropology, Southern Illinois University Edwardsville, ²Department of Anthropology, National Museum, Prague

The Early Middle Age society of Great Moravia (9th-10th century) is credited by historians as the first Slavic state, and for their contribution of bringing Christianity to Central Europe. The Czech Kingdom that emerged during the High Middle Ages (11th-14th) had a significant cultural impact on much of Europe, gaining great wealth and power through cultural networks and the expansion of the Holy Roman Empire. History provides information about these processes throughout the Middle Ages, but little is known about the effects of migratory networks on cultural processes. Further, cultural development is often attributed to male socio-political interactions in historic records, and female interaction networks are under-represented.

We used dental morphological and metric data to calculate biological distances among Middle Age samples to evaluate population mobility. We first examine the degree of population continuity and replacement during the Early to High Middle Ages transition, including samples from the surrounding regions. We next examine the differences in population structures among males and females during both temporal periods. Our results show a high degree of population continuity among samples from Great Moravian and Czech Kingdom sites. Females among Great Moravian samples have high intra-site variation when compared to males. Females among Czech Kingdom samples show even higher intra-site variation, and low inter-site variation when compared to males. We conclude female mobility patterns were an important part of Great Moravian and Czech Kingdom networks, and may have played a key role in the spread of cultural relationships around Central Europe through migration.

An evolutionary-neuroscience approach to behavioral interventions linking exercise and brain health

DAVID A. RAICHLÉN¹, PRADYUMNA K. BHARADWAJ^{2,3}, LAUREN A. NGUYEN^{2,3},

MARY KATHRYN FRANCHETTI^{2,3}, ERIKA K. ZIGMAN^{2,3}, ABIGAIL R. SOLORIO^{2,3} and GENE E. ALEXANDER^{2,3,4,5,6,7,8}

¹Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California, ²Department of Psychology, University of Arizona, ³Evelyn F. McKnight Brain Institute, University of Arizona, ⁴Department of Psychiatry, University of Arizona, ⁵Neuroscience Graduate Interdisciplinary Program, University of Arizona, ⁶Physiological Sciences Graduate Interdisciplinary Program, University of Arizona, ⁷BIO5 Institute, University of Arizona, ⁸Arizona Alzheimer's Consortium

Recent work suggests exercise can have important beneficial effects on the aging brain, however the underlying mechanisms remain poorly understood. We have argued an evolutionary-neuroscience approach may help us better understand these mechanisms and can provide a foundation for developing novel interventions to improve brain aging (Raichlen & Alexander, 2017, *TINS*, 40:408-421). Here, we suggest that, from an evolutionary perspective, physical activity mainly occurred during foraging, which combines aerobic activity with cognitively demanding tasks (e.g., spatial navigation and executive cognitive functions). Thus, mechanisms linked to neuroplasticity, including hippocampal neurogenesis, may be triggered by physical activity as a way to enhance cognitive needs during foraging tasks. If correct, simultaneous physical and cognitive challenges may lead to the strongest brain benefits.

To begin testing this hypothesis, we developed a novel intervention that combines aerobic exercise with cognitive demands targeted by foraging (including spatial navigation and executive cognitive functions) presented on a tablet computer. In a 12-week randomized controlled trial, older adults (age 60-74) significantly improved cognitive performance (serial subtraction while walking) following the intervention ($p = 3.5e-7$). Individuals who exercised alone or used the cognitive challenge without exercise also improved cognitive performance (p 's=0.048) but effect sizes were less than half as large as the simultaneous intervention. Our results support the hypothesis, grounded in an evolutionary medicine perspective, that combined aerobic and cognitive challenges will have beneficial effects on the brain. We suggest this study demonstrates the power of using an evolutionary-neuroscience approach to design interventions that can improve health and aging in modern populations.

A review of biomechanical studies examining the impact of mobility on long bone morphology

REBECCA RAINVILLE

Anthropology, Université de Montréal

ABSTRACTS

Biomechanical analyses are used to understand patterns in past human behavior. More precisely, cross-sectional properties of long bones have been used to explore the relationship between skeletal morphology and mobility. The rapidly growing interest in this field has created an influx of data, however, the variation in methods limits comparisons across populations, while studies that are comparable often appear to yield conflicting results. For the present study, the general assumption that decreasing levels of physical activity lead to a reduction in postcranial robusticity is tested by comparing the results of studies on skeletal populations with different mobility patterns. The compiled data reveal that cross-sectional properties do not show a consistent pattern with studies indicating either decreased, stable or even increased skeletal robusticity with reduced mobility. Thus, there is no overall trend of skeletal gracilization with decreasing levels of mobility rather, changes in postcranial morphology vary according to time and space. Different measures of body size standardization and methodology can only partly explain this variation. Furthermore, given the complexity involved in the bone modeling process, it is difficult to discern whether adaptations in bone structure are the result of changes in physical activity or, rather, in other factors such as genetics, nutrition and health. Thus, inconsistencies may simply reflect multiple, regionally specific factors interacting to influence bone deposition. The current study underscores the difficulty of using cross-sectional properties to infer mobility or important shifts in modes of subsistence in past populations.

DNA integrity in forensic samples

SAMANTHA RAMEY and MERADETH H. SNOW
Anthropology, University of Montana

Studies have been conducted on cross-contamination throughout the investigation process. However, no published studies have examined the potential for contamination during the storage process. This study tested two DNA collection methods for the potential of cross-contamination during storage. Three different dry times of buccal swabs and Whatman cards were tested: none, one hour and 24 hours, in triplicate, and then placed into storage with a uncontaminated sample for one of the following times: 72 hours, 14 days, or 45 days. Cross-contamination was detected in the 72 hours and 45 days blank samples. There was no detection of cross-contamination in any of the blank 14 days samples. The statistics revealed there is a statistical significance for the storage time but not dry time. The Fisher exact test yielded a 0.00 p-value ($\alpha = 0.05$) for the Whatman card, while the buccal swabs yielded a 0.054 p-value ($\alpha = 0.05$). Cross-contamination was detected upon removal from storage demonstrating that further research is needed to better understand cross-contamination during storage.

Social relationships in a group of wild spider monkeys (*Ateles belzebuth*) in the Ecuadorian Amazon

SEBASTIAN RAMIREZ AMAYA^{1,4}, KEVIN LANGERGRABER¹, ANDRES LINK^{3,4} and ANTHONY DI FIORE^{2,4}

¹School of Human Evolution and Social Change, Arizona State University, ²Department of Anthropology and Primate Molecular Ecology and Evolution Laboratory, University of Texas at Austin, ³Departamento de Ciencias Biológicas, Universidad de Los Andes, ⁴Atelines Project, Fundacion Proyecto Primates

Theory predicts that the nature of the social relationships among group living primates is predicted by the balance between the strength of within and between group competition over resources that limit reproduction. We used this theory to predict the patterns of male and female social relationships in a wild community of spider monkeys living in a pristine lowland site in the Yasuní Biosphere Reserve, Ecuador. We used five years of data on co-association in the same subgroup and on close spatial proximity collected at 15-min intervals during focal-individual-follows of adults to characterize the social relationships within the group. We used permutation tests to identify differentiated dyadic social relationships from random chance alone among dyad classes. We then used multi-group models to quantify and compare the strength and patterns of differentiation of social relationships of male-male, female-female, and mixed-sex dyads. The average strength of same-sex relationships was higher than mixed-sex relationships, and males had stronger same-sex relationships than females. Relationships among all dyad types were differentiated, F-F dyads exhibited more highly differentiated relationships than either M-M or mixed-sex dyads. We discuss potential adaptive benefits for males of forming relationships with close kin. We compare our results with those obtained from chimpanzee communities where males have been shown to also form strong social relationships with each other, presumably in response to high levels of intragroup contests over access to females. In contrast to male chimpanzees, male spiders do not form dominance relationships with one another, and intragroup M-M contests are extremely rare.

Funded by NSF BCS-1062540, BCS-1633882, the National Geographic Society, the Wenner-Gren Foundation for Anthropological Research, the Harry Frank Guggenheim Foundation, and the University of Texas at Austin.

Early life growth disruption and effect on mortality in Arkhangai, Aimag, Mongolia (745-840 AD).

NATALIE RAMIREZ and CHRISTINE LEE
Anthropology, California State University Los Angeles

This study analyzes evidence for early life growth disruption and its effect on mortality in nomadic pastoralist population from Arkhangai, Aimag, Mongolia. Fifteen burials (7 infants and 8 juveniles/adults) were analyzed. Porotic hyperostosis, cribra orbitalia, periostitis, and enamel defects were considered in relation to age of death. 100% of the burials exhibit evidence of malnutrition or illness or both. All of the infants present with the presence of cribra orbitalia, porotic hyperostosis, and periostitis and 71.42% present with enamel defects. Of juveniles and adults, 62.5% show evidence of cribra orbitalia and porotic hyperostosis, while 37.5% exhibit evidence of enamel defects. Uyghurs raised livestock and consumed agricultural based products. A dzud, extremes snowfalls, cold temperatures, and winds, are known to cause a high mortality of livestock. Historical records indicate that a period during 839-840 AD a dzud provoked famine, epidemics and the loss of animals. Difficult environmental conditions can allow us to think that a reduction of resources occurred at this time. Meat and milk consumption was affected by livestock mortality along with limited agricultural products reduced by droughts. We can suggest the Uyghur suffered from a lack of nutrient intake in their population. Poor nutrition and physiological stress provoked by nutritional deficiencies weakens the immune system of the human body making it prone to the development of infectious diseases and premature death.

Load paths in a skeletal element with heterogeneous elasticity

ANDREW J. RAPOFF¹, DAVID A. HODGSON¹, W. SCOTT. MCGRAW² and DAVID J. DAEGLING³

¹Mechanical Engineering, Union College, ²Anthropology, Ohio State University, ³Anthropology, University of Florida

A load path in a structural element (e.g., a bone) is the stiffest route through the element and represents the primary route through which internal forces are transmitted. For example, most of the load through two springs in parallel will pass through the stiffest spring. A load path analysis seeks to determine this route and is used to design weight efficient structures. Its use in anthropology permits functional inferences between species for homologous skeletal elements. For example, the endocondylar ridge was found to be the load path in the *Macaca* mandible from tooth row to condyle during simulated feeding events (Ross et al. *AJPA* 168:209); variations in load paths in mandibles of other extant species and the fossil record may provide insight into feeding mechanics. We introduce a load path analysis that incorporates heterogeneous orthotropic elasticity about a nutrient foramen in an equine metacarpus. Orthotropic elastic constants (elastic and shear moduli and Poisson's ratio) were determined using microindentation (*ASME SBC* 2003). Load paths

ABSTRACTS

on either side around the foramen were determined by stepping through locations proximally to distally. We generally found the load paths to start longitudinally, to pass medially and laterally a distance of two foramen diameters away from the foramen and finally to converge longitudinally again. These paths reflect both the predominant loading direction in this skeletal element as well as demonstrate material strategies for avoiding stress concentrations around holes. This analysis illustrates the need to consider both structural and material properties in modeling the mechanical stress environment.

Impacts of lifestyle on diffuse idiopathic skeletal hyperostosis (DISH) within the Texas State Donated Skeletal Collection

LAUREN E. RATLIFF¹, MICHELLE D. HAMILTON², NICHOLAS P. HERRMANN² and DANIEL J. WESCOTT²

¹, Tennessee Valley Archaeological Research, ²Anthropology, Texas State University

Diffuse idiopathic skeletal hyperostosis (DISH) is a condition that causes fusion along that right side of vertebral bodies in a “candle-wax” pattern that has no known etiology. Physiological, social, and demographic factors have been correlated to DISH, including obesity, socioeconomic status, sex, ancestry, age, gout, and diabetes. This study drew upon previous works to examine associations with these factors within modern individuals from the Texas State Donated Skeletal Collection. A total of 247 individuals were examined, and 45 met the criteria for having DISH under an adjusted definition adopted for this research.

Results indicated males, older individuals, and individuals with gout were more likely to develop DISH. The results also supported previous work identifying which vertebrae were most affected, with T9-T10 and surrounding joints being most affected. This study also addressed the varying definitions of DISH and how these criteria changed the results depending on definition. Finally, this research suggests standardized definitions and criteria to use when identifying DISH in skeletal remains. The importance of this research is that it adds to the body of literature on the hard tissue expression of DISH as well as interactions between the condition and different aspects of lifestyle.

Molecular Findings of Combined Application of Forensic Toxicology and Ancient DNA techniques on Egyptian canopic jar contents

ENRIQUE RAYO¹, ABIGAIL BOUWMAN¹, LANA BROCKBALS², THOMAS KRAEMER², MICHAEL

HABICHT¹, PATRICK EPPENBERGER¹, VERENA SCHUENEMANN¹ and FRANK RUEHLI¹

¹Institute of Evolutionary Medicine, University of Zurich, ²Institute of Forensic Medicine, University of Zurich

Ancient Egyptian remains have been of interest for anthropological research for decades. Despite a multitude of investigations, the ritual vessels for the internal organs removed during body preparation — liver, lungs, stomach, intestines, of Egyptian mummies are rarely used for palaeopathological or medical investigations. These artifacts, commonly referred to as canopic jars, are the perfect combination of cultural and biological material and present an untapped resource for both Egyptological and medical fields. We applied next-generation sequencing to assess ancient DNA preservation and gas chromatography/high-resolution mass spectrometry to identify any embalming components in a total of 140 jars. Due to the complicated nature of the samples, several ancient DNA extraction and library preparation methods were tested on the tissues, with the single-stranded library preparation method yielding authentic ancient DNA fragments for one jar based on the characteristic ancient DNA damage profile. This is the first-ever recorded evidence of ancient human DNA found in Ancient Egyptian canopic jars. In addition, we also present the complex molecular fingerprint of these vessels — differing from the profile of mummified Egyptian remains. These results are a component of ‘The Canopic Jar Project’ launched by the Institute of Evolutionary Medicine at Zurich, which is laying the foundation for multidisciplinary research procedures by examining a large series of samples from European and American museum collections.

Climate colonialism and “adaptive capacity” in the Arctic

ELSPETH READY

Human Behavior, Ecology and Culture, Max Planck Institute for Evolutionary Anthropology

Historical narratives of the Arctic frequently imagined a future where it would be tamed through climate change. A warmer Arctic is one no longer hostile to capitalist expansion. But even without this encroachment, climate change represents an external regime imposed upon Arctic indigenous peoples without their consent, that threatens their lands, resources, and traditional practices. In this respect, climate change can be considered a passive form of colonialism. I argue that viewing climate change as one of many ongoing forms of colonial creep raises deeper questions about its potentially negative consequences, particularly for health. Much Arctic climate change research focuses on “adaptive capacity,” asking how Inuit can modify their behaviors to “successfully adapt” to climate change, but fails to address the complex relationship between

culture and well-being. Drawing on my research in the Canadian Arctic, I suggest that the problems faced by Inuit communities today highlight important gaps in our discipline’s theory and approach that need to be addressed for us to meaningfully engage with the problem of “climate change adaptation.” First, we need to grapple with some of the major questions in our broader discipline that have been sidestepped over the past century, namely, where does culture come from, and how does it change? Second, we need to investigate the consequences of rapid change (cultural, ecological, economic and social) for health—especially mental health—and well-being. Third, we need to reconfigure the relationship between pure and applied research.

Preliminary Analysis of the Commingled Ossuary at Brădești (Fenyéd), Harghita County, Transylvania, Romania

SOPHIA I. RECK¹, JOSÉ L. MARRERO-ROSADO², ROBERT E. MITCHELL³, MEAGHAN J. CHAMPNEY⁴, JOHANNA E. YOUNG⁵, MARLA BARREIRO SANCHEZ⁶, ANDRE GONCIAR⁷, ZSOLT NYÁRÁDI⁸ and FRANKIE WEST⁹

¹Department of Geography & Anthropology, Louisiana State University, ²Department of Anthropology, University of California at Berkeley, ³Department of Anthropology, California State University, Los Angeles, ⁴Anthropology Department, Binghamton University, ⁵Forensic Science Program, George Mason University, ⁶Department of Anthropology, University of South Florida, ⁷ArchaeoTek, BioArch Canada, ⁸Haáz Rezső Museum, Romania, ⁹Forensic Science Program, Western Carolina University

In Transylvania, ossuaries are commonly associated with medieval Catholic churches. These secondary burials allowed for continued occupancy of consecrated ground while opening new space for primary interments in the church graveyard. The site at Brădești (Fenyéd), Harghita County, Transylvania, Romania contains an example of one such church, graveyard, and ossuary. Remains were removed from the ossuary in 2013 and subsequently curated and analyzed over several field seasons. Analysis yielded a minimum number of individuals (MNI) of 158 from the left petrous portion (using MNI from White, 1953) and 145 from the linea aspera of the left femur (Mack et al., 2016). Fragmentation analysis (Lambacher et al., 2016) revealed the following percent completeness for each element: radii 22.59% (n=172), ulnae 23.15% (n=210), humeri 18.17% (n=554), femora 12.62% (n=820), tibiae 12.21% (n=524), and mandibles 56.68% (n=182). Ultimately, more individuals were observed in the ossuary than the number of burials (n=54) in the Brădești (Fenyéd) graveyard. Results of this preliminary analysis provide a greater understanding of the extent to which the site was used over time, while elucidating the preservation and taphonomy of skeletal elements

ABSTRACTS

in ossuaries, especially regarding human agency over these processes. The results also show the effectiveness of landmark analysis when assessing MNI in an extremely commingled and fragmented context. In the future, the results of the present study could be compared to a fragmentation analysis of the primary interments at the site to quantify the taphonomic effects of secondary burial in one population.

Hominin community structure: ecological patterns and niche construction

AMY L. RECTOR¹ and KAYE E. REED²

¹Anthropology, Virginia Commonwealth University, ²Institute of Human Origins and School of Human Evolution and Social Change, Arizona State University

Hominin paleohabitat reconstructions usually rely on identifying patterns from the fossil record and comparing them to variation in modern African habitats to detect similarity in ecological parameters. Often, faunal communities as units of analysis do not explicitly include hominins; if they are included, hominin species are not considered as biologically or ecologically different in terms of their influence on faunal community structure. However, this ignores the fact that different hominin species may have an active role in their structuring their communities and possibly changing the trajectory of evolution within the community.

Here, we approach the question of the ecological context for the evolution of earliest *Homo* through the lens of the extended evolutionary synthesis: How did earliest *Homo* influence the paleocommunity within which the taxon existed? How do patterns in the fossil record and large mammal communities reflect possible niche construction by *Homo*? How did *Homo* possibly change the historical outcome of other species? To address these questions, large datasets of fossil and extant African mammalian communities were analyzed to detect changes in functional and species richness and evenness, as well as turn over patterns in these communities, before, concomitant with, and after the evolution of *Homo*.

Results show that mammalian community structures changed through time and were influenced by the evolution of *Homo* compared with communities evolving with earlier hominins. While climate was also important, we suggest that the advent of obligatory stone tool use in scavenging or hunting in the *Homo* lineage also was responsible for change.

Preliminary description of the fossil cercopithecids from Galili, Ethiopia

HAILAY G. REDA¹, STEPHEN R. FROST¹, JAY QUADE², HASEN SAID³ and SCOTT W. SIMPSON^{4,5}

¹Anthropology, University of Oregon, ²Geosciences, University of Arizona, ³Ethiopian Studies, Addis Ababa University, ⁴Anatomy, Case Western Reserve University, ⁵Laboratory of Physical Anthropology, Cleveland Museum of Natural History

The Galili Research site has furnished over 650 fossil cercopithecids collected by previous and current research groups, including a few complete crania, but isolated teeth predominate. The majority come from the Dhidinley (4.4-3.9 Ma) and Shabeley Laag (ca. 3.9 Ma) members. The Galili cercopithecids are important because few African sites preserve cercopithecoid taxa during this time. Galili cercopithecids were compared with those from broadly contemporary localities using qualitative features and standard dental metrics. To date, at least five cercopithecoid taxa have been identified: an early member of the *Theropithecus oswaldi* lineage, two other papionins and two colobines. The *T. oswaldi* lineage material has simpler, more primitive molars than that from Woranso-Mille, Hadar, Omo, and Koobi Fora. They are also smaller than all of these populations, but not significantly than Woranso-Mille, perhaps due to the limited Galili sample. Together these facts suggest an older date for Galili. The most common papionin from Galili is close in size to papionini gen. sp. indet. from Woranso-Mille as well as *Pliopapio alemui*. The predominant Galili colobines are close in size to *Cercopithecoides meaveae* and *Kuseracolobus aramisi*. A larger papionin and colobine are also present, but very rare. Overall, the relatively diverse assemblage suggests a range of available vegetation and habitat types, but the predominance of non-*Theropithecus* papionins compared to colobines (15%) at Galili suggests that it may have been a somewhat open habitat. That *Theropithecus* is present, but rare (5-10%) is similar to Kanopoi, but unlike Woranso-Mille where the genus greatly predominates.

This research supported by NSF-BCS 1640342 to SS and University of Oregon to SF.

Variation in adolescent male chimpanzee reproductive tactics: implications for understanding what is a "population" of chimpanzees

RACHNA B. REDDY

Anthropology, University of Michigan

Chimpanzees have been studied in the wild for nearly six decades. Although this length of time is impressive, it is shorter than the species maximum lifespan. Consequently, many questions about chimpanzee behavior remain unresolved, and we do not know the extent to which observations from a single group can be generalized to

the entire chimpanzee "population" we want to characterize. My study of a large cohort of adolescent male chimpanzees (9 – 15 y) at Ngogo in Kibale National Park, Uganda, reveals heretofore undocumented behavior, making it difficult, if not impossible, to define what is species typical. Prior research indicates that adult male chimpanzees sexually coerce females, and those who do so reproduce with them. In my research I found that some adolescent males were able to reproduce despite the fact that they were unable to compete effectively with adult males, as they were young, low ranking, and still physically and socially immature. Instead of coercing females into mating with them, these adolescent males adopted a novel mating tactic: they formed affiliative bonds with specific females. These bonds are similar, yet different, from the well-known friendships formed between adult male and female baboons. I discuss how some unusual demographic and social factors at Ngogo may explain why such male – female affiliative bonds have not been described in other chimpanzee communities. Results of this study show that considerable inter-community differences in chimpanzee behavior exist. This makes it problematic to define a chimpanzee population.

This research was supported by the National Geographic Society, the National Science Foundation (BCS-1540259; DGE-1256260), the Nacey-Maggioncalda Foundation, the L.S.B. Leakey Foundation, and the University of Michigan.

Virtual reconstruction and description of the lower face and dentition of StW 498 – a Sterkfontein *Australopithecus*

SHANI REDDY^{1,4}, RONALD J. CLARKE¹, KRISTIAN J. CARLSON^{1,2}, JOSÉ BRAGA^{1,3} and DOMINIC J. STRATFORD⁴

¹Evolutionary Studies Institute, University of the Witwatersrand, ²Department of Integrative Anatomical Sciences, University of Southern California, ³Laboratoire d'Anthropologie Moléculaire et Imagerie de Synthèse, Université de Toulouse (Paul Sabatier), ⁴School of Geography, Archaeology and Environmental Studies, University of the Witwatersrand

The cranial vault fragments, relatively complete left and right maxillae, and mandibles of StW 498 were excavated from square P/41 at Sterkfontein Member 4 in 1988 by Alun Hughes and Phillip Tobias. While the mandibular and maxillary dentition is complete, the right hemi-mandible and right maxilla are fragmentary and anatomically displaced. Because of its badly crushed condition, a physical reconstruction was not advisable. The unreconstructed anatomy of this specimen has been briefly described by Schwartz and Tattersall (2005), and the fragmented dentition briefly described by Moggi-Cecchi *et al.* (2006). The primary purpose of this research was to virtually reconstruct StW 498 using high resolution image data acquired from microCT scanning, which provided a valuable opportunity to conduct

ABSTRACTS

new, detailed quantitative analyses and qualitative observations in order to place it within a framework of hominid cranio-dental variation, focusing in particular on *Australopithecus africanus*, *Australopithecus prometheus* and *Paranthropus robustus*. Based on the internal morphology and size of the dental arcade, StW 498 is a young adolescent male. The specimen exhibits dental pathology, specifically crowding of the maxillary dentition which resulted in the atypical eruption and position of the left maxillary canine. However, contra to the suggestion by Schwartz and Tattersall (2005), the right lower canine reflects taphonomic disruption of the intact anatomy rather than an eruptive anomaly. The results of this research indicate that StW 498 is morphologically more similar to specimens attributed to *A. prometheus*, such as MLD 9, StW 252, and StW 573, than to *A. africanus* and *P. robustus*.

This research was generously funded by the DST-NRF Centre of Excellence in Palaeosciences (CoE-Pal) (grant number - COE2016-366) and by the Palaeontological Scientific Trust (PAST), Johannesburg, South Africa.

Perestroika in paleoanthropology: The Eyasi Plateau Paleontological Expedition (EPPE), Laetoli (Tanzania) fossil specimen database and the importance of promoting open-access and reproducibility in paleoanthropology.

DENNÉ REED¹, TERRY HARRISON² and AMANDUS KWEKASON³

¹Anthropology, University of Texas at Austin, ²Anthropology, New York University, ³Anthropology, National Museum of Tanzania

Laetoli is renowned for the discovery of important hominin fossils, including the lectotype for *Australopithecus afarensis*. The Eyasi Plateau Paleontological Expedition (EPPE) Laetoli fossil specimen database contains over 13,000 records of plant and animal fossils (ca. 28,248 specimens) that were collected by EPPE field teams working at Laetoli, in northern Tanzania and documents the discovery, stratigraphic provenience and taxonomic diversity of Plio-Pleistocene fauna and flora between 4.4 Ma and >200 ka.

In 2019 the AAPA put forth a statement on data access in biological anthropology recommending that publications should include access to the primary data used in any analyses. The EPPE database is one of the few open-access paleoanthropological fossil specimen datasets available. Our aim was to demonstrate the feasibility of publishing original specimen data in a manner 1) consistent with AAPA recommendations, 2) that conforms to international standards allowing for discovery through data aggregation platforms, and 3) that is sufficiently validated to allow reuse and analysis of the data.

Data were digitized from the hard-copy field catalog into spreadsheets, then read into the Paleo Core database (<http://paleocore.org>) using custom Python scripts. During this process the data were mapped to standard definitions (e.g., Darwin Core) and the entries were harmonized to standardized vocabularies and data formats. The process of cleaning and standardizing the data demonstrated that it is feasible to publish original fossil specimen data, and also revealed structural changes (i.e., incentives, training) that must be addressed as well as technical hurdles that hinder broader open-access data sharing in paleoanthropology.

Field work funded by NSF (BCS-0309513, BCS-0216683, BCS 1350023), the National Geographic Society, the Leakey Foundation, and NYU University Research Challenge Fund grants. Paleo Core funded by NSF (Grant BCS-1244735).

Physical anthropology, testosterone, and white nationalism: a call to action

MEREDITH W. REICHES

Anthropology, University of Massachusetts Boston

Since 2002, endocrinology researchers have warned that American men's testosterone levels are in decline. While the etiology of the decline is uncertain and average levels remain within normal range, fear for the future of men has become a rallying cry among white nationalists, who view declining testosterone as evidence of slipping social and political power. The science and rhetoric of testosterone decline claims merit urgent attention from physical anthropologists for two reasons. First, physical anthropologists have unique methodological expertise with which to assess their validity, functional importance, and ecological variability. Physical anthropologists recognize that cross-population comparative data reveal no single, optimal level of testosterone for fertility and longevity. They distinguish between bound and bioactive hormone, consider receptor density and sensitivity, and analyze hormone levels both as developmentally modulated individual traits and as states that react to diurnal, energetic, immune, and psychosocial context. Second, when human biology data are mobilized to support discriminatory agendas, physical anthropologists have an opportunity and a responsibility to educate the public about human variation. While the discipline has made strides in the discourse on genetics and race, physical anthropology research and approaches have low uptake in popular dialogue around testosterone. In a Google news search for testosterone, 12 of 30 articles published between July and October of 2019 concern low testosterone in men. None mentions physical anthropology findings or

principles. This paper proposes a research and public outreach agenda to intervene in the narrative linking testosterone to masculinity and white nationalism.

No funding to declare.

A New Discovery of Human Sacrifice in the Lambayeque Valley: Wari Imperialism and Ritual Violence at Huaca Santa Rosa, North Coast Peru

FRANCESCA A. REIMER¹, HAAGEN D. KLAUS¹, OLHA LYSÁ¹, KATHERINE SARGENT¹, EDGAR BRACAMONTE² and WALTER ALVA²

¹Sociology & Anthropology, George Mason University, ²Dirección, Museo Tumbas Reales de Sipán

The nature and extent of imperialism as practiced by the highland Wari culture has long been debated in Andean archaeology. Despite longstanding suspicions of a Wari incursion in the Lambayeque region (north coast), there has never been any direct evidence to indicate their presence - until now. In 2019, evidence was found of a Wari outpost installed at the Late Moche site of Huaca Santa Rosa (mid Lambayeque Valley) around A.D. 650. It included an unmistakable D-shaped ritual structure that exemplified Wari imperial strategies involving procurement and caching of trophy heads. In this poster, we describe the 14 human skeletons of young/middle adult males, females, and a child buried under the floor of this structure. All the bodies were placed in splayed or haphazard positions consistent with north coast sacrifice. Three individuals exhibited perimortem sharp-force trauma from throat slitting and one male was decapitated. While the Wari occupation of Santa Rosa appears to have been short-lived (50-100 years), these rituals appear as a hybrid form between local and foreign traditions, likely a product of syncretism and compromise in a setting of cultural contact. This new evidence deepens the reconstruction of sacrifice on the north coast of Peru and sheds new light on Wari statecraft and Andean ritual killing.

This research was generously supported by a Rust Family Foundation Grant to HDK.

Immortal, though he lies under the ground: Osteobiographies of three individuals from the first Battle of Himera (480 BCE)

KATHERINE L. REINBERGER¹, LAURIE J. REITSEMA¹, BRITNEY KYLE² and STEFANO VASSALLO³

¹Department of Anthropology, University of Georgia, ²Department of Anthropology, University of Northern Colorado, ³Archaeological Heritage Section, Superintendency of Palermo

The term "osteobiography" refers to an individualized approach that emphasizes the identity and life histories of ancient persons. For a field that typically takes population level approaches

ABSTRACTS

and gained its earliest positions by focusing on biology and health, osteobiographies enrich bioarchaeology by providing a more intimate view of individual past lives in social contexts. The ancient Greek world is frequently studied through historical documents that shine a light on individuals, especially the elite. Osteobiographies are eminently compatible with these accounts, yet are underexplored. Bioarchaeology of the ancient Mediterranean continues to utilize bioarchaeology's strengths in population studies and is well suited to consider less-visible individuals of past societies.

The Battles of Himera were two violent conflicts between Greeks and Carthaginians in Sicily and the mass graves from the battles have been well studied in terms of historical narrative, mortuary archaeology, and osteology. In this study, we present osteobiographies of three individuals who died in the 480 BCE Battle of Himera, reporting their unusual lead, strontium, oxygen, carbon, and nitrogen isotopic and paleopathological data. We contextualize the data in a rich framework of historical records of the battles and indicators of health and trauma among Himera's general populace and other soldiers. All three individuals have non-local signatures, and we explore variations in their diet and childhood stress. Osteobiographies more deeply engage researchers and audiences with lived experiences of ancient war veterans, discovering who they were as individuals, in addition to being members of the armies with which they fought and died.

NSF REU award numbers 1560227 and 1560158, the University of Georgia, the University of Northern Colorado, UGA Innovative and Interdisciplinary Research Grant, UGA OVPF Faculty Research Grant

Napping in the wild: How slow lorises balance their intrinsic circadian rhythms and sleep homeostasis against environmental factors

KATHLEEN D. REINHARDT^{1,2}, R. ADRIANA HERNANDEZ-AGUILAR³, MUHAMMAD A. IMRON³, VLADYSLAV V. VYAZOVSKIY⁴ and K. ANNA I. NEKARIS¹

¹Anthropology and Geography, Oxford Brookes University, ²Center for Ecological and Evolutionary Synthesis, University of Oslo, ³Department of Forest Resources Conservation, Universitas Gadjah Mada, ⁴Physiology, Anatomy and Genetics, University of Oxford

Sleep is mediated by numerous intrinsic factors, including circadian rhythms, sleep homeostasis and sleep-wake history. These drivers are further influenced by external factors in nature, where an animal must balance sleep need against environmental pressures. Non-human primates display a variation of activity patterns which can be assumed to superimpose the flexibility of one's sleep architecture across a 24-h period. While research on primate sleep architecture

has increased in the last decade, information is still lacking for wild populations. We recorded locomotor activity of wild Javan slow lorises (*Nycticebus javanicus*; $n = 7$) over 321 days using accelerometer devices, and monitoring environmental factors (temperature and light) in their natural habitat. Slow lorises displayed strict nocturnal activity patterns, with rare occurrence of activity during the day. Monophasic sleep occurred during the day (09:41 ± 03:30 (hh:mm) duration) with pronounced activity changes in anticipation of day-night transitions. Individuals napped at varying quantities and durations during their active period, subsequent to brief arousals during daytime rest. Nap occurrence increased substantially towards the middle of the slow loris active period, where temperature fluctuations were inversely related to rest consolidation. Increased consolidation of rest at the beginning of their habitual sleep period may reflect increased sleep intensity or direct influence of ambient temperature. The distribution of nap occurrence indicate sleep pressure and homeostatic sleep need. Our research poses an intriguing question of how primates compensate for sleep loss while adjusting their sleep pattern to fluctuations in the environment.

Human provisioning is associated with increased telomere length in long tailed-macaque (*Macaca fascicularis*) populations with a longer history of access to human-derived foods

PETER H. REJ¹, AMY R. KLEGARTH^{1,2}, CRYSTAL M. RILEY KOENIG³, MICHAEL D. GUMERT⁴, LISA JONES-ENGEL¹ and DAN TA. EISENBERG^{1,2}

¹Anthropology, University of Washington, ²Center for Studies in Demography and Ecology, University of Washington, ³History, Sociology, and Anthropology, Southern Utah University, ⁴Psychology, Nanyang Technological University

Emerging evidence suggests that short telomere length (TL) increases an organism's predisposition to disease and accelerated aging. However, it is not well understood why these effects do not select for longer telomeres. The 'thrifty telomere' hypothesis provides one possibility: while longer telomeres improve an organism's ability to repair tissue through less constrained cell proliferation, cell proliferation requires energy that might be more adaptively used for other physiological processes. Thus, natural selection may favor shorter telomeres in low resource environments. Here we present an experimental assessment of the thrifty telomere hypothesis carried out across urban long-tailed macaques (*Macaca fascicularis*) in Bali, Indonesia and Singapore. Groups of macaques in Bali have been regularly/ritually provisioned by humans for over 1000 years and are somewhat genetically distinct. Thus, current provisioning levels likely reflect past natural selection. Conversely, in Singapore, groups are less

genetically distinct, and regular human contact/provisioning is a much more recent phenomenon. Therefore, differences across Singaporean groups are more likely to be due to environmental exposures affecting TL within a generation. We measured TL in 168 wild macaques from across both islands. Two different measures of anthropogenic contact were collected from the Bali and Singapore animals. Consistent with the thrifty telomere hypothesis, we observed a positive association between TL and anthropogenic contact within Bali, but not Singapore. Inconsistent with predictions, there were no significant differences in TL across islands. These results provide provisional support for the thrifty telomere hypothesis, suggesting that increased energetic availability may allow selection for longer telomeres.

Supported by UW: RRF (#A111561); Leakey Foundation; NSF: IGERT GLOBES (#0504495), East Asia Pacific Summer Institute (Singapore); National Geographic: Waitt Grant, Young-Explorer's Grant (9234-12); US Student Fulbright Program (Singapore 2013-2014).

Using normal variation in mouse ossification to identify genes underlying growth plate formation

PHILIP L. RENO¹, CATHERINE ROBERTS², EMILY K. SCHUETZ¹, KELSEY M. KJOSNESS¹ and DOUGLAS B. MENKE³

¹Bio-Medical Sciences, Philadelphia College of Osteopathic Medicine, ²Anthropology, Pennsylvania State University, ³Genetics, University of Georgia

The great diversity in primate skeletal shape is in large part dictated by variation in growth rate. Longitudinal growth occurs at growth plates, which amplify and maintain the process of chondrocyte differentiation throughout ontogeny. Thanks to experiments in model organisms such as the mouse, knowledge of growth plate physiology has blossomed; yet, little is known about how growth plate location and behavior are patterned to produce the normal diversity in skeletal shapes. Fortunately, substantial anatomical variation exists within the mammalian skeleton that can be used to identify the mechanisms underlying growth plate formation. The pisiform (in non-human mammals) and calcaneus each form an active growth plate unlike the other carpals and tarsals, and the metatarsals form a growth plate at only one end. In each of these cases, growth plate containing tissues can be paired with tissues undergoing generalized endochondral ossification that control for the effects of age, systemic growth factors, and biomechanical environment. We performed global transcriptome sequencing (RNA-seq) on 0-, 4- and 9-day old mouse growth plate forming and non-forming tissues to identify growth plate-specific genes. Significant differences in gene expression were detected with differentially expressed genes enriched in gene ontology categories associated with cartilage

ABSTRACTS

and skeletal development. Expression differences were also found in genes previously not known to have a role in skeletal development. Identification of the genes involved in the natural formation of mouse growth plates will aid our understanding of the mechanisms underlying differences in skeletal shape among primates.

Funding provided by NSF grants IOS-1656315 & BCS-1638812.

The association among the C677T mutation in the MTHFR gene, skin color measures and UV radiation suggests local adaptation rather than sweeping clines.

LUCIO REYES, CAROLINE MACCLEAN, DAVID GODFRE, FRANCISCO GONZALEZ-HERNÁNDEZ and LORENA MADRIGAL

Anthropology, University of South Florida

The evolutionary forces that lead to the distribution of the C677T mutation in the MTHFR gene is debated. We ask why this allele, notorious for its deleterious effects, is highly frequent in several human populations.

We look at the correlation between insolation, T-allele-frequency and skin-color-measures taken in the same population. We present skin-color-measures obtained with the three filters most frequently used in the EEL apparatus: F425 mμ, F545 mμ, and F685 mμ. Most of the populations which were surveyed were from Eurasia.

Our sample size includes at least 30 data points for which we have data for all the variables. The correlation between the T allele and insolation is negative and highly significant ($r_s = -0.57, n = 36, p = 0.0002$), confirming that the T allele has low frequencies in populations exposed to high solar radiation. The correlation between the T-allele-frequency and the measures taken by the three filters at the same populations were significantly negative. Thus, the allele is not found in darkly-pigmented populations. The correlation was particularly strong and linear for the F685 filter ($r_s = 0.73, n = 35, p = 0.0001$). The MTHFR gene is involved in the folate cycle and is thus affected by UV radiation. Here we have shown that the distribution of the allele is correlated with skin color and insolation. However, the eventual phenotype of this mutation (hyperhomocysteinemia) may have been naturally-selected for an entirely different reason, despite its many poor health effects. Indeed, the world-wide distribution of this allele does not form a smooth cline (such as the skin-color cline), suggesting localized adaptation.

Matriline predicts lower inflammation for women in the Mosuo of Southwest China

ADAM Z. REYNOLDS¹, SIOBHAN M. MATTISON¹, MELISSA EMERY THOMPSON¹, PAUL L. HOOPER¹, KATHRINE E. STARKWEATHER¹, CHUN-YI SUM², SU

MINGJIE³, LI HUI³, TAMI BLUMENFELD¹, MARY K. SHENK⁴ and KATHERINE WANDER⁵

¹Anthropology, University of New Mexico, ²Anthropology, University of Rochester, ³MOE Key Laboratory, Fudan University, ⁴Anthropology, Pennsylvania State University, ⁵Anthropology, Binghamton University (SUNY)

Kinship systems underlie all of human social life and are associated with important inequalities between men and women. It is well-established that members of the favored gender in matrilineal and patrilineal societies enjoy increased autonomy, resource access, and social support. However, it remains unknown whether these gender inequalities lead to disparities in long-term health and disease risk. Here we use C-reactive protein (CRP), a dominant inflammatory protein that indexes risk for many chronic diseases, to investigate gender disparities in long-term inflammation and disease risk among matrilineal and patrilineal populations of Mosuo agriculturalists in Southwest China. Our results show that (i) while women experience higher rates of elevated CRP than men in patriline, (ii) this gender disparity is reversed in matriline, where men face higher rates of elevated CRP than women. Chronic inflammation and disease risk thus depend not only on gender, but also on the kinship system in which one is embedded. This work contributes to a body of biocultural research showing that culture matters to physiological function, long-term health, and disease risk.

This work was funded by the National Science Foundation (BCS 1461514).

Using genomic data to track cultural evolution in South African populations over the past 200 years

AUSTIN W. REYNOLDS¹, MARK N. GROTE¹, JUSTIN W. MYRICK¹, REBECCA L. SIFORD³, CEDRIC J. WERELY^{4,5,6}, EILEEN G. HOAL^{4,5}, CHRISTOPHER R. GIGNOUX^{7,8}, MARLO MÄLLER^{4,5,6} and BRENNAN M. HENNI^{1,2}

¹Department of Anthropology, University of California, Davis, ²Genome Center, University of California, Davis, ³School of Human Evolution and Social Change, Arizona State University, ⁴DST-NRF Centre of Excellence for Biomedical Tuberculosis Research, South African Medical Research Council Centre for Tuberculosis Research, Stellenbosch University, ⁵Division of Molecular Biology and Human Genetics, Stellenbosch University, ⁶Faculty of Medicine and Health Sciences, Stellenbosch University, ⁷Colorado Center for Personalized Medicine, University of Colorado, ⁸Department of Biostatistics, University of Colorado

The colonial-period arrival of Europeans in southern Africa is associated with large demographic shifts that displaced indigenous Khoekhoe and San populations. The South African Coloured population from Cape Town, for example is understood to have experienced male-biased European gene flow during the 17th century. However the

demographic and genetic impacts of colonialism are poorly understood in regions further north, where indigenous groups persisted for a much longer period of time. Here we examine the spatial and temporal impacts of this colonial expansion using genomic and demographic data representing over 2500 individuals living in three distinct regions of the Northern and Western Cape Provinces of South Africa. Rather than ask how cultural features influence genetic patterns, we reverse this approach to understand cultural evolution. We use genetic ancestry as a proxy for the level of European cultural exposure, as a family unit, to track the influence of colonial interaction. Furthermore, via extensive demographic interviews, we test whether present-day populations retain social signatures from the earlier KhoeSan inhabitants such as matrilocal residence or lower dispersal distances for women. Our genomic data show an increase in KhoeSan ancestry in groups living further from Cape Town. Our demographic analysis suggests that matrilocal residence preference is retained in the Richtersveld and Karoo regions of the Northern Cape. Temporally we find evidence for increased migration rates in all regions, starting in the early 20th Century. Using a generalized additive mixed model, we demonstrate that an individual's birthplace, among other factors significantly influences their likelihood of migrating.

Portions of this work were funded by the Leakey Foundation.

Preliminary zooarchaeological report on the Late Pleistocene faunal remains of a newly discovered fossil assemblage at Koobi Fora, Kenya

MATHILDE RIBORDY¹ and FRANCES L. FORREST^{2,3}
¹Human Evolutionary Biology, Harvard University, ²Hall of Human Origins Laboratory for Comparative Genomics and Human origins, American Museum of Natural History, ³New York Consortium in Evolutionary Primatology

We describe the faunal assemblage of a new fossil locality discovered by researchers from the Koobi Fora Research and Training Program during the summer of 2019 in area 8A, in the Ileret sub-region of the Koobi Fora formation. Attributed to the KBS member (1.87 to 1.56 million years ago), this locality yielded numerous fossils, including several with anthropogenic modifications, including cutmarks and percussion damage. This preliminary study focused on a sample of 197 mammalian fossils, which were identified to taxon and element, and examined for surface modifications. We provide a general description of the taxonomic composition, bovid size class distribution, weathering stages, frequency and anatomical placement of surface modifications, skeletal element representation, and epiphysis to shaft ratios. Data were then compared to published experimental models to determine

ABSTRACTS

the timing of hominin carcass acquisition. The assemblage was dominated by size 3 bovines. Cutmarks and percussion marks were present in the assemblage in greater numbers than carnivore modifications (6.1%, 2.5% and 1%, respectively). The distribution of skeletal elements suggests that carcasses were transported to the site. Our results show that hominins butchered carcasses in Koobi Fora between 1.87 and 1.56 million years ago, and likely had early access to carcasses. These preliminary results are promising, and we suggest conducting further research at this location. We would suggest doing further collections, as a larger sample size would provide more accurate results, but also collecting elements more systematically, including non-mammalian fauna to have a better understanding of the depositional context of these remains.

NSF REU #1930719, NSF ARCH #1624398, David Rockefeller International Experience Fund Grant

Signatures of Development in the Gastrointestinal Microbiome of Wild Savanna Monkeys

ALICIA M. RICH¹, SANKWETE PRUDENT MOKGOKONG², MARYJKA B. BLASZCZYK³, DESIRÉ L. DALTON^{2,4}, KATHERINE R. AMATO⁵ and CHRISTOPHER A. SCHMITT¹

¹Anthropology, Boston University, ²Genetics, South African National Biodiversity Institute, ³Anthropology, The University of Texas at Austin, ⁴Zoology, University of Venda, ⁵Anthropology, Northwestern University

Access to anthropogenic food enhancement can have a significant effect on the development of synanthropic primates. A closer examination of the relationship between anthropogenic food enhancement and primate development may provide insight into how the advent of agriculture altered patterns in human life history. Given their ubiquity on both farms and nature reserves, South African vervet monkeys (*Chlorocebus pygerythrus*) provide an excellent model system to test these effects. We investigated whether free-ranging vervets on a private farm, with access to ample human waste, cultivated crops, and livestock feed, experience altered development compared to wild-foraging vervets in a nature reserve, and whether these patterns covaried with gut microbial composition. Between 2016 and 2018, we gathered cross-sectional samples of anthropometric data and gut microbiomes from feces ($N=63$). Female vervets on the farm ($N=23$) present significantly greater suprailiac skinfold thickness than in the nature reserve, suggesting increased fat deposition ($t[10]=2.48$, $p<0.05$, two-tailed). Ordinal logistic regressions of parity status based on nipple length in females indicate an earlier onset of reproduction, with age category four on the farm showing signs of parity ($\beta=49.94$, $p<0.01$), but not in the nature reserve. Gut microbial communities also associate with these

patterns. Overall, these results are consistent with an effect of anthropogenic food-enhancement on gut microbial composition, which may be linked to both body fat deposition and an earlier onset of reproductive maturation in females.

This research was funded by the Wenner-Gren Foundation, Northwestern University, and Boston University.

Paleolithic mobility shifts as hominin niche construction

JULIEN RIEL-SALVATORE¹, FABIO NEGRINO² and GENEVIÈVE POTHIER BOUCHARD¹

¹Département d'anthropologie, Université de Montréal, ²DAFIST, Università degli studi di Genova

Recent work has shown human behavioral ecology to be the adaptive force by which human niche construction accrues over the long-term. By virtue of the time-averaged nature of the data they normally deal with, paleoanthropologists have in recent years developed a series of tools to extract from palimpsests human behavioral strategies that often would not be perceptible from snapshots of 'pristine' one-off assemblages. These signals reveal some dimensions of hominin niche construction and, in turn, permit a finer-grained understanding of multimillennial processes like the Middle-Upper Paleolithic transition by highlighting the shifting dynamics of human cultural and biological adaptations and of the ecological niches they occupy and alter over time. This paper presents a case study illustrating the interpretive power of these approaches. It begins with a review of the overarching principles that can tease out meaningful signals from palimpsests which agent-based models have recently identified. It then moves to an analysis of the regional record from Liguria to show how time-transgressive trends in mobility shifts help both distinguish Neanderthal from modern human adaptations and reveal internal variability within the industries of both groups that are equally if not more important in explaining the lasting evolutionary success of the latter beginning ca. 42,000BP. By underscoring these differences in how differently two groups of hominins exploited, navigated and impacted a similar landscape over 10,000 years, palimpsest data are shown to be uniquely powerful in shedding important new light on the evolutionary dynamics of the perennial question of Neanderthal disappearance in Western Europe.

SSHRC Insight Grant 435-2017-1520 FRQ-SC Grant 2016-NP-193048

Ancient DNA Mimicry? Bleach-Based Decontamination Treatment and Cytosine Deamination in Modern DNA Contaminants

ANNE M. RILEY¹, MARGARET STATON² and GRACIELA S. CABANA¹

¹Anthropology, University of Tennessee, Knoxville, ²Genome Science & Technology, University of Tennessee, Knoxville

Ancient DNA (aDNA) has typically undergone degradative processes that make its effective recovery vulnerable to contaminating DNA. Specialists have developed several decontamination protocols, but one has become standard: the soaking of ancient specimens (especially bones and teeth) in household bleach solutions.

Research from the last decade has shown that bleach does not fully eliminate modern DNA contamination, and worse, may degrade it to the point of mimicking aDNA damage patterns that researchers rely on to authenticate aDNA sequences. Bleach has been shown to reduce contaminant DNA to low copy numbers and small fragments, two distinguishing features of aDNA. A third feature is cytosine deamination, characterized by increased cytosine to thymine substitutions. The effect of bleach solutions on cytosine deamination in aDNA research contexts is as yet an open question.

We investigate whether bleach treatment induces cytosine deamination in contaminant human mitochondrial DNA from museum-curated zooarchaeological bones and teeth. Frequencies and distributions of deaminated DNA bases, as inferred by mapDamage2.0, were statistically evaluated using a mixed effect three-way ANOVA.

Results show a tendency toward higher levels of cytosine deamination in bleach-treated relative to untreated specimens, which suggests that bleach may have a role in inducing this damage pattern in modern contaminants. Unexpectedly, among bleach-treated groups, we observed a negative correlation between specimen submersion time and cytosine to thymine substitution frequencies. These findings suggest that bleach treatment is effective in eliminating superficial, recently deposited contaminant DNA, but appears to be less effective on more deeply penetrated contaminants.

Primate populations/communities, the role of humans in shaping them, and why it matters

ERIN P. RILEY

Anthropology, San Diego State University

In primatology, the term "population" is often variably defined. It is invoked to refer to one's study species or the animals one is studying ("study population") or it is used to mean a biological

ABSTRACTS

population – that is, a subset of a species that is partially or completely separated from others. More often than not, however, the term is used, but not explicitly defined. Accordingly, just as it is for its mother field (i.e., biological anthropology), the question of “what is a population?” is a relevant concern for primatology as well. In this talk, offering a view from primatology, I discuss two issues related to this symposium’s focus on population as a foundational, yet troubling concept. First, I explore the issue of level of analysis, the historical legacy of studying the population ecology of primates, and the importance of also studying primates as members of ecological communities. Second, I explore how and why the tendency to envision “population” as a natural unit is problematic. Namely, it ignores the role that humans have played in constructing and shaping what we call “primate populations.” I draw from current field research on the human-primate interface, including my own work in Indonesia and Florida, to illustrate these issues. I argue that these critiques matter because the way that we think and write about primates shapes how we study them and how we interpret their patterns of behavior.

Follow my lead: energy expenditures in utero resemble maternal allometry in humans and chimpanzees

REBECCA RIMBACH^{1,2} and HERMAN PONTZER^{1,3}

¹Evolutionary Anthropology, Duke University, USA, ²Animal, Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa, ³Duke Global Health Institute, Duke University, USA

In humans and other animals, metabolic rate is closely related to body size in a power-law relationship commonly known as Kleiber’s Law, in which the rate of energy expenditure increases with mass^{0.75}. Kleiber’s Law predicts high mass-specific metabolic rates (energy expenditure/gram) for the embryo and fetus during gestation, but little is known about fetal energy requirements due to the difficulty in obtaining direct measurements. Here, we use published measurements of daily energy expenditure (DEE, kcal/d) and basal metabolic rate (BMR, kcal/d) in infants and adults to reconstruct fetal energy requirements in humans. From birth, BMR and DEE increase in Kleiber’s Law manner as the infant grows, with high mass-specific metabolic rates compared to adults. However, the relationship between metabolic rate and body mass in infancy clearly differs from that in utero. Instead, DEE and BMR at birth indicate that fetal mass-specific metabolic rates match those of the mother. Thus, neonates transition from an adult mass-specific metabolic rate in utero to a much higher mass-specific metabolic rate in infancy and childhood. Available comparative data from chimpanzees indicates that they follow a similar pattern, suggesting metabolic

regimes in utero are evolutionarily conserved. Metabolic rates in human children begin to exceed those of chimpanzees at approximately two years of age, in parallel with the ontogenetic divergence in brain size. We discuss the implications of these results for understanding maternal and fetal energy demand, the timing of parturition, and metabolic ontogeny in humans and other apes.

Supported by NFS BCS-1824466

The Arch and Anth Podcast: education, outreach and representation

MICHAEL B. C. RIVERA

The Arch and Anth Podcast

The Arch and Anth Podcast is a public communication project aiming to educate general audiences about human history, biology and cultures through expert interviews. This audio medium is relatively new, but recent efforts to use podcasts as outreach tools have greatly contributed to our discipline’s public communication goals and needs. Here, I argue podcasting is an effective means of disseminating both the content and the importance of our work to broad audiences worldwide.

In-person access to anthropology in schools, museums and laboratories is often limited by geographical, logistical and financial barriers. Conversely, The Arch and Anth Podcast’s interviews are free to download or stream online at any time. The podcast averages 9,000–10,000 listens per month, and the episodes have been heard by consumers in over 100 countries. Stakeholders and general audiences are made and kept interested in our scholarship, the evolutionary concepts that ground it, the breadth of our discipline, the personal journeys taken to become anthropologists, and anthropology’s wider impacts among society, particularly related to issues such as climate change, racism, the non-binary natures of sex and gender, colonial histories, and much more.

Through careful selection of podcast guests, there is also broad representation of experts of all subdisciplines within anthropology, as well as genders, nationalities, socioeconomic backgrounds, academic stages, ethnicities, sexualities and other significant axes. This has helped give many women, racialized scholars and minoritized anthropologists a large platform to highlight research, share their academic journeys, develop public outreach skills, and grow their professional and public networks.

Exercise increases nonshivering thermogenesis but not bone mass during cold exposure in a mouse model of humans

AMY ROBBINS, CHRISTINA A. TOM, MIRANDA N. COSMAN, REBECCA TUTINO, TAYLOR M. SPENCER,

CLEO MOURSI, RACHEL HURWITZ and MAUREEN J. DEVLIN

Anthropology, University of Michigan

Recent studies suggest exercise can activate brown adipose tissue (BAT) in humans, producing heat. This finding is surprising since exercise itself generates heat, and BAT upregulation is more commonly associated with cold stress. To understand the effects of exercise and cold on uncoupling protein (UCP1) in BAT and on bone mass, we studied male C57BL/6J mice at 26C (thermoneutrality) and 16C (moderate cold) from 3-6 weeks of age. Half of each group had running wheels (exercise, EX) and half did not (control, CON). We hypothesized that exercise would increase UCP1 and cortical and trabecular bone volume at both temperatures. Results indicate that both exercise (+32-91%) and cold (+31-52%) increased UCP1 protein expression (p<0.03 for all) in BAT, such that it was highest in 16C EX and lowest in 26C CON. In the distal femur, EX mice had 27-28% lower trabecular bone volume fraction (BV/TV), 18-24% lower connectivity density (Conn.D), and 7-8% lower trabecular number (Tb.N) vs. controls at 16C and 26C (p<0.05 for all). Cold mice had 24% lower BV/TV, 8% lower Tb.N and 25-35% lower Conn.D independent of exercise (p<0.05 for all), such that trabecular bone properties were lowest in 16C EX and highest in 26C CON. There were no differences in midshaft femur cortical bone. These results show that exercise does increase UCP1 expression, but contrary to our hypothesis exercise and cold have inverse effects on UCP1 and trabecular bone microarchitecture. Low bone mass in cold-dwelling humans may reflect energetic tradeoffs among thermogenesis, activity, and skeletal acquisition.

This project was supported by NSF BCS-1638553 to MD.

Middle Pleistocene environments from Markaytoli (lower Awash Valley, Ethiopia) inferred from dental stable isotopes

JOSHUA R. ROBINSON¹, CHRISTOPHER J. CAMPISANO² and KAYE E. REED²

¹Archaeology, Boston University, ²Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University

Compared with the Pliocene and Early Pleistocene, Middle Pleistocene local paleoenvironments in eastern Africa are considerably under-sampled. To fill this lacuna, 68 faunal dental samples collected during the 2012 and 2015 field seasons at the Markaytoli site in the Ledi-Geraru Research Project area of the lower Awash Valley of Ethiopia were analyzed for stable carbon and oxygen isotopes. Based on a combination of biochronological and paleomagnetic analyses, the Markaytoli site dates to either close to 1.0 million years ago or 0.78-0.5 million years ago. The vast majority of samples, ~ 85%, consumed ≥ 80% C₄ resources, indicating that Markaytoli was open and grassy. The most

ABSTRACTS

commonly sampled taxa, reduncins, have significantly higher carbon values than other Middle Pleistocene assemblages, such as the Asbole fauna in the lower Awash Valley and penecontemporaneous sediments in the Omo-Turkana Basin. Low carbon values for tragelaphins and small-bodied primates, which account for ~ 15% of the faunal assemblage, suggest the presence of a wooded component. Oxygen isotope values are generally high – ~ 65% are more positive than -2.0‰ – indicative of arid environments. Low oxygen values for Hippopotamidae and Thryonomidae attest to the presence of standing water, likely the river system. The oxygen isotope profile of the assemblage is very similar to that of the Asbole site, although caution is necessary when comparing oxygen isotope values between different regions. Taken together, the carbon and oxygen isotope data shows that Markaytoli was an open floodplain environment close to a river system associated with denser vegetation.

National Science Foundation (BCS-1157351) and John Templeton Foundation. The opinions expressed in this publication are those of the authors and do not necessarily reflect the views of John Templeton Foundation.

Variation in the Juvenile Bony Pelvis

ALEXANDRA N. ROCCA

Anthropology, University of Alberta

The bony pelvis is an important bone in studies of archaeological populations and human evolution as it balances upright walking and the birthing of large-brained infants. It has been previously thought that the female pelvis is selectively constrained by these functions; however, new research demonstrates the pelvis is impacted by developmental plasticity and morphological variation. This research studied two archaeological human skeletal collections consisting of 60 juvenile individuals from 0-16 years of age and 20 adults. This research explored when in pelvic growth morphological differences arise in the iliac crest and if there are differences between populations. Geometric morphometric analysis of 3D semilandmark data was used. This approach is a novel way of exploring human bone adaptability and constraints in morphological variation. When the results of the patterns of shape change were examined, the majority of landmark movement occurred in the mediolateral plane. The greatest difference in mean shape occurred between the first and fourth developmental cohort. Correlation tests revealed a positive relationship between shape and size. All results were the same between the two populations. The adult populations did not differ by sex but allowed maturation trajectories to be explored. Both size and shape maturation demonstrated highly significant positive correlations with age. This research was limited in its analysis by the fact it only examined the iliac crest. Future studies should look at the entire shape of

the pelvis over maturation and should further explore different populations to better understand the impact of developmental plasticity in different geographic contexts.

I would like to thank the Natural Science and Engineering Research Council of Canada for their support of this research through the Alexander Graham Bell Master's Scholarship.

Ancestral Affiliation and the Production of Social Identity: Investigations of Mortuary Practices among Persistent Hunter-Gatherers in Archaic Indian Knoll, Kentucky

REBECCA L. RODAN and DANIEL H. TEMPLE

Anthropology, George Mason University

The Archaic cemetery at Indian Knoll (ca. 4600-3500 BP) in Kentucky represents a mortuary location utilized as a persistent landscape. Reconstructing mortuary practices and population structure among hunter-gatherers helps explain the formation of persistent places through identities affiliated with the ancestral dead. Grave good presence and absence as well as burial location within the midden was recorded. Buccolingual and mesiodistal measurements were collected for each permanent tooth ($n = 139$). An R-matrix evaluated within-group phenotypic variation for the full sample and within layers of the midden. Mantel's partial correlation tests were employed to evaluate the relationship biological distance and spatial distance within the total cemetery and between occupational layers. Phenotypic variation increased between the Deep and Shell midden layers ($t = 46.9, P < 0.0001$) and contracted between the Shell and Low Shell midden layers ($t = 2.39, P < 0.0263$). Grave good usage became more inclusive between the Deep and Shell midden occupation ($t = 41, P < 0.0001$), then contracted between the Shell and Low Shell midden ($t = 14.4, P < 0.0001$). There were no significant correlations between biological and spatial distances. These results suggest that the social structure of the site moved from a more restricted, closely related group to a more diverse population, with a contraction in this diversity during the latest occupational phase. Burial proximity was likely a symbolic social strategy aimed at preserving the site as a persistent landscape through maintenance of social memory via adjacency to ancestral occupants.

How positive and negative social experiences vary with cortisol concentration in women of color scientists

MICHELLE A. RODRIGUES^{1,2}, MARIEL GALVAN², DENISE HERRERA², BRYANA RIVERA², RACHEL NEUBAUER², FATIMATA SOUMARE², IFEOLUWA ATUNNISE², RUBY MENDENHALL^{3,4}, ELIZABETH

A.L. STINE-MORROW^{1,5} and KATHRYN B.H. CLANCY^{1,2}

¹Beckman Institute for Advanced Science and Technology, University of Illinois, Urbana-Champaign, ²Department of Anthropology, University of Illinois, Urbana-Champaign, ³Department of Sociology, University of Illinois, Urbana-Champaign, ⁴Carle Illinois School of Medicine, University of Illinois, Urbana-Champaign, ⁵Department of Educational Psychology, University of Illinois, Urbana-Champaign

Social support is embodied through stress pathways, and these mechanisms impact health and shape human evolutionary history. However, negative social experiences may also be embodied through these pathways. Here, we examined how daily social support and negative workplace interactions varied with daily cortisol concentration in women of color scientists, a population that likely experiences the intersection of gender and racial discrimination. Participants collected daily urine samples over one menstrual cycle, and we assayed samples for cortisol concentration via enzyme-linked immunosorbent assays. Preliminary analysis of mean daily negative workplace interactions over a month indicate that they significantly correlate with experiences of racial microaggressions ($r=0.659, N=10, p=0.038$). In preliminary analyses of daily variation in social support, negative interactions, sleep, and symptoms of somatic stress in a subset of participants ($N=10$), cortisol concentrations were weakly positively correlated with talking to family ($r=0.150, N=236, p=0.022$), weakly negatively correlated with negative workplace interactions ($r=-0.146, N=236, p=0.025$), and positively correlated with social media use ($r=0.284, N=236, p<0.001$). In a general linear mixed model, symptoms of somatic stress ($F_{1,228}=4.166, p=0.042$) and social media use ($F_{1,228}=3.195, p=0.049$) were significantly associated with cortisol concentrations. Our preliminary findings suggest negative workplace experiences may be a proxy for experiences of discrimination, but social media use has the largest association with daily cortisol concentrations. We will present analyses from the full dataset ($N=20$ women of color scientists) to address how the confluence of supportive interactions and negative interactions impact cortisol concentration, and how these factors may impact health over the lifespan.

Research was funded by a Beckman Postdoctoral Fellowship, the American Association of Physical Anthropologists Professional Development Fund, and the Wenner-Gren Foundation.

ABSTRACTS

Association between distal humerus measurements and body mass in modern humans: applications for fossil hominin MK3

AMANDA L. RODRIGUEZ¹, DEBORAH L. CUNNINGHAM¹, DANIEL J. WESCOTT¹ and ROBERT C. MCCARTHY²

¹Anthropology, Texas State University, ²Biological Sciences, Benedictine University

The 1.39 Ma distal humerus MK3 is argued to be more similar morphologically to *Homo* than *Pan* or *Gorilla*. The body mass estimate for MK3 computed using the product of capitular height (CPSI) and distal articular width (HDML) is approximately 90 kg using a human model. In this study, we compared body mass estimates from these humeral articular dimensions and femoral head diameter (FHD) in a known-body mass sample of 46 normal-BMI males from the Texas State Donated Skeletal Collection (TXSTDSC) to determine if distal humeral measures can accurately approximate body mass. In addition, we examined the allometric relationship between the two humeral measures in humans and gorillas. All methods of body mass assessment tend to overestimate lower body mass values and underestimate higher values. Estimates of body mass from distal humerus measurements nearly mirror the accuracy of FHD, indicating that the estimate for MK3 is a reasonable extrapolation from the modern human data. However, while twelve males from the TXSTDSC have a CPSI greater than that of MK3, none exceeded the fossil's HDML. This implies a different allometric relationship of humeral structures for MK3 when compared to modern humans. MK3 scales like female gorillas. Therefore, the estimate based on modern humans may incorrectly approximate body mass for this specimen.

Neanderthal-Denisovan ancestors interbred with a distantly-related hominin

ALAN R. ROGERS, NATHAN S. HARRIS and ALAN A. ACHENBACH

Anthropology, University of Utah

Previous research has shown that modern Eurasians interbred with their Neanderthal and Denisovan predecessors. We show here that hundreds of thousands of years earlier, the ancestors of Neanderthals and Denisovans interbred with their own Eurasian predecessors—members of a “superarchaic” population that separated from other humans about 2 mya. The superarchaic population was large, with an effective size between 20 and 50 thousand individuals. We confirm previous findings that: (1) Denisovans also interbred with superarchaics, (2) Neanderthals and Denisovans separated early in the middle Pleistocene, (3) their ancestors endured a bottleneck of population size, and (4)

the Neanderthal population was large at first but then declined in size. We provide qualified support for the view that (5) Neanderthals interbred with the ancestors of modern humans.

This work was supported by NSF BCS 1638840 (ARR), NSF GRF 1747505 (AAA), and the Center for High Performance Computing at the University of Utah (ARR).

Maize, migration, and mobility: Variation in long bone functional adaptation in the pre- and protohistoric American Southwest

JACKLYN J. ROGERS¹, DANIEL H. TEMPLE¹ and DAVID HUNT²

¹Department of Sociology and Anthropology, George Mason University, ²Department of Anthropology, Smithsonian National Museum of Natural History

This study evaluates changes in behavior that occurred within indigenous populations from the American Southwest during agricultural intensification and European colonization. Long bone diaphyses from Pueblo Bonito (ca. 800-1200 BP) a pre-contact Pueblo II site, and Hawikku (ca. 1400-1680 BP), a protohistoric Pueblo IV site were included in this work. Computed tomographic images and Moment Macro software were used to measure areas and second moments of area for adult humeri, radii, femora, and tibiae. All measurements were standardized for body size using body mass and powers of bone length. Standardized areas and second moments of area were compared between males and females from Pueblo Bonito and Hawikku using MANOVA with a Games-Howell post-hoc test. Significant increases in M-L bending rigidity of humeri in females ($p \leq 0.027$) and males ($p \leq 0.021$) and torsional rigidity of humeri in females ($p \leq 0.047$) and males ($p < 0.043$) were found at the Hawikku compared to Pueblo Bonito site. No significant differences were found in any additional cross-sectional properties between the Hawikku and Pueblo Bonito samples. These results are consistent with increased loading of the upper limb during the intensification of agricultural economies through Spanish colonization, likely the processing of maize. These findings also support archaeological research that suggests similar degrees of mobility over time that may be traced to site dispersals and regional migration across the American Southwest. In this sense, the agricultural transition did not reduce mobility through increased sedentism, but did intensify habitual activity in the upper limb.

Reconstructing the postcranial morphology of the last common ancestor of humans and chimpanzees

CAMPBELL ROLIAN¹, JULIEN CLAVEL², KELSEY D. PUGH³ and PIERRE LEMELIN⁴

¹Comparative Biology and Experimental Medicine, University of Calgary, ²Life Sciences, Natural

History Museum, ³Graduate Center of the City University of New York, City University of New York, ⁴Division of Anatomy, University of Alberta

Evolutionary anthropologists have long been interested in the postcranial anatomy and locomotor behavior of our last common ancestor (LCA) with chimpanzees, and in the evolutionary trajectories that have shaped the two lineages since their divergence. The morphology and behavior of the LCA has been hypothesized at times to be hylobatid-like, African ape-like, or to have a more generalized postcranial morphology associated with above-branch arboreal locomotion. To evaluate these hypotheses, we applied multivariate phylogenetic comparative and quantitative genetics tools to limb bone data from a taxonomically broad sample of extinct and extant primates, in order to reconstruct postcranial morphology and evolution in the *Pan-Homo* LCA. Using Ornstein-Uhlenbeck models of multivariate evolution, we find that although it differs from all extant lineages, the LCA's limb morphology most closely resembles *Pan*. Specifically, the LCA is five times closer to *Pan* in morphospace than to arboreal cercopithecines, and three times closer than to other extant hominoids. Quantitative genetic analyses suggest that evolution towards *Pan* was marked by weaker selection than towards *Homo*, sometimes indistinguishable from drift, resulting in minor change in the lengths of the proximal limbs, and moderate increases in the lengths of the hands, and feet. In contrast, evolution towards *Homo* was marked by strong selection for reduced forelimb and hand length, and for increased femur, tibia and metatarsal length. These data support the hypothesis that the *Pan-Homo* LCA was chimpanzee-like, and provide new morphological standards to evaluate the tempo and mode of evolutionary change in Hominidae.

Campbell Rolian was supported by the University of Calgary Faculty of Veterinary Medicine, and by Discovery Grant 4181932 from the Natural Sciences and Engineering Research Council of Canada

Women of Zhenghan: documenting gender inequality based on skeletal assemblages from Eastern Zhou China

AIDA ROMERA BARBERA¹, KATE PECHENKINA², MELANIE MILLER³, SIAN HALCROW³ and WENQUAN FAN⁴

¹Anthropology, The Graduate Center, CUNY, ²Anthropology, Queens College of CUNY, New York Consortium in Evolutionary Primatology (NYCEP), ³Anatomy, University of Otago, ⁴Research Division of Shang and Zhou Dynasties, Henan Provincial Institute of Cultural Relics and Archaeology

Skeletal collections examined for this study are associated with the Zhenghan Ancient City and were excavated from archaeological sites located in modern Xinzheng. Zhenghan city was established during the Western Zhou era (1046 – 771 BC) and flourished during the era preceding

ABSTRACTS

the unification of China by Qin Shi Huang in 221 BC. Remains of 277 individuals from Zhengnan were sufficiently well preserved for the analysis, of which 162 were assigned as males and 115 as females. Analyzing association between the sex of the deceased and grave complexity and elaboration shows clear bias against female graves. Earlier, using the stable isotope analysis of human bone samples from this site, we have demonstrated a significant divergence on male and female diets in Zhengnan. The male-female dietary differences were further supported by sex differences in the distribution of skeletal stress markers and oral health. Although skeletal trauma was infrequent in Zhengnan skeletal assemblages, with only 18% of skeletons displaying traumatic injuries, the patterns of trauma differed greatly between males and females. Traumas typically linked to face-to-face combat, such as parry and boxing fractures, were prevalent in males. Female skeletons displayed traumas characteristic of systemic abuse, including depressed fractures of the skull inflicted by downward bows and multiple fractures of the face bones. The distribution of squatting facets suggests gender-specific habitual postures, with female skeletons frequently displaying facets characteristic for squatting and kneeling postures. Taken together, these lines of evidence suggest a well established male-female inequality in the urban population of Zhengnan.

This research has been supported by PSC-CUNY research Grant to KP and Marsden foundation Grant to SH and MM.

Analysis of landmark variation in the study of cranial fluctuating asymmetry

ASHLY N. ROMERO, DAVID R. MITCHELL and CLAIRE E. TERHUNE

Department of Anthropology, University of Arkansas

Estimating fluctuating asymmetry (FA) in various primates provides an understanding of the developmental stability of these groups. While it is important to calculate how much asymmetry one individual, population, or species exhibits, it is unclear how much asymmetry each cranial region contributes to this overall asymmetry score. Here, we analyzed landmark variation of the FA component of 120 landmark configurations of *Gorilla gorilla gorilla* (F=22; M=22), *Pan troglodytes troglodytes* (F=17; M=20), and *Macaca fascicularis fascicularis* (F=19; M=20). We placed 74 landmarks across these crania, using 8 midline landmarks and 33 bilateral landmarks. Across-sample results suggest that the bilateral landmarks on the most lateral point on the zygomatic arch and the most lateral point on the posterior cranial vault exhibit the most variation. Landmarks on the mastoid process, orbits, postorbital constriction, and pterygoid hamulus are the second most variable set of bilateral landmarks. Landmarks around the

foramen magnum and alveolar processes are among those with the least asymmetric variation. These results do not suggest any one area of the cranium exhibits greater asymmetry than another but may indicate landmarks that are not particularly useful for assessing asymmetry and can be eliminated in future studies. Further, landmarks that greatly contribute to asymmetry may be avoided for shape analyses on symmetric structures when possible because they are likely to distort data and influence findings. While our findings here compared across groups, further analyses should examine these data at the level of species and sex to investigate patterns specific to these groupings.

Learning From Those Who Served: Application of Regression-based Body Mass Estimation Methods to The USS Oklahoma Population

MAXWELL S. ROONEY and EMILY HAMMERL

Anthropology, University of Nebraska - Lincoln

Current methodologies in body mass estimation are lacking in accuracy when compared to the methods of sex, age, and ancestry estimation familiar to forensic anthropologists. For this reason, the practical application of body mass estimation remains underutilized, hindering the study of a potentially advantageous aspect of the bioprofile.

This project highlights body mass estimation in a forensic context while sidestepping the osteological paradox through the utilization of a unique population; the US Military personnel killed on the USS Oklahoma attack on Pearl Harbor. Because these individuals were similar in age (18-40) and their deaths were traumatic and not pathological, it provides an opportunity to control for many variables that other populations cannot. To demonstrate, I applied the methodology in Dr. Christopher Ruff's 1991 study estimating body mass, utilizing measurements taken from AP radiographs of the proximal femur and their subsequent application to regression equations. These data were cross-referenced to weight data collected by the US Military during the individual's enlistment. The mean standard of estimate yielded by the Ruff '91 equations on the sample population was 104.12 and 62 for regression involving femoral head breadth and shaft breadth, respectively. This differs from the mean standard of estimate, 73.49 and 56.01, yielded by the equations created for USS Oklahoma data. While these results are expected in sample-specific linear regression, the controlled attributes of the sample and the equations produced offer another opportunity through which we can further our understanding of body mass estimation.

The Impact of Facial Reduction on Canine Paranasal Sinuses

CIELE ROSENBERG, MOLLY SELBA and VALERIE DELEON

Anthropology, University of Florida

Selective breeding in domestic dogs (*Canis lupus familiaris*) has drastically impacted their cranial morphology. Artificial selection has been driven by the desire for canines with paedomorphic features, which has led to extreme facial reduction. This study tests how facial reduction affects the size and shape of paranasal sinuses. It may provide deeper insight about this phenomenon in primate evolution. Normocephalic and brachycephalic (short-faced) dogs of similar body size were compared to understand how selective breeding has influenced sinus development. The size of the neurocranium (braincase) was used as a proxy for body size. The sample consisted of clinically obtained CT image volumes of normocephalic beagles (N = 10) and brachycephalic English bulldogs (N = 10). It was hypothesized that there would be a significant difference of volume and surface area of sinuses between breeds. The frontal sinuses and maxillary recesses of each dog were segmented out digitally using the post-processing software Amira. Surface area and volume of each sinus were calculated in Amira. Results showed no significant effect of brachycephaly in the frontal sinuses. However, there was a significant effect of brachycephaly on maxillary sinuses, which had both smaller surface area (p=0.030) and volume (p=0.026). Additional findings show that the brachycephalic group exhibited a significantly higher degree of asymmetry in their maxillary sinuses, but not their frontal sinuses. These results indicate that facial reduction in dogs affects the maxillary sinuses. Asymmetry of maxillary sinuses suggests that development of the sinuses is disrupted by rapid morphological changes imposed by selective breeding.

How Dr. Eric Delson Shaped Cladistic Analysis: Lessons from the Platyrrhines

ALFRED L. ROSENBERGER

Anthropology, Graduate Center City University of New York

Dr. Eric Delson and colleagues led the revolution that transformed our understanding of primate evolution, the methods of phylogeny reconstruction, and primate classification during a prolific ten years, 1975-1985. The principles of cladistic analysis he described and implemented in his studies of catarrhines are time-tested. They remain central to paleoanthropology and evolutionary primatology even though practices and data sources have evolved considerably since then.

The modernization of platyrrhine systematics illustrates several key concepts that he promulgated. Characters and synapomorphy:

ABSTRACTS

Reconstructing the affinities of a radiation requires assessment of multiple systems. The interrelationships within and among platyrrhine clades are most securely delineated by crania (cebines), postcrania (atelines), dentitions (pitheciines), reproduction (callitrichins), and behavior (homunculines). Samples, morphotypes and morphocline polarity: Commonality and out-group comparisons of seriated patterns reliably point to the ancestral morphologies of specific study groups. Upper molars of "crown" platyrrhines probably evolved from a four-cusped design, though this inference may not hold for the group's ultimate, much older beginnings. Identifying ancestors: With evidence from morphology, time, and geography, sister-group relationships can be reformulated into robust ancestor-descendant hypotheses. Ancestral-descendant lineages highlight the macro-evolutionary history of modern platyrrhines, e.g., the 12-14 million year old *La Venta* links (*Neosaimiri-Saimiri*; *Stirtonia-Alouatta*; *Aotus dindensis-Aotus* sp.) and older ties to 20 million year old forms from Argentina (*Dolichocebus-Neosaimiri-Saimiri*; *Tremacebus-Aotus*). Scenarios: Unstable storylines have no scientific standing in evolutionary reconstructions. A penetrating example is the platyrrhine origins scenario that claims the dispersal mechanism behind New World monkey ancestry involved rafting across the Atlantic Ocean.

A Possible Case of Chiari Malformation Type in a Soldier from the Tuchengzi fortress site (Qin Dynasty 221-206 BCE) along the Great Wall, China

DAVID S. ROSETTE and CHRISTINE LEE

Anthropology, California State University, Los Angeles

Chiari malformations are a type of structural defect caused by crowding of the brainstem, cerebellum, and tonsils. The defects caused by Chiari malformations result in the cerebellar tonsils being projected downward through the foramen magnum and cause various neurological symptoms.

The case study comes from a sample of six skulls excavated at the Tuchengzi site in modern day Inner Mongolia. During the Qin dynasty (221-206 BCE) Tuchengzi served as a border military outpost along the Great Wall that saw combat in times of war and served as an agricultural settlement in times of peace. Using macroscopic non-metric analysis of photographs the sample skulls are all Asian males and all show similar patterns of blunt force trauma and/or sharp force trauma consistent with warfare. The individual in question (aged 25-30) is differentiated from his compatriots by skeletal deformations specific to Chiari malformations. The individual was

then compared with modern day cases of Chiari malformations to determine that he was most likely afflicted with Type I Chiari malformation as opposed to similar pathologies.

Dam health effects: Drinking water salinity is a key risk factor for hypertension and dilute urine among Daasanach pastoralists in Northern Kenya

ASHER Y. ROSINGER^{1,2}, HILARY BETHANCOURT¹, ZANE S. SWANSON³, JESSICA SAUNDERS³, SHIVA DHANASEKAR⁴, W. LARRY KENNEY⁵, SERA L. YOUNG⁶, ROSEMARY NZUNZA⁷ and HERMAN PONTZER^{3,8}

¹Department of Biobehavioral Health, Pennsylvania State University, ²Department of Anthropology, Pennsylvania State University, ³Department of Evolutionary Anthropology, Duke University, ⁴Department of Anthropology, Emory University, ⁵Department of Kinesiology, Pennsylvania State University, ⁶Department of Anthropology, Northwestern University, ⁷SERU, Kenya Medical Research Institute (KEMRI), ⁸Global Health Institute, Duke University

Socioecological changes impact water security, lifestyle, human biology, and health. The Gilgel Gibe III Dam completed in 2015 in southern Ethiopia has stopped flood pulses, causing increased salinity and shrinking of Lake Turkana. Daasanach pastoralists living in northern Kenya complain about the saltiness of their drinking water, a key component of water insecurity. However, the relationship between water salinity and health in this population remains unknown. Therefore, we tested how water salinity and milk consumption (a traditional/alternative hydration source) relate to hypertension (blood pressure³140/90 mmHg) and hyperdilute urine (urine specific gravity <1.003 g/ml), which can indicate kidney damage. Data come from the 2019 Water Insecurity, Stress, and Hydration (WISH) study, which tested water quality in seven communities and collected health biomarkers and survey data from 218 non-pregnant adults aged 18+ from 128 households. The salinity of drinking water ranged from 120-520 mg/L, while water from Lake Turkana reached 2000 mg/L, exceeding the 500 mg/L cutoff of freshwater. Logistic regression models with standard errors clustered on households indicate that each additional 100 mg/L of salt in drinking water was associated with 41% (95% CI: 1.08-1.84, p=0.01) increased odds of hypertension and 32% (95% CI: 1.01-1.73, p=0.043) increased odds of hyperdilute urine adjusting for sex, age, BMI, heat index, milk intake, and reported kidney problems. Daily milk consumption was associated with 43-56% lower odds of both health outcomes.

Increased water salinity has critical implications for blood pressure and kidney function of lean pastoralists relying more on water than milk for hydration.

NSF ARCH #1624398; NSF REU #1930719; This work was funded by the PSU SSRI Human Health and Environment Seed Grant

Revisiting Helton: Navigating identity through selective Mississippianization on the fringes of Cahokia

AMANDA N. ROSSILLO

Anthropology, Barnard College of Columbia University, Evolutionary Anthropology, Duke University

Stone box graves were a major component of the Mississippian mortuary tradition in the American southeast for centuries. They numbered in the tens of thousands in Tennessee and Kentucky alone, and were also common further west in the American Bottom and Central Illinois River Valley. Yet, they are conspicuously absent from the nearby Lower Illinois River Valley except for four limestone boxes at the Helton site, dating to ~1260 CE in a local Jersey Bluff cemetery located less than 100km from Cahokia. Three of the four contained infant skeletal remains, two of which were buried with one sherd each from the same ceramic vessel, while the fourth lay empty. Additionally, the disarticulated remains suggest secondary burial, while one limestone slab had been burned. Dental and osteological analyses revealed that all three individuals were less than three years of age at time of death and experienced minimal taphonomic wear. Pathological observations indicated periosteal new bone addition along the sagittal sutures of two individuals, one of whom also exhibited evidence of cribra orbitalia in both eye orbits. Contextualizing these burials within the culture-historical framework of the Late Woodland and Mississippian southeast points to numerous possibilities as to why these infants were given specialized mortuary treatment that was virtually non-existent locally yet common elsewhere. Given the proximity of Helton to Cahokia, this Jersey Bluff community likely navigated changing religious, social, political, and/or economic landscapes through selective Mississippianization while retaining certain local traditions, which may have been tied to these infants' young ages.

This work was funded in part by a Tow Summer Research Fellowship granted through the Tow Foundation.

Infant Mortality in Archaic Athens (ca. 700-480 BCE): An investigation into the Jar Burials of Phaleron Cemetery

JESSICA E. ROTHWELL¹, ELENI ANNA PREVEDOROU^{1,2} and JANE E. BUIKSTRA¹

¹Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona

ABSTRACTS

State University, ²Malcolm H. Wiener Laboratory for Archaeological Science, American School of Classical Studies at Athens

The lives of non-elites, especially non-elite children, in ancient Greece are significantly understudied. This study investigates a sample of 45 of Jar Burials from Phaleron Cemetery in Athens, Greece, in order to understand the health outcomes of non-elite infants and young children during the Archaic Period (ca. 700-480 BCE). Our goals include determining whether infants at Phaleron survived beyond the first few weeks after birth and whether they survived long enough to elicit a bony response to physiological stress. To address these questions, age-at-death was estimated using standard methods based on dental and skeletal development. Pathological bony changes in the cranium and postcranium were also recorded.

Although most infants survived birth and lived beyond the first few weeks after birth, approximately 20% died within two weeks of birth and 67% after two weeks, but before the age of 2. For the 36 individuals for whom dental age estimation was possible, the largest number of individuals died between 3 and 9 months of age. Also, 29% of 45 individuals lived with chronic physiological stress sufficiently long to elicit a bony response. These results suggest that the Jar Burials represent children who were accepted into their family after birth but were unable to survive early life physiological stressors. Furthermore, the presence of bony responses to physiological stress suggests that, for at least some of these individuals, stressors were chronic, rather than acute.

The Malcolm Hewitt Wiener Foundation, The Paul and Alexandra Canellopoulos Foundation, The Desnick Family, The National Endowment for the Humanities (RZ-255623-17), The National Science Foundation (DGE-1311230, BCS-1828645), and ASU/GPSA Research.

New Neandertal fossils from Trou Magrite, Belgium, and their contribution to our understanding of Neandertal diversity

HÉLÈNE ROUGIER¹, ISABELLE CREVECOEUR², COSIMO POSTH³, HERVÉ BOCHERENS^{4,5}, PAULINE COLOMBET², DAMIEN FLAS^{6,7}, JOHANNES KRAUSE³, PATRICK SEMAL⁸ and CHRISTOPH WISSING⁴

¹Department of Anthropology, California State University Northridge, ²UMR 5199-PACEA, CNRS, University of Bordeaux, ³Department of Archaeogenetics, Max Planck Institute for the Science of Human History, ⁴Department of Geosciences, Biogeology, University of Tübingen, ⁵Senckenberg Centre for Human Evolution and Palaeoenvironment, University of Tübingen, ⁶Department of Prehistoric Archaeology, University of Liège, ⁷UMR 5608-TRACES, Toulouse - Jean Jaurès University, ⁸Scientific Heritage Service, Royal Belgian Institute of Natural Sciences

Belgium has yielded an exceptional Neandertal fossil record that has played a major role in Neandertal studies since the 19th century. Here we present the outcome of a new multidisciplinary project that aimed at re-assessing the skeletal collections from the Belgian site of Trou Magrite. This site yielded rich archeological assemblages spanning from the Middle and Upper Paleolithic to the Mesolithic, Neolithic, and Iron Age. We revised the already known human collection, conducted a systematic sorting of the faunal material, and combined the use of morphometrics, taphonomy, stable isotopes, dating, and genetic analyses to perform taxonomic and chronocultural identifications. This resulted in the identification of two new Neandertal fossils among the faunal material excavated in the 19th century: an upper right permanent canine representing an adult individual, and the left femur diaphysis of a ca. 8-10-month-old infant. We will present the biological characteristics and mitochondrial DNA phylogenetic position of the Trou Magrite Neandertals, in particular with regard to the other Northern European Neandertals. Our project adds a ninth site to the list of Belgian sites that have yielded Neandertal fossils, and emphasizes the existence of a low genetic diversity among Late Neandertals, which is to be compared to their significant behavioral (mortuary and technical) variability. As such, Belgian Neandertals continue to contribute significantly to our understanding of the population processes that resulted in the disappearance of this group.

This research was funded by the College of Social and Behavioral Sciences of CSUN and the CSUN Competition for Research, Scholarship and Creative Activity Awards.

Arthropod consumption in lemurs: an exploratory analysis using DNA metabarcoding

AMANDA K. ROWE¹, MARIAH E. DONOHUE², ELIZABETH L. CLARE³, ROSIE DRINKWATER³, ANDREAS KOENIG^{1,4}, ZACHARY M. RIDGWAY⁵, LUKE D. MARTIN⁶, EVA S. NOMENJANAHARY⁷, FRANCOIS ZAKAMANANA⁸, LOVASOA J. RANDRIAMANANAZA⁸, THIERRY E. RAKOTONIRINA⁸ and PATRICIA C. WRIGHT⁸

¹Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, ²Department of Biology, University of Kentucky, ³School of Biological and Chemical Sciences, Queen Mary University of London, ⁴Department of Anthropology, Stony Brook University, ⁵Department of Chemistry, Stony Brook University, ⁶School of Archaeology and Anthropology, Australian National University, ⁷Department of Biological Anthropology, University of Antananarivo, ⁸Centre ValBio Research Station, Stony Brook University

Arthropods can fulfill major nutritional requirements for primates, but because of the limitations of traditional methods, we know very little about the frequency and importance of arthropod consumption for many primate species. As such,

most lemur research to date reports arthropod consumption as general animal prey, insects, spiders, or broad common name groups. To aid in a more complete understanding of arthropod consumption, we performed an exploratory analysis using DNA metabarcoding to identify prey fragments found in lemur fecal samples. Using live-trapping or focal follows of the study species, we opportunistically collected 170 fecal samples from 10 lemur species found in three national parks in Madagascar (genera *Avahi*, *Cheirogaleus*, *Eulemur*, *Microcebus*, *Mirza*, *Phaner*, *Propithecus*). We then performed DNA metabarcoding analyses on the prey fragments found in the fecal samples to identify consumed arthropods. Arthropod DNA was present in the fecal samples of all 10 lemur species. Lemurs of the family Cheirogaleidae displayed the highest frequencies and had the richest diet in terms of arthropods when compared to non-cheirogaleids. To our knowledge, this study presents the first evidence of arthropod consumption in *Phaner pallescens*, *Avahi laniger*, and *Propithecus verreauxi*. We identified more than 35 families of arthropods as probable food items that have not been published as lemur dietary items to date. Our results suggest that arthropods represent an important nutritional source for many lemur species. Furthermore, this exploratory analysis emphasizes the role DNA metabarcoding can play in elucidating an animal's diet.

Sigma Xi, RW Primate Fund, American Society of Primatologists, Animal Behavior Society, Lemur Conservation Action Fund, SBU GSEU, SBU IDPAS, Society of Systematic Biologists, and Gertrude F. Ribble Trust.

Body mass estimation from footprint size in early hominins

CHRISTOPHER B. RUFF¹, ROSHNA E. WUNDERLICH², KEVIN G. HATALA³, RUSSELL H. TUTTLE⁴, CHARLES E. HILTON⁵, DAVID M. WEBB⁶, BENEDIKT HALLGRIMSSON⁷, CHARLES MUSIBA⁸ and MICHAEL G. BAKSH⁹

¹Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, ²Biology, James Madison University, ³Biology, Chatham University, ⁴Anthropology, University of Chicago, ⁵Anthropology, University of North Carolina, ⁶Anthropology and Sociology, Kutztown University, ⁷Cell Biology and Anatomy, University of Calgary, ⁸Anthropology, University of Colorado Denver, ⁹Environmental Planning, Tierra Environmental Services

Preserved footprints provide important information on early hominin locomotor behavior and ecology. They have also been used by several authors to reconstruct body size, based on relationships between footprint size, stature, and body mass in living humans. However, a comprehensive comparative study of body mass relative to foot/footprint size in humans has not yet been carried out. Here we examine these

ABSTRACTS

relationships in five adult, habitually unshod or minimally shod modern human populations of varying body size and shape: Machinguenga (n=47), Daasanach (n=29), Pumé (n=34), Hadzabe (n=49), and Samoans (n=35). Average body mass indices (BMI) vary from 18.4 (Daasanach) to 27.4 (Samoans), with a total range of body masses from 36 to 99 kg. Samples with higher BMIs have larger body masses relative to foot areas (foot length x breadth). Thus, the best prediction of body mass is obtained from a multiple regression of body mass against foot area and BMI ($r = 0.96$, %SEE = 7.0%). The best fit of body mass on foot area alone is a quadratic equation ($r = 0.86$, %SEE = 13.7%). When applied to footprint samples of presumed *Australopithecus afarensis* from Laetoli, probable *Homo erectus* from Ileret, and possible *Homo antecessor* from Happisburgh, UK, body mass estimates 13-34% higher than previous estimates based on a single linear modern human reference sample are obtained. These results illustrate the importance of considering a range of human body forms when attempting to reconstruct body mass in early hominins from footprint dimensions.

We thank the National Science Foundation (BCS-1232522), Leakey Foundation, and Wenner-Gren Foundation for funding support to collect these data, and the Commission for Science and Technology in Tanzania.

Factors associated with age at natural menopause among Nagas in Nagaland, India

PETENEINUO RULU¹, MEENAL DHALL² and LYNNETTE LEIDY. SIEVERT¹

¹Anthropology, University of Massachusetts, Amherst, ²Anthropology, University of Delhi, Delhi India

The age at which natural menopause occurs can be determined by the final menstrual period and is influenced by cultural and as well environmental factors. Mean and median ages at menopause vary by methodological technique. Age at menopause is associated with health outcomes, such as breast cancer and osteoporosis, as well as longevity. The present study aims to determine age at menopause among Nagas residing in Nagaland and factors associated with variation in age at menopause. Cross-sectional data were obtained (n=352) through interviews, and age at natural menopause was queried by recall method. Mean age of the population was 47.8±8.6 years, ranging from 35 to 65 years, and mean recalled age at menopause among naturally postmenopausal women was 48 years, ranging from 41 to 53 years. Probit analysis, applied to determine age at natural menopause among the entire sample, resulted in a median of 50.48 years (95% Fieller Bounds: 49.88 – 51.13 years). Among Naga women, 68% had obtained a high school degree or higher and almost all (98%) were married. Based on the Asian cut offs for Body Mass Index (BMI),

54.3% had normal weight, 16.2% were underweight, 12.2% were overweight, and 16.2% were obese. Factors influencing age at menopause were assessed using Cox regression models, indicating inverse, non-significant associations with education and socioeconomic status, and positive, non-significant associations with BMI, number of conceptions, age at menarche, and menstrual regularity.

Lagothrix variation in skeletal and linear variables

JACQUELINE RUNESTAD CONNOUR¹, STEPHANIE L. CANINGTON² and KAYLA NIDA¹

¹Dept. Biological Sciences, Ohio Northern University, ²Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

This project explores skeletal properties and linear dimensions in *Lagothrix* to evaluate sexual dimorphism, and whether subspecies/species from neighboring regions are similar. Skeletal properties include limb bone midshaft cross-sectional cortical areas estimated from radiographs. Linear dimensions include head+body lengths obtained from either literature sources (available upon request) or the on-line databases of the American Museum of Natural History, the Field Museum of Natural History, and the National Museum of Natural History.

Analysis includes genus and subspecies levels, and uses Mann-Whitney tests to determine p-values. At the genus level, *Lagothrix* males are greater in body mass than females (p-value 0.01, N = 11 males, 12 females). Males also have longer bodies (p-value 0.02, N = 55, 49), and humeral midshaft cross-sectional cortical area is greater in males (p-value 0.02, N = 4, 6). At the subspecies/species level, *poepigii* males have longer head+body lengths than females (p-value 0.02, N = 13, 9). Comparing subspecies/species to each other, *cana* females are shorter in head+body length than the other females (p-values less than 0.02, N = 9 or more). *Lugens* males are longer in head+body length than males of either *lagothricha* or *cana*, and *poepigii* males are longer than *lagothricha* males (p-values less than 0.05, N = 10 or more).

In conclusion, *Lagothrix* demonstrates sexual dimorphism in greater body size in males. Among subspecies/species, data do not group taxa that literature and museum sources suggest are neighbors. More information is needed regarding ancestral distribution patterns of *Lagothrix*.

Trabecular mapping: Effects of intra- and interobserver error on sliding semilandmark placement

C. KINLEY RUSSELL¹, DEVORA S. GLEIBER², DANIEL J. WESCOTT², DEBORAH L. CUNNINGHAM² and ADAM D. SYLVESTER¹

¹Center for Functional Anatomy & Evolution, The Johns Hopkins University School of Medicine, ²Department of Anthropology, Texas State University

Trabecular mapping combines geometric morphometric and bone microstructural analyses to overcome the limitations of single volume of interest (VOI) analyses. In this method, sliding semilandmarks are utilized to locate multiple VOIs within the trabecular structure. Here we quantify the effects of intra- and interobserver error in medial tibial condyle delineation on sliding semilandmark placement and collected trabecular properties.

Micro-computed tomography was used to scan 12 proximal tibiae from the Texas State University Donated Skeletal Collection (Forensic Anthropology Center at Texas State). Surface models were generated from converted binary image stacks. Each of two observers created three trims of every condyle from its full surface model. Sliding semilandmarks (n=141) were distributed across each condyle and slid to minimize the bending energy of the thin-plate spline function relative to the updated Procrustes average. VOIs were located deep to each semilandmark. The effect of semilandmark position on collected properties was investigated by moving each VOI 0.5-1.5 mm to ten adjacent positions. Correlations were calculated between 10,000 randomized bootstrap samples of the 11 positions for each VOI.

Intraobserver error in sliding semilandmark position averaged 0.33 mm. Interobserver error in landmark placement was 0.22 mm. Intra- and interobserver error was higher in edge landmarks than those distributed across the surface. Though bone volume fraction and trabecular thickness vary with VOI position, there is a strong correlation between the 11 collected values for these properties ($r \geq 0.80$). These results indicate that VOIs placed using sliding semilandmarks provide reliable information on bone microstructural properties.

This work was supported in part by instrumentation funded by the NSF under grant NSF: MRI 1338044.

Placental synchronicity: Placental phenotypes of demand have developmental roots in maternal early life characteristics

JULIENNE N. RUTHERFORD¹, VICTORIA A. DEMARTELLY², CORINNA N. ROSS^{3,4}, TONI E. ZIEGLER⁵ and SUZETTE D. TARDIF⁴

¹Women, Children, and Family Health Science, College of Nursing, University of Illinois at

ABSTRACTS

Chicago, ²Obstetrics & Gynecology, University of Chicago, ³Biology, Texas A&M University - San Antonio, ⁴Southwest National Primate Research Center, Texas Biomedical Research Foundation, ⁵Wisconsin National Primate Research Center, University of Wisconsin Madison

Development of placental compartments related to fetal demand and maternal supply may be shaped by a combination of current maternal condition and early life maternal characteristics, clarifying mechanisms of intergenerational phenotypic transfer. The marmoset monkey, a fast-reproducing, litter-bearing primate, is an ideal model to explore intergenerational intrauterine processes. We evaluated the effect of maternal gestational weight and maternal litter size on 1) trabecular surface area, the microscopic placental interface ("demand"), and 2) intertrabecular volume, the maternal blood space ("supply"), in 29 marmoset placentas. Surface area was not correlated with placental volume, maternal gestational weight, or litter weight but was inversely associated with maternal litter size ($\beta=-24.4$, $p=0.02$, $r^2=0.19$). Placentas from mothers who were triplets had significantly reduced microscopic surface area compared to those from twin females (mean(SD)=9.0(7.9) vs. 6.6(6.1) m², $p=0.02$). The volume of the maternal blood space was predicted by placental volume and maternal gestational weight in bivariate regression models (respectively $\beta=0.11$, $p<0.0001$, $r^2=0.58$; $\beta=0.004$, $p=0.001$, $r^2=0.38$). In multiple regression, placental volume remained significant ($\beta=0.12$, $p=0.002$; overall model $p=0.0001$, $r^2=0.64$). We have previously shown that placentas of triplet fetuses have reduced surface area (Rutherford & Tardif, 2009); here, we show that the placentas of their offspring have a similarly restricted phenotype. Supply is linked to current conditions, whereas demand may have developmental origins: offspring of triplet females, who themselves experienced in utero restriction, downregulate demand via reduced surface area, perhaps in physiological synchronization toward expected deprivation. Treating fetoplacental demand as an intergenerational intrauterine phenomenon may guide improvements in outcomes.

This work was funded by the NIH: R01HD076018 (Rutherford), R01DK077639 (Tardif), and OD P51 OD011133 (Southwest National Primate Research Center).

DNA methylation measurements using dried blood spots on the Illumina EPIC array yield high quality data comparable to whole blood measured using the 450k array

CALLEN P. RYAN¹, DAVID S. LIN², MICHAEL S. KOBOR², THOMAS W. MCDADE¹ and CHRISTOPHER W. KUZAWA¹

¹Department of Anthropology, Northwestern University, ²Centre for Molecular Medicine and Therapeutics, University of British-Columbia

DNA methylation (DNAm) is an epigenetic process involved in transcriptional regulation and disease and is increasingly measured in biological anthropology to study the impact of social and environmental exposures. Global measures of DNAm are often obtained from whole blood applied to microarray technologies, such as Illumina's Infinium Methylation450 Beadchip array. However, field conditions often pose challenges to acquiring and storing whole blood samples that are required for measuring DNAm. Furthermore, the legacy 450k array has been replaced by the expanded Infinium MethylationEPIC Beadchip (EPIC) array, raising questions about the comparability between these two platforms. To study the utility of the EPIC array for measuring DNAm in DBS, we compared the latter with samples taken from whole blood belonging to the same individuals at the same time point, measured using the 450k array ($n = 8$). We examined estimated bisulfite conversion rates, compared normalized β -values across 391,445 overlapping sites, and compared imputed immune epithelial, fibroblast, and immune cells between the two approaches. Bisulfite conversion rates were ≥ 0.95 for EPIC, and Pearson correlations of β -values using the two methods were >0.99 . Imputed proportions of B-cells, CD4T, CD8T, Granulocytes, Monocytes, Natural Killer cells, and Plasma Blastocytes were comparable across the methods. We also did not see evidence of contamination from epithelial cells or fibroblasts in the DBS sample. In conjunction with other research, these findings support the validity of DBS measured on the EPIC array to measure DNAm, leading to new opportunities for the study of epigenetic phenomenon using field-friendly, minimally invasive methods.

CPR gratefully acknowledges funding provided by the National Science Foundation (#1751912) and the Natural Science and Engineering Research Council of Canada (NSERC).

The confluence of functional matrices on the sphenoid bone and local effects of soft-tissue anatomy on intracranial space variation

KATHARINE G. J. RYAN¹, BENJAMIN AUERBACH¹ and LAUREN BUTARIC²

¹Department of Anthropology, University of Tennessee, Knoxville, ²Department of Anatomy, Des Moines University

Moss's Functional Matrix Hypothesis suggests that the development of soft-tissues of the head drives variation in the craniofacial skeleton. How multiple soft-tissues with different developmental origins interact to influence skull variation remains unresolved. We examined the sphenoid, which interfaces with the dura mater, the cavernous sinus and several cranial nerves and vessels, pituitary gland, and mucosa of the sphenoidal sinus and the nasopharynx. We compared the orbits and palate, two intracranial facial capsules under

local soft-tissue influences, which we hypothesize would vary semi-independently of the sphenoid despite integration between the facial skeleton and basicranium. We obtained 12 virtual landmarks from 30 microCT scans of human crania. Regions were compared through Partial Least Squares analyses and Klingenberg's morphological integration and modularity tests. Results show that most of cranial variance occurs in the anteroposterior length and superoinferior depth. This is reflected by the sphenoid body shortening and rotating superoposteriorly along with increases in the cranial base angle (CBA). This morphological variance provides covarying changes in the orbits and palate ($p=0.0034$), which lengthen with increased anteroposterior space for the face. When CBA does not vary, most of the variation is in anterosuperior expansion of the lesser sphenoid wing and an inferior expansion of the sphenoid body which we hypothesize to be driven by local soft-tissue interfacing. Shifts in the position of the sphenoid results in changes in the anteroposterior length of the anterior cranial fossa, but no anteroposterior changes in the rest of the face, which are semi-independent of the sphenoid ($p=0.045$, $RV=0.37$).

Variation in cortical and trabecular bone structure in relation to subsistence strategy in a diverse sample of modern humans

TIMOTHY M. RYAN¹, LILY J. DEMARS¹, NICHOLAS B. STEPHENS¹, KARA PETERS¹, JAAP P. P. SAERS², MARK R. DOWDESWELL³, TEA JASHASHVILI^{4,5,6}, KRISTIAN J. CARLSON^{6,7}, JAY T. STOCK⁸ and ADAM D. GORDON⁹

¹Department of Anthropology, Pennsylvania State University, ²Department of Archaeology, Cambridge University, ³School of Statistics and Actuarial Science, University of the Witwatersrand, ⁴Molecular Imaging Center, Department of Radiology, Keck School of Medicine, University of Southern California, ⁵Department of Geology and Paleontology, Georgian National Museum, ⁶Evolutionary Studies Institute, University of the Witwatersrand, ⁷Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, ⁸Department of Anthropology, Western University, ⁹Department of Anthropology, University at Albany, SUNY

Many studies have analyzed trabecular bone structural variation in relation to behavioral differences in modern humans, providing some evidence for a link between activity/mobility and trabecular bone structure. However, most have been limited to a small number of postcranial elements, and few have analyzed covariation between trabecular and cortical bone within the same individuals. We use microCT scans to characterize trabecular and cortical bone structure in multiple skeletal elements (seventh cervical vertebra, proximal humerus, proximal femur, and distal tibia) from a large, diverse sample of

ABSTRACTS

modern human groups (n=10). The groups represent a behavioral/mobility gradient ranging from foragers to post-industrial societies. We interpret the variation relative to their inferred mobility and activity patterns. Bone volume fraction (BV/TV) and degree of anisotropy (DA) were quantified using Medtool 4.3. Midshaft cortical bone cross-sectional geometry was quantified using BoneJ. Patterns of trabecular bone variation were generally similar across all elements. BV/TV was highest in the C7, followed by the proximal femur, distal tibia, and proximal humerus. Between-group differences in cortical bone generally followed predictions, with some notable exceptions. Humeral trabecular and cortical bone had similar patterns of variation in some groups, but this pattern was not found consistently in other long bones. There is a significant amount of within and between group variation in trabecular and cortical bone structure that likely reflects both mechanical and non-mechanical factors. A better understanding of variation in both cortical and trabecular bone, and how they covary, will provide further insights into factors affecting modern human skeletal phenotype.

Funding: NSF BCS-1719187, NSF BCS-1719140, RCUK/BBSRC BB/R01292X/1, NIH S0RR027665, NIH S100D018500

Saving Bones: a direct comparison of FTIR-ATR, whole bone percent nitrogen, and NIR

CHRISTINA M. RYDER¹, MATTHEW SPONHEIMER¹, HUSSEIN SHOKRY², IGNACIO A. LAZAGABASTER³, NIMROD MAROM³, GILLIANE F. MONNIER⁴, MATTHEW J. COLLINS², THIBAUT DEVIÈSE⁵ and THOMAS HIGHAM⁵

¹Department of Anthropology, University of Colorado, Boulder, ²The GLOBE INSTITUTE, University of Copenhagen, ³The Leon Recanati Institute for Maritime Studies and Departments of Maritime Civilizations and Archaeology, University of Haifa, ⁴Department of Anthropology, University of Minnesota, ⁵School of Archaeology, University of Oxford

Well-preserved collagen, an organic component of bone, can reveal much about the human past. While archaeological collagen can help illuminate the history of past populations, diagenetic processes can result in rapid and sometimes inconspicuous collagen degradation. As a result, recent sites may have poor preservation, while ancient sites may have some specimens that are surprisingly well-preserved. Consequently, there has been considerable interest in potential methods to prescreen bone for collagen content. Here we compare the efficacy of FTIR-ATR, whole bone percent nitrogen (%N), and NIR to select well-preserved samples from collections of unprocessed bone. FTIR utilizes the presence of Amide I (1651 cm⁻¹) and Amide II (1553 cm⁻¹) peaks and the Amide I/Phosphate peak-to-peak ratio to identify well-preserved specimen.

A threshold of 0.76 %N suggests a sample preserves a sufficient amount of collagen. NIR uses chemometric models, built using PCA and PLSR of from specimens of known collagen yield, to characterize well-preserved specimens. Here, we compare FTIR-ATR and NIR spectra taken on samples from the Judean Desert, Israel, and the northern Saqqara region of Egypt. We then compare %N to NIR spectra from specimens from Zafarraya, a Neanderthal cave site in Spain. The results show agreement between FTIR-ATR and NIR, but among the Zafarraya collection, NIR correctly characterizes collagen content in 78.6% of samples compared to only 72.0% for %N. Near-infrared light proves to be advantageous because it penetrates deeply and can predict the collagen yield of unprocessed bone in a timely, cost-efficient, and non-destructive manner.

Center to Advance Research and Teaching in the Social Sciences, CU Boulder VCR Innovative Seed Grant Program, CU Boulder Arts and Sciences Fund for Excellence, CU Boulder

Morphometrics and the analysis of fragmentary remains: the case of the Megalopolis isolated upper M3

CAROLIN RÄDING¹, JULIA ZASTROW², HEIKE SCHERF¹, CONSTANTIN DOUKAS³ and KATERINA HARVATI^{1,2}

¹Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoenvironment, Eberhard Karls University of Tübingen, ²DFG Centre of Advanced Studies 'Words, Bones, Genes, Tools', Eberhard Karls University of Tübingen, ³Department of Geology, National and Kapodistrian University of Athens

The isolated left upper third molar from the Megalopolis basin, Greece, is enigmatic due to its problematic preservation and context. We applied the method of crown outline analysis to upper third molars in an attempt to shed light on its affinities. As the Megalopolis molar was a surface find during geological surveys in 1962-63, its actual geological age is unknown. It was proposed to possibly be one of the oldest human fossils in Europe based on the faunal assemblage collected at the same time. Only a tooth crown with noticeable occlusal wear is preserved. Crown outline analysis provides a framework in which teeth can be analyzed independently of their shape, presence of the dental root and to a certain degree occlusal wear. We applied the method on a sample of 45 upper third molars ranging from *Homo erectus* to recent modern humans and successfully combined CT scans of original specimens with CT scans of high resolution dental casts. Principal component and linear discriminant function analyses of the size-independent crown outline grouped the Megalopolis molar with our Neanderthal comparative sample. We conclude that its most likely identification is as a member of the Neanderthal lineage. However, we urge further analyses with an increased fossil

comparative sample. The Megalopolis molar contributes to the scarce Pleistocene human fossil record of Greece and, thereby, highlights the potential of methodological improvements enabling new insights from known fragmentary fossil material.

This research was supported by the European Research Council (ERC CoG no. 724703) and the German Research Foundation (DFG FOR 2237).

The crash-weaning diet: two case studies on the consequences of unusually early and fast weaning among East African chimpanzees (*Pan troglodytes schweinfurthii*)

KRIS H. SABBI and MELISSA EMERY THOMPSON
Anthropology, University of New Mexico

Among mammals, the transition from relying entirely on mother's milk toward independent foraging has important fitness consequences. This is especially true for long-lived, large-bodied great apes with complex foraging niches, like chimpanzees. Infant chimpanzees may experiment with their first solid foods prior to their first birthday, but typically continue to breastfeed regularly until they are 4 to 6 y.o. During this time, they gain nutritional independence gradually, falling back on mother's milk to support growth and development while they learn to locate and process foods. In this study we document the cases of two wild infant chimpanzees in Kibale National Park, Uganda, that weaned several years younger than expected (1.8-2.3 y.o.) over the span of a few months rather than a few years because their mothers became pregnant again quickly. In line with normal development, each infant had begun to eat solid foods prior to weaning, however, increased independent foraging effort during weaning did not seem to compensate for decreased maternal nutrition. Both infants became dramatically less active and spent far less time playing (<10 sec/hour observed) than similarly-aged infants (307±453 sec/hour; p<0.001). Energetic decline culminated in the death of one infant, and several developmental delays persist in the surviving infant. These cases provide rare opportunities to observe the potential consequences of early weaning when surviving mothers could provide aspects of maternal care other than nutrition from milk, underscoring multifaceted constraints on life history and development.

This research was funded by the Leakey Foundation, the Nacey Maggioncalda Foundation, the Wenner-Gren Foundation, the American Philosophical Society, and the University of New Mexico.

ABSTRACTS

Validation of a method for quantifying urinary C-peptide in platyrrhines

ALEXANDRA J. SACCO¹, MICHAEL C. GRANATOSKY^{2,3}, LAURA ABONDANO^{1,4}, MYRA F. LAIRD^{3,5} and KRISTA M. MILICH¹

¹Department of Anthropology, Washington University in St. Louis, ²Department of Anatomy, New York Institute of Technology, ³Department of Organismal Biology and Anatomy, University of Chicago, ⁴Department of Anthropology, University of Texas at Austin, ⁵Department of Integrative Anatomical Sciences, University of Southern California

Urinary C-peptide (UCP) is a biomarker for insulin production and often investigated in conjunction with ecological and behavioral data as a non-invasive physiological measure of energy balance in non-human primates. Methods to quantify UCP have been validated in catarrhines, but genetic evidence suggests that divergent evolution has led to variation in the organization of the insulin gene in platyrrhines. This variation complicates the application of these methods to measure UCP in platyrrhine taxa. Here, we evaluated a method for quantifying UCP in this primate group. Urine samples were opportunistically collected from laboratory-housed tufted capuchins (*Sapajus apella*) (n=3) during an ongoing experiment in which individuals participated in exercise activities for predetermined time intervals. To test the effects of energetic expenditure on UCP concentrations, we analyzed urine samples collected before and after the exercise activity. UCP concentrations were measured using a commercially available human C-peptide radioimmunoassay, and assay values were standardized using specific gravity. UCP concentrations varied significantly before and after exercise ($H(1) = 4.247, p = 0.039$). In each paired sample of UCP concentrations for given individuals, the concentrations were lower after exercise than they were prior to exercise. These results provide a biological validation of the use of these methods for measuring UCP in a platyrrhine species. Additionally, parallelism of serial dilutions of urine samples were calculated as a validation of the assay techniques. Given the evidence of divergent evolution resulting in genetic variation in platyrrhines, our results provide important methodological considerations for investigating questions related to energy balance in this taxon.

This research was supported by NSF-BCS-1440516, NSF-BCS-1627206, NSF-BCS-1440542, NSF-BCS-1638822, Washington University in St. Louis, and the AAPA Cobb Award.

Investigating the relationship between skin color and vitamin D deficiency in baboons (*Papio*)

SRISHTI SADHIR^{1,2,3}, ANDREA R. ELLER¹, STEPHANIE L. CANINGTON^{1,4} and SABRINA B. SHOLTS¹

¹Department of Biological Anthropology, National Museum of Natural History, Smithsonian

Institution, ²Department of Anthropology, University of Connecticut, ³Department of Ecology and Evolutionary Biology, University of Connecticut, ⁴Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Zoo primates found in historical museum collections show higher rates of cranial and dental pathologies than their wild counterparts, including metabolic bone diseases (MBD) attributed to vitamin D deficiency. Recent evidence in baboons (*Papio*) has also shown that exposed skin pigmentation influences UV absorption and consequent vitamin D₃ production, with the lowest levels found in darker baboon subspecies. In this study, we investigated the relationship between observed MBD pathology, captivity status, and exposed skin pigmentation in baboon crania at the Smithsonian Institution's National Museum of Natural History (NMNH). We hypothesized that the frequency of MBD would differ significantly between individuals of different skin color, with darker subspecies exhibiting higher frequencies. Presence or absence of MBD pathology (maxillary thickening and inflammation) was recorded for each specimen (N=176). Baboon subspecies were also categorized into "dark," "medium," and "light" skin color categories. In the total sample, 10.2% of specimens showed maxillary thickening and inflammation, while captive specimens (n=88) showed a significantly higher frequency of 19.3% ($\chi^2 = 0.05, p = 0.00$). MBD pathology was less frequent in the dark- and medium-colored subspecies (17.0% and 20.9%, respectively) than the light-colored subspecies (27.3%). There was no correlation between MBD and skin color, nor a higher frequency of MBD in dark-skinned specimens ($\chi^2 = 0.05, p = 0.72$). Given the limitations of a small sample size, ongoing research with additional museum collections may shed more light on the relationship between health and phenotypic variation in historical and modern baboon populations.

This research was funded by the Smithsonian Women's Committee and the National Science Foundation REU Site: Natural History Research Experiences (NHRE), OCE-1560088.

Distinct combinations of cortical and trabecular structure characterize loading history of the tibia: a pQCT study of athletes and controls

JAAP P.P. SAERS¹, LILY J. DOERSHUK², NICHOLAS B. STEPHENS², TEA JASHASHVILI^{3,4}, KRISTIAN J. CARLSON^{5,6}, ADAM D. GORDON⁷, COLIN N. SHAW¹, TIMOTHY M. RYAN² and JAY T. STOCK^{1,8}

¹Department of Archaeology, University of Cambridge, ²Department of Anthropology, Pennsylvania State University, ³Department of Radiology, University of Southern California, ⁴Department of Geology and Paleontology, Georgian National Museum, ⁵Department of Integrative Anatomical Sciences, University of Southern California, ⁶Evolutionary Studies Institute,

University of the Witwatersrand, ⁷Department of Anthropology, University at Albany, SUNY, ⁸Department of Anthropology, Western University

Variation in trabecular and cortical bone structure is often used to infer habitual behavior in the past. However, signals from both types of bone are rarely considered together and may even contradict each other. Here we examine trabecular and cortical bone structure in living people to understand the mechanical signals hidden in both types of bone.

We compare trabecular and cortical bone mechanical properties in pQCT scans of the tibia between groups of 83 male athletes (running, hockey, swimming, cricket) and sedentary controls using a Bayesian multilevel model.

All groups show distinct combinations of mean tibia midshaft $J^{0.73}$, I_{max}/I_{min} , and trabecular bone density in the distal tibia. There is a very minor but credible correlation between midshaft cross-sectional properties and trabecular bone density ($R^2 = 0.06$), but no relationship within any sporting categories.

All sporting groups have a credibly higher mean trabecular bone density compared to controls, but do not differ amongst each other. Cortical bone $J^{0.73}$ is greater in high impact sports (cricket, running, hockey) compared to controls, but not between low impact swimming and controls. These results suggest that diaphyseal cortical bone adapts to high impact bending loads while trabecular bone density increases under any kind of high activity.

Individuals from the different categories overlap substantially, but the posterior distributions of mean mechanical properties are clearly separated by unique combinations of cortical and trabecular variables. As such, detailed group-level behavioral inferences are possible by combining cortical and trabecular properties in our analyses of past human behavior.

Funding: RCUK/BBSRC grant BB/R01292X/1, NSF BCS-1719187, NSF BCS-1719140

Investigating health effects of urbanization on macaque crania

SANA T. SAIYEDI¹, ANDREA R. ELLER², RITA M. AUSTIN^{2,3,4}, STEPHANIE CANINGTON⁵, SABRINA B. SHOLTS² and AGUSTIN FUENTES¹

¹Department of Anthropology, University of Notre Dame, ²Department of Anthropology, Smithsonian Institution, National Museum of Natural History, ³Department of Anthropology, University of Oklahoma, ⁴Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, ⁵Center for Functional Anatomy and Evolution, Johns Hopkins University

Macaques compose a widely distributed nonhuman primate genus (*Macaca*) that thrives in various environments, including urban environments densely populated by humans. Research

ABSTRACTS

demonstrates that macaques alter aspects of their behavior, such as activity and diet, to adjust to urban environments, but the evolutionary and health implications of these adjustments are not fully understood. These questions are the focus of the EMPHASIS (Environmental Mismatches in Primates: Anthropogenic Settings and Impacts Survey) project, which investigates potential evolutionary patterns using health markers on human and nonhuman primate skeletal remains from a variety of anthropogenic environments. Here we report on an EMPHASIS project that analyzed skeletal pathology and dental calculus in macaque cranial specimens (N=323) collected from urban (n=27) and rural environments (n=296) to explore potential health outcomes related to exposure to urbanization, or proximity to human establishments such as towns and residential areas. Of all specimens, rural and urban, 21% exhibited skeletal pathology, while 15% exhibited dental calculus. Chi-squared tests revealed no differences in the presence of skeletal pathology ($p=0.699$) or dental calculus ($p=0.794$) between rural and urban macaques. Our results suggest skeletal pathology and dental calculus are not clearly differentially influenced by an urban environment, yet additional research with more sampling from urban regions is needed. As macaques grow in population, and especially around urban areas, continued research on skeletal health markers may help us better understand how adaptations to anthropogenic environments affect primate health through evolutionary trade-offs.

Using great ape cerebral cortex organoids to study brain evolution and disease

SOFIE R. SALAMA^{1,2,3}, GARY L. MANTALAS^{2,4}, ANDREW R. FIELD^{2,4}, IAN T. FIDDES^{1,2}, COLLEEN M. BOSWORTH^{1,2}, GIFTI GEMEDA², TAYLOR REAL², NICHOLAS HEYER², BENEDICT PATEN^{1,2} and DAVID HAUSSLER^{1,2,3}

¹Biomolecular Engineering, University of California, Santa Cruz, ²UC Santa Cruz Genomics Institute, University of California, Santa Cruz, ³Howard Hughes Medical Institute, University of California, Santa Cruz, ⁴Molecular, Cellular and Developmental Biology, University of California, Santa Cruz

Understanding the relationship between genome evolution and the evolution of complex organs such as the large and highly interconnected human brain is a challenging and fascinating problem. Improved genome assemblies for great apes and old world monkeys based on long and linked read data and improved comparative gene annotation have greatly improved our ability to resolve orthologous and paralogous gene relationships and to identify lineage specific genome rearrangements. Further, the ability to recapitulate many features of early brain development in vitro using pluripotent stem cell derived cerebral cortex organoids enable a comparative approach to identify the molecular innovations underlying the

recently evolved features of primate and human brain development. Here we performed comparative gene expression analysis of a five-week time course of cerebral organoids from human, chimpanzee, orangutan and macaque. We identified lncRNAs with both sequence and timing of gene expression conservation in order to enrich for those that regulate neurodevelopmental gene expression. We also identified human-specific NOTCH2NL genes that arose from recent segmental duplications. NOTCH2NL is affected in recurrent copy number variation events associated with neurodevelopmental diseases including autism and schizophrenia. Functional characterization in cerebral organoids suggest that NOTCH2NL contributes to the prolonged proliferation and expansion of neural stem cells that ultimately leads to more cortical projection neurons in humans. Current efforts are aimed at using CRISPRi and CRISPR knockout approaches to establish specific roles for these newly evolved genes in cerebral cortex organoid formation and function and, by extension, in human brain development.

This work is supported by Howard Hughes Medical Institute, Schmidt Futures Foundation, Simons Foundation Autism Research Initiative Award 643417 and the UCSC Institute for the Biology of Stem Cells

New insight into the corpse handling during cremation. Contribution of experimental archaeology and biogeochemical analyses on burnt bones

KEVIN SALESSE^{1,2}, CHRISTOPHE SNOECK^{3,4}, IOANNIS KONTOPOULOS⁵, ELISAVET STAMATAKI⁵, GIACOMO CAPUZZO¹, AMANDA SENGELOV¹, MATHIEU BOUDIN⁵, MARTA HLAD⁵, RICA ANNAERT⁵, SARAH DALLE⁷, GUY DE MULDER⁷, CHARLOTTE SABAUX⁷, DRIES TYS⁵, BARBARA VESELKA⁵, EUGÈNE WARMENBOL⁸ and MARTINE VERCAUTEREN¹

¹Research Unit of Anthropology and Human Genetics, Université Libre de Bruxelles, ²UMR 5199: PACEA, University of Bordeaux, ³Research Unit: Analytical, Environmental & Geo-Chemistry, Vrije Universiteit Brussel, ⁴G-Time Laboratory, Université Libre de Bruxelles, ⁵Maritime Cultures Research Institute, Vrije Universiteit Brussel, ⁶Royal Institute for Cultural Heritage, ⁷Department of Archaeology, Ghent University, ⁸Centre de Recherches en Archéologie et Patrimoine, Université Libre de Bruxelles

Cremation has been employed in a wide range of geographic and cultural contexts, since prehistorical times to the present. It is generally a sophisticated process, involving a complex suite of activities before, during and after the disposal of the dead body by fire. If post-cremation life histories of burnt human remains can be readily investigated, understanding the treatment of the corpse during the burning act itself is a much more challenging venture. Archaeologically, very limited – if none – evidences about the

management of the deceased on the pyre are generally available. In this study, we aimed at bringing new insights into the corpse handling during the burning act. This was possible through experimental archeology and state-of-the-art biogeochemical techniques (elemental, structural and isotope analyses) applied on cremated remains. Outdoor burning sessions and laboratory heating experiments, implicating modern pigs as human proxies, were repeatedly carried out in Belgium. Based on this experimental material, we were able to demonstrate that stable isotope evidences ($\delta^{13}\text{C}$, $\delta^{18}\text{O}$) were valuable indicators to discuss the initial position of a body in a pyre as well as the presence of garments worn by the deceased. While these results are preliminary, they are reproducible. In addition, through structural (Fourier-transform infrared spectroscopy) and morphological characterization (Scanning Electron Microscopy and Energy-Dispersive X-Ray Spectroscopy) evidences, we were able to strengthen the previous results but also better characterize the heating conditions experienced by the deceased. This study brings new breakthrough in the field of archeology of cremation.

The CRUMBEL Project (No. 30999782) has received funding from the Excellence of Science (EOS) framework (Belgium)

Home range overlap between two groups of wild western gorillas (*Gorilla gorilla*)

ROBERTA SALMI¹, KRISTEN MORROW^{1,2}, JESSICA LODWICK³, CLARA SCARRY⁴ and DIANE M. DORAN-SHEEHY⁵

¹Department of Anthropology, University of Georgia, ²Integrative Conservation Graduate Program, University of Georgia, ³Department of Ecology and Evolutionary Biology, University of Connecticut, ⁴Department of Anthropology, Sacramento State University, ⁵Department of Anthropology, Stony Brook University

Although various ecological and social factors explain differences in home range use among primate species, the effects of conspecific neighbors in movement decisions by non-territorial species has received little attention. Western gorillas in Central Africa overlap in their home range use and engage in frequent, often peaceful, intergroup encounters, despite their preference for contestable resources, such as seasonal fruits. To assess the degree to which neighboring groups overlap in their home range use, we recorded the daily ranging behavior of two groups of wild western gorillas at the Mondika Research Center (Republic of Congo) from October 2002 to August 2003. We analyzed spatial dimensions of home range size and patterns of use on a quasi-annual and monthly basis using multiple methods (GS, KDE, and MCP). The two groups displayed extensive quasi-annual home range overlap (GS: $75\pm 2\%$; KDE: $68\pm 6\%$; MCP: $71\pm 0\%$; the highest recorded for this species) and substantial

ABSTRACTS

quasi-annual core area overlap (GS: 48±4%; KDE: 19±1%; MCP: 40±9%). On a monthly basis, the two groups shared half of their range (GS: 50±1%; KDE: 60±2%; MCP: 49±1%) and a quarter of their core area (GS: 23±4%; KDE: 24±2%; MCP: 24±1%). Despite the significant overlap, interactions between the two groups were limited (8) and concentrated in the months of high-fruit availability, suggesting that the two groups were able to limit competition by spatiotemporal segregation at smaller scale. We discuss result differences across methods of home range estimation and the effect of population density on home range overlap in this species.

This study was funded by the National Science Foundation (SBR-972912), and Stony Brook University.

Group sleep reduces pathogen exposure: experimental support for the encounter dilution effect in wild chimpanzees (*Pan troglodytes schweinfurthii*)

DAVID R. SAMSON^{1,2}, LUKE A. LOUDEN³, KATIE GERSTNER⁴, SAMANTHA WILEY⁵, BEN LAKE⁶, BRADLEY J. WHITE⁷, CHARLES L. NUNN^{2,8} and KEVIN D. HUNT⁹

¹Anthropology, University of Toronto Mississauga, ²Department of Evolutionary Anthropology, Duke University, ³Department of Biological Sciences, Purdue University, ⁴Department of Anthropology, Wayne State University, ⁵Department of Anthropology, University of Nevada, Las Vegas, ⁶Lester E. Fisher center for the study and conservation of Apes, Lincoln Park Zoo, ⁷Department of Entomology at the Center for Disease Vector Research, University of California, ⁸Duke Global Health Institute, Duke University, ⁹Department of Anthropology, Indiana University

While asleep, an organism is vulnerable to abiotic and biotic forces, which include pathogen exposure by way of biting insects. The encounter-dilution hypothesis proposes that the formation of groups at sleep sites is influenced by a 'selfish herd' behavior, where individuals sleep within groups as a counter to predation risk. We employed multiple light traps that were also baited with non-toxic chemical attractants to capture insects throughout nighttime periods to test the encounter dilution hypothesis in the context of chimpanzee sleep site selection. Across 74 night with 294 traps, we collected 65,545 individual insects. Consistent with the encounter-dilution hypothesis, we found that insect exposure, inferred by absolute values of caught insects in nighttime traps, was strongly influenced by the grouping of traps. Specifically, single traps caught more insects – including vector transmitting female mosquitoes – than grouped traps, and the distance between traps within the grouped context influenced the number of insects caught. Moreover, our linear mixed effect model revealed that "trap location" was among the two most important predictive factors, with ground sleep sites showing less exposure

to insects than arboreal sleep sites. Additionally, traps associated with tree-species *Cynometra alexandri* resulted in significantly lower catch rates than *Pseudospondias microcarpa* associated traps. Our results identify potential disease-related selective pressures on sleep site sociality in primates and reveal novel defensive strategies wild chimpanzees use to avoid disease.

Funding provided by Indiana University and Duke University

Reproductive status predicts oxidative stress profiles in young women

AMELIA SANCILIO^{1,2}, WILLIAM FUNK³, NATHAN MONTGOMERY³ and CHRISTOPHER KUZAWA^{2,4}

¹Center for Health and the Social Sciences, University of Chicago, ²Anthropology, Northwestern University, ³Department of Preventive Medicine, Northwestern University, ⁴Institute for Policy Research, Northwestern University

Increased investment in reproduction at the expense of somatic maintenance is posited to accelerate senescence and decrease lifespan, trade-offs which represent potential "costs of reproduction." The physiological or metabolic pathways that govern these trade-offs are only partially understood. Oxidative damage has been implicated in the gradual deterioration of somatic function that characterizes senescence, and therefore represents a potential cost of reproduction. Here we investigate the potential costs of reproduction by examining the link between reproductive status and protein adduct biomarkers of oxidative stress and antioxidant defense. We compared levels of 18 protein adduct biomarkers of associated with oxidative stress, antioxidant defense, lipid peroxidation, and other endogenous processes in a sample of women (age 20–22) in the Philippines who were either pregnant, breastfeeding, nulliparous, or previously reproductive (total N = 80). We predicted that reproductive status would be associated with levels of protein adduct biomarkers that indicate the generation of oxidative stress, with currently reproductive individuals demonstrating higher levels of oxidative stress and lower antioxidant levels than women who are nulliparous or parous but not currently breastfeeding or pregnant. We report statistically significant differences across reproductive groups for 4 of the protein adduct biomarkers measured here, indicating increased oxidative stress and decreased antioxidant protection for women who are currently pregnant or breastfeeding. Ongoing applications of these methods will contribute to a greater understanding of the costs of reproduction, as well as the physiological, health, and evolutionary significance of the trade-offs faced by women over the course of their lives.

Fathers and father figures: Kin and age effects on chimpanzee (*Pan troglodytes*) social relationships

AARON A. SANDEL

Department of Anthropology, University of Texas at Austin

In most mammals, mothers form social bonds with their offspring, but fathers do not. The exceptions are pair bonded species, including humans, where fathers often care for infants. But even in polygynandrous primates, fathers bias behavior toward their offspring. To explore father biases, I studied male chimpanzees at Ngogo, Kibale National Park, Uganda, during 12 months in 2014-2015 (period 1) and 8 months in 2017-2018 (period 2). In period 1, I found that adolescent/young adult male chimpanzees biased grooming toward old males, especially their fathers. In period 2, there was a bias to groom old males; 25% of males had an old male (>35 years old) as their top grooming partner. However, there was no bias for fathers. One adolescent had his father as a top grooming partner, but none of the males that had groomed frequently with their fathers in period 1 did so in period 2. In general, relationships did not persist: grooming rates in period 1 were weak predictors of grooming rates in period 2. The lack of enduring bonds may be due to different social strategies as males mature and enter the dominance hierarchy. It is also due to a shift in the community structure at Ngogo, which began to divide in 2015, and exhibited two incipient communities by 2017 with three father-son pairs on opposite sides of the divide. Despite these changes, the bias for old males, regardless of relatedness, suggests a role of "father figures" during the transition to adulthood in male chimpanzees.

The Leakey Foundation, University of Michigan, Arizona State University, the Nacey-Maggioncalda Foundation, the National Science Foundation (1540259 and F031543)

A catalog and methodology in the study of the fourth bone of the rib to estimate the age in the population of Durango, Mexico

CINDY C. SANDOVAL¹ and VÁCTOR M. LÓPEZ²

¹LABORATORIO DE ANTROPOLOGÍA, FISCALIA GENERAL DEL ESTADO DE DURANGO, ²DEPARTAMENTO DE IDENTIFICACIÓN HUMANA, FISCALIA GENERAL DEL ESTADO DE DURANGO

The objective of the study has applied the method of Iscan for estimation of age as an indicator of Mexican population.

The study of the sternal end of the rib through direct observation, change analysis, establishment and bone maturation standard is the way to compare our results with those contributed by other authors. Furthermore, in forensic anthropology, this work has allowed us to obtain an evaluation of human remains of adult origin from Durango, Mexico. In addition, the techniques help and confirm the difficulty of estimating the age of

ABSTRACTS

death in individuals over 60 years of age and the application of macroscopic studies as a reference in the Mexican population, mainly in Durango. The materials used for the study were 100 individuals of known age and sex. This allowed establishing parameters for the sex of each individual and determining some phases with approximately more useful age ranges for the final estimation of the age of the individuals at the time of death, applied in forensic cases. This study has shown that the sternal rib can provide an accurate estimate of the age of death in the Mexican population in an age range in men and women by the principle of the individual analysis of the fourth rib.

Geometric Morphometric Analysis of the dental remains from the Early Upper Paleolithic of Manot Cave, Israel

RACHEL SARIG^{1,2}, CINZIA FORNAI^{3,4}, HILA MAY^{2,5}, OMRY BARZILAI⁶ and GERHARD W. WEBER^{3,7}

¹Department of Oral Biology, The Goldschleger School of Dental Medicine, Sackler Faculty of Medicine, Tel Aviv University, Tel Aviv, Israel, ²Dan David Center for Human Evolution and Biohistory Research, Sackler Faculty of Medicine, Tel Aviv University, Tel Aviv, Israel, ³Department of Evolutionary Anthropology, University of Vienna, Althanstr 14, A-1090 Vienna, Austria, ⁴Institute of Evolutionary Medicine, University of Zurich, Winterthurerstr. 190, CH-8057 Zurich, Switzerland, ⁵Department of Anatomy and Anthropology, Sackler Faculty of Medicine, Tel Aviv University, Tel Aviv, Israel, ⁶Archaeological Research Department, Israel Antiquities Authority, POB 586, Jerusalem 91004, Israel, ⁷Core Facility for Micro-Computed Tomography, University of Vienna, Althanstr 14, A-1090 Vienna, Austria

This study presents the dental remains discovered at Manot Cave (MC), Western Galilee, Israel. Human occupation at the cave is evident during the Early Upper Paleolithic period (46-33 ka), mainly represented by Early Ahmarian (~46-42 ka) and Levantine Aurignacian (~38-34 ka). Six teeth were found at the site, of which four could be thoroughly analysed (two deciduous and two permanent). We applied Geometric Morphometric analyses using a large comparative sample in order to assess the morphological affinities of the Manot specimens with other *Homo* groups. Based on micro-CT scans, the occlusal surface of the enamel-dentin-junction (EDJ), the cervical and the crown outlines were captured by landmarks/semilandmarks/pseudolandmarks. Furthermore, EDJ and cervical outline were combined into a fourth type of dataset that includes the height of the tooth crowns. The Manot teeth show a remarkably heterogenous mixture of modern human and Neanderthal trait expressions: the upper first premolar (MC-9 P³) is very modern human-like; the upper deciduous second molar (MC-10 dm²) and the upper second permanent molar (MC-8 M²) might be modern humans but they show also Neanderthal characteristics; the

lower second deciduous molar (MC-7 dm²) might be a Neanderthal. Our analysis could not supply conclusive answers to the question regarding the origin of the Manot Aurignacian. However, as our results show, this industry could be related either to modern humans or some kind of hybrid population of Neanderthals and modern humans. Whether they arrived from Europe or if they were a local Levantine variant cannot be answered with our data.

This work was supported by the Dan David Foundation, Binational Science Foundation (no. 2015303), Israel Science Foundation (no. 338/14), The Leakey Foundation, CARE Archaeological Foundation and Case Western Reserve University.

Changes in body composition during short-term acclimatization to highly challenging environments

MALLIKA S. SARMA¹, CARA J. COBOCK¹, SHANNON ROCHELLE², SARAH MARTIN² and LEE T. GETTLER¹

¹Anthropology, University of Notre Dame, ²Rocky Mountain, National Outdoor Leadership School

Under ecological stressors like high altitude and cold stress, humans experience rapid physiological changes as they acclimatize to the surrounding conditions. This often results in relatively swift negative outcomes (e.g. extreme weight loss) within the acclimatization period (~2-3 weeks). However, bodies can rebound from stressors and return to baseline once acclimatized, though it is unknown how individual factors such as sex or age may affect acclimatization success. Working with the National Outdoor Leadership School, we looked at healthy individuals (n = 71) on ~90-day expeditions through the Rocky Mountains where prior work demonstrated that ecological demands lead to negative energy balance. Assessing within-individual changes, we tested how sex and age predicted body composition changes in high altitude and cold environments. Individuals' body fat declined from the beginning to the end of the expedition, on average, as did their body weight in the early expedition stages (ps < 0.05) but the effect sizes were small. Notably, they had typically returned to their baseline body weight by the expedition's end. Finally, for the first three quarters of the expedition, both men and women gained significant lean muscle mass (p < 0.05). Neither sex nor age were significantly linked to body composition changes. Under these metabolically demanding conditions, it is unexpected that participants experienced relatively minimal overall declines in body fat, rebounds in body mass, and upticks in muscle mass. This suggests future work should

explore the possibility that individuals may use behavioral strategies or alternative physiological mechanisms to metabolically acclimatize alongside expending of energy stores.

This project is supported by the NSF GRFP, the Institute for Scholarship in the Liberal Arts, the NSF DDRIG, PEO Scholar Award, and AAUW Women American Fellowship.

Why are they hanging around? The role of suspension during feeding in chimpanzees

LAUREN SARRINGHAUS¹, SHARIFAH NAMAGANDA² and LAURA MACLATCHY¹

¹Department of Anthropology, University of Michigan, ²Department of Zoology, Entomology & Fisheries Sciences, Makerere University

Positional behavioral versatility is a hallmark of extant hominoids, with orthograde forelimb suspension and vertical climbing constituting key components of this versatility. A prominent hypothesis regarding the origin of orthograde suspensory behavior is that it evolved to facilitate feeding on ripe fruit in terminal branches in the forest canopy. However, some of the earliest fossil apes to exhibit locomotor versatility, such as *Morotopithecus* and *Rangwapithecus*, had a reliance on folivory. In this study, chimpanzees are used as a model to determine if certain positional behaviors such as forelimb suspension are used preferentially while consuming fruit compared to leaves, as both food types are of potential evolutionary relevance. Positional behavior data in the context of feeding were collected from 2-minute instantaneous focal sampling of adult and subadult chimpanzees from the Ngogo community, Kibale National Park, Uganda, over two field seasons. Orthograde forelimb suspension was the second most frequent positional behavior employed (after sit) while feeding on both fruit and leaves. This was true for all individuals combined and when individuals were divided by age class. Although 77% of the 887 observed feeding bouts involved eating fruit, and only 14 % involved eating leaves, the percentage of bouts in which orthograde forelimb suspension was used during feeding for fruit (17%) and leaves (22%) was not significantly different (z-score = -1.34, p = 0.18). Thus positional behavioral versatility contributes to leaf-eating in chimpanzees, suggesting that both fruit and leaves should be considered in future investigations of the evolution of versatility in hominoids.

This research was funded by the National Science Foundation and the Leakey Foundation.

Temporal Changes of Periodontal Disease in the Neolithic Jomon, Japan

AIKO SASO¹, KATHERINE HAMPSON² and OSAMU KONDO²

¹Department of Physical Therapy, Niigata University of Health and Welfare, ²Department of Biological

ABSTRACTS

Sciences, Graduate School of Science, The University of Tokyo

Concerning temporal changes in oral health in Jomon populations, previous studies showed that the rate of dental caries gradually increased from the Early to the Middle, and the Late to the Final Jomon period. In the Middle period, the caries rate reached over 10%, which is almost equivalent to the level of "agricultural" group.

In this study, we evaluated periodontal disease by distance from the cement enamel junction to the alveolar crest (CEF-AC distance) and by morphological change in the interdental septum, and tested the changes between time periods, sex and site locations. In addition, we performed a correspondence analysis to confirm relationships between the periodontal disease scores, and caries rate, antemortem tooth loss rate, wear score, and chipping score.

In the results, the temporal changes of periodontal disease rate showed a different pattern from that of caries rate. Furthermore, we found also clear differences in rates of periodontal disease between site locations (inland and coastal areas) and between the time periods (Early and Middle Jomon). Recent archeobotanical evidence has suggested the plant utilizations occurred at different times along the Japanese archipelago. We may link the observed data on the oral health indicators to a more geographically and periodically detailed map on the archeological evidence.

This work was supported by JSPS KAKENHI

Human Biology and the Koobi Fora Field School: New Work with the Daasanach, a Small-Scale Pastoralist Population

JESSICA SAUNDERS¹, ZANE S. SWANSON¹, HILARY BETHANCOURT², SHIVA DHANASEKAR³, ROSEMARY NZUNZA⁴, ASHER Y. ROSINGER^{2,5} and HERMAN PONTZER^{1,6}

¹Evolutionary Anthropology, Duke University, ²Department of Biobehavioral Health, Pennsylvania State University, ³Department of Anthropology, Emory University, ⁴Kenya Medical Research Institute, KEMRI, ⁵Department of Anthropology, Pennsylvania State University, ⁶Global Health Institute, Duke University

The Koobi Fora Field School (KFFS), currently operated by George Washington University and the National Museums of Kenya, has been working along the eastern margin of Lake Turkana Basin for several decades. In that time, field school research has primarily focused on paleoanthropology, geology, and archaeology. Recently, however, human biology research has been integrated into the structure of the KFFS, with work now being conducted in conjunction with Daasanach communities living in and around the town of Illeret, Kenya. Early work has involved collecting survey, anthropometric, dried blood spot, doubly labeled water, and water quality

data to investigate the effects of ecological, environmental, and lifestyle variation on the life history, energetics, and health of this traditionally semi-nomadic pastoralist population. Data collection in the summer of 2019 resulted in the participation of 242 adults and 218 children from 137 households across 7 Daasanach communities of varying distance from the Illeret town center (<0.5km - 14km). Analyses on cardiometabolic health, one facet of the KFFS human biology project, found higher than expected rates of hypertension among Daasanach (32.6% of adults 40–65 yrs and 44.4% of adults 65+ yrs). However, blood lipids, another indicator of cardiometabolic health, were low relative to US norms. Additionally, age-adjusted diastolic blood pressures for adult males and females both varied significantly by community and distance from the town center. These results demonstrate how human biology research and collaboration with Daasanach will broaden our understanding of how diverse ecological contexts, subsistence patterns, and lifestyles affect human biological variation.

NSF ARCH #1624398; NSF REU #1930719; This work was funded by the PSU SSRI Human Health and Environment Seed Grant, and the Triangle Center for Evolutionary Medicine (TriCEM) Graduate Research Grant.

Longitudinal biometric analyses of a temperate, high altitude, large nocturnal primate, *Otolemur crassicaudatus*: Sex and environmental effects

MICHELLE L. SAUTHER¹, FRANK P. CUOZZO², JAMES MILLETTE III¹, ADRIAN SW. TORDIFFE³, BIBI LINDEN^{2,4} and JABU LINDEN^{2,4}

¹Anthropology, University of Colorado - Boulder, ²Nocturnal Primate Biology Project, Lajuma Research Centre, ³University of Pretoria, Department of Paraclinical Sciences, ⁴University of Venda, Department of Zoology

Primates are mostly tropical, with only a few, primarily larger bodied haplorhine genera adapting to the more stressful ecology of temperate habitats. To better understand how a strepsirrhine primate is affected by such environmental stressors, we carried out a 7-year (2013-2019) study of wild thick-tailed galagos, *Otolemur crassicaudatus*, in a high altitude, seasonal habitat at the Lajuma Research Centre, South Africa. Biometric data were collected on individuals captured in Havahart traps (n = 102, 67 adults, 35 subadults, 206 total repeat captures). Adult males were heavier, had greater subscapular body fat, greater linear measurements and muscle mass (circumference data) compared to adult females (one way ANOVA, Tukey post-hoc analyses; p < .05). Subadults exhibited no sex differences other than subadult females having higher suprailiac skin fold values than subadult males. More fine-tuned growth and development data taken on the same individuals across 2017-18 reveals that males increase their body weights at

a more rapid trajectory than females, who take longer to achieve adult weights. Seasonality (hot wet versus cold dry) impacts adult and subadult body weights, with lower measures during the cold season when insect resources are reduced (t-test, p = .0001). Weight, circumferences and body fat (skin folds), also varied by year, being lower during years characterized by dramatically high amounts of rainfall and cooler temperatures which may affect resource availability (e.g. 2013, 2014). This study demonstrates the importance of longitudinal data and informs how primates living in changing, fluctuating environments may be impacted by increasing climate change.

National Science Foundation BCS Biological Anthropology #1638833

Population history and the evolution of human variation

KRISTEN R. R. SAVELL¹ and CHARLES C. ROSEMAN²

¹Department of Biology, Sacred Heart University, ²School of Integrative Biology, University of Illinois at Urbana-Champaign

Population history is the order and timing of population-level events which structure the effects of gene flow and genetic drift on variation across populations. As such, population history encompasses migration and founder effects, as well as relatedness at local, regional, and global scales. Contemporary anthropological work in evolutionary quantitative genetics treats population history as little more than a variable for which we must account in our investigations of natural selection's role in evolutionary processes. Moreover, there is an unexamined conceptual relationship between population history at the micro-evolutionary level and phylogenetic constraint at the macro-evolutionary level.

Here, our approach is twofold. First, we review the treatment of population history in the quantitative genetic literature, focusing on its role as an extension of the neutral model of evolution as well as the attempts that have been made to disentangle the various influences of gene flow and genetic drift. Secondly, we examine the role of population history at different evolutionary scales. We argue that population history is more than a nuisance variable and that it plays a crucial and constructive role in human adaptation. To this effect, we critically examine the framing of core problems in hominin evolution as being macro- or micro-evolutionary. Results of our simulation and theoretical work indicate that most of the major evolutionary transitions in the fossil record, from the evolution of brain size to the accumulation of cranial differences between Neandertals and recent humans, are neither macro- nor micro-evolutionary as conventionally understood.

ABSTRACTS

How well do feeding observations match fecal stable isotope values? An evaluation among Verreaux's sifaka (*Propithecus verreauxi*) and ring-tailed lemurs (*Lemur catta*)

NORA W. SAWYER¹, JAMES E. LOUDON¹, RYAN SCHACHT¹, MICHELLE L. SAUTHER² and MATT SPONHEIMER²

¹Department of Anthropology, East Carolina University, ²Department of Anthropology, University of Colorado, Boulder

Primatologists have paired stable isotope analyses with observational data to gain a fuller understanding of nonhuman primate (NHP) behavioral ecology. The stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotope values of animals are recorded in their tissues and excreta and reflect the values of the foods they have consumed. Fecal $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values represent the undigested portion of the foods consumed, providing dietary data on the order of days or weeks, depending on gut transit rates. We evaluate how well feeding observations match fecal $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values for sympatric Verreaux's sifaka (*Propithecus verreauxi*) and ring-tailed lemurs (*Lemur catta*) at the Beza Mahafaly Special Reserve over an eight-month period. We developed a simple equation to predict the fecal $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of the sifaka and lemurs that included their feeding observations ($n=7291$), the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of the plants they consumed ($n=128$), and adjustments for fecal-plant fractionation. We sampled two social groups of sifaka and lemurs ($n=224$ fecal samples) on a monthly basis. We regressed our observed $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values against measured $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ fecal values. We found that our observed values were significantly associated with fecal $\delta^{15}\text{N}$ isotope values ($p=0.02$). However, our model did not significantly predict fecal $\delta^{13}\text{C}$ isotope values ($p=0.17$). In sum, we found mixed support for expectations that fecal values represent observations of diet. $\delta^{15}\text{N}$ values were closely matched, but $\delta^{13}\text{C}$ values were not. Thus, while fecal isotope values provide useful dietary information, they may not completely correspond with NHP feeding observations.

This project was funded by the National Science Foundation (BCS 0525109).

Global Variation of Rocker Jaw

ANDREA SBEI, SCARLETT BOLING, MASON MCKINNEY and G. RICHARD SCOTT

Anthropology, University of Nevada, Reno

Turner et al. (1991) included three mandibular traits in the Arizona State University Dental Anthropology System: palatine torus, mandibular torus, and rocker jaw. While frequencies of tori have been reported for global samples, less is known about the distribution of the rocker jaw trait. The term rocker jaw refers to a mandible with an inferiorly bowing body, which is curved in

such a way that when set on a flat surface, the mandible rocks back and forth for one or two seconds (grade 1) or longer (grade 2). Although many have noted rocker jaw as a common trait in Polynesians, no systematic analysis has been done to investigate its global variation.

In this project, we calculate the worldwide frequencies of rocker jaw using the C.G. Turner database to compile data on multiple samples from 16 major geographic regions ($n=6044$). Individuals were scored for rocker jaw on a scale from 0 to 2, with a breakpoint of 1 to derive total frequencies. Rocker jaw variation displayed four major frequency patterns: 0-10% - South America, Micronesia, Sub-Saharan Africa, India, and Europe; 11-20% - North America, East Asia, Central Asia, Southeast Asia, New Guinea, Siberia, North Africa, and Nubia; 21-30% - Australia and Melanesia; 31-50% - none; 51% and over - Polynesia. The results of this study confirm that rocker jaw is present in much higher frequencies among Polynesian groups. More work is needed to study the genetics and development of rocker jaw to fully interpret its unusual pattern of global variation.

Single and Dual Isoscape Models for Establishing Local Strontium and Oxygen Isotope Signatures of Human Skeletons in the Prehistoric Andes

BETH K. SCAFFIDI¹, KELLY KNUDSON¹ and TIFFINY TUNG²

¹School of Human Evolution and Social Change, Arizona State University, ²Department of Anthropology, Vanderbilt University

Strontium and oxygen isotopes are robust markers of residential history. The ratio of bioavailable strontium isotopes ($^{87}\text{Sr}/^{86}\text{Sr}$) in the food chain varies according to bedrock age and composition and does not fractionate in the body, so that tissues reflect the geological signature of diet. Oxygen isotopes vary according to altitude and latitude, so enamel $\delta^{18}\text{O}$ values reflect the drinking water consumed during childhood. If mostly-local food and water were consumed, enamel strontium and/or oxygen values beyond the local range indicate non-local childhood. While these isotopes have been used to statistically parse non-locals within a population, variation within and between sites throughout the Andes has not been thoroughly characterized. This study compiles published human strontium ($n = 1390$) and oxygen ($n = 893$) values, plots them in coordinate space, and generates single and dual geostatistical models (or isoscapes) for establishing expected local ranges of skeletal isotope values.

Skeletal $^{87}\text{Sr}/^{86}\text{Sr}$ values range from 0.7019 to 0.7239 (mean = 0.7071, sd = 0.002) and are normally distributed (Ryan-Joiner = 0.765, p -value < 0.010). Skeletal $\delta^{18}\text{O}_{\text{dwSMOW}}$ values ranged from

-19.6‰ to -3.5‰ (mean = -11.34, sd = 4.18), and are normally distributed (Ryan-Joiner p -value < 0.010). The dual isotope model has a root-mean-square = 1.18 and root-mean-square standardized = 1.04. Paired oxygen and strontium isotope values from known provenience ($n = 30$) were used to validate the dual-isotope model, resulting in 100.00% falling within the mean \pm 2SD for each isotope prediction. Future work will compare these datasets to environmental isoscape models for the region.

National Science Foundation SBE Postdoctoral Research Fellowship (award number 1809470)

Travel costs of intergroup aggression among Argentine tufted capuchin monkeys

CLARA J. SCARRY

Department of Anthropology, California State University, Sacramento

In choosing whether to participate in intergroup aggression, individuals are expected to assess both the relative costs and benefits, as well as the probable outcome of an encounter. While intergroup dominance correlates with home range size or quality in many primate species, the immediate costs of engaging in aggressive intergroup encounters are rarely measured. In the current study I examine the potential costs of intergroup aggression among Argentine tufted capuchin monkeys (*Sapajus nigritus*), focusing on immediate travel costs because intergroup encounters rarely involve direct physical aggression and are instead characterized by long-distance chases. During all-day group follows ($N = 70$ days) of four social groups, I recorded the group's center-of-mass at 15-minute intervals to construct complete daily paths between sleeping sites, as well as recording all occurrences of intergroup encounters and their outcomes. Losing an encounter appears to entail immediate energetic costs, as measured by increased daily travel distance (22%) in the absence of a concomitant increase in time spent feeding. Instead, following an intergroup encounter, losing groups move faster, suggesting they are foraging less intensively, with no changes in the amount of time spent stationary or the overall sinuosity of the daily path. In contrast, both daily path length and average travel speed by winning groups are indistinguishable from days without encounters. Despite both these costs and the highly predictable nature of outcomes, subordinate group frequently initiate intergroup encounters, suggesting that their long-term benefits for home range maintenance may outweigh the short-term costs.

This study was funded by the Leakey Foundation, the National Geographic Society, the National Science Foundation (BCS-0752683), and the Wenner-Gren Foundation.

ABSTRACTS

What can you do when the standard biological profile can't help? A case of identical twins

AUDREY D. SCHAEFER^{1,2} and CARRIE B. LEGARDE²
¹SNA International, ²Defense POW/MIA Accounting Agency

In a large commingled assemblage of human remains, mtDNA is often the starting point for analysis, particularly when the individuals are all men of similar age, ancestry, and stature. Siblings can pose a particular problem since they have the same mtDNA and Y-chromosome DNA, which yield the best results. Differences in age or stature, or both, may allow for segregation of the skeletal remains, but what are our options when the unknowns are identical twins who have the same DNA, age, ancestry, and stature. Our typical anthropological toolkit cannot help. How similar are the bones of identical twins? Can we reliably pair match elements? Individuating characteristics become the most important portion of this biological profile, but this also relies on the presence of antemortem records.

This presentation outlines a case involving the identification of twin brothers and discusses the importance of observations beyond the standard biological profile and the collaboration between anthropology and odontology for forensic cases. In our case, we were able to individually identify the crania based on dental comparison and this was supported by individuating characteristics confirmed with antemortem records. There was no duplication in the postcranial elements, which prevented us from identifying postcranial elements to a single individual. This case presented a unique challenge where we had to rely on observations outside of the biological profile and collaborate with other disciplines to individually identify twin brothers.

Social Identities of Tributes during the Late Horizon (1470-1532 CE) in the Lambayeque Valley, Peru

BENJAMIN J. SCHAEFER^{1,2,3} and BETHANY L. TURNER⁴

¹Anthropology, University of Illinois at Chicago, ²Gender and Women's Studies, University of Illinois at Chicago, ³Latin American and Latino Studies, University of Illinois at Chicago, ⁴Anthropology, Georgia State University

A key question in Andean archaeology centers on the varied life histories of sacrificial victims, particularly the period when Andean South America was dominated by the Inka Empire (1450-1532 CE). The flexible nature of Inka statecraft meant that some subject polities were incorporated with minimal change to local traditions, while others saw significant and often-forceful change. Inka control of the north coast aligned with the former: Muchik local communities largely continued their own forms of governance within a hegemonic

tributary economy. This study reconstructs and theorizes individual life histories of female sacrificial victims (N=4) from the Inka phase at the Huaca de Los Sacrificios of the Chotuna-Chornancap Archaeological Complex in Peru's Lambayeque Valley. This site served as a ritual and ceremonial space by the Chimú, and then Inka, empires. Previous mortuary, osteological, and stable isotope analyses suggest that, in contrast to better-known Inka *capacocha* sacrifices, these individuals were regionally local, consumed typical coastal diets, and were sacrificed in violent fashion involving significant perimortem trauma. Here, cortisol levels are analyzed in mummified hair to infer psychosocial stress preceding death. Cortisol values have a mean of 317 nMol/L with a breadth spanning 74-1026 nMol/L. These values exceed clinically normal levels, indicating chronic activation of the hypothalamic-pituitary-adrenal (HPA) axis and suggesting pregnancy or elevated stress. None of these individuals were found in association with fetal remains, making pregnancy less likely. Instead, results suggest that these individuals embodied various forms of psychosocial stressors before death, adding an important dimension to their life histories.

The Massachusetts Cultural Council - Tyringham Local Council

Quantitative Genetics of Body Mass and Color in Mandrills (*Mandrillus sphinx*)

JERRED K. SCHAEFER¹, ADAM D. GORDON¹, BARTHELEMY NGOUBANGOYE², SHARON E. KESSLER³, MARIE CHARPENTIER⁴ and JOANNA M. SETCHELL^{5,6}

¹Department of Anthropology, University at Albany-SUNY, ²Centre de Primatologie, Centre International de Recherches Médicales, ³Department of Psychology, University of Stirling, ⁴Institut des Sciences de l'Evolution de Montpellier, Université de Montpellier, ⁵Department of Anthropology, Durham University, ⁶Behaviour Ecology and Evolution Research (BEER) Centre, Durham University

Sexual dimorphism is widespread across primate species, yet little is known about the underlying proximate mechanisms that produce such patterns. Mandrills (*Mandrillus sphinx*) provide one of the best examples of sexual selection in the order Primates due to their high levels of sexual dichromatism and size dimorphism, and data are available for 132 pedigreed individuals from a semi-free-ranging colony at the Centre International de Recherches Médicales, Franceville, Gabon. In this study, we use a multi-response, multivariate mixed (i.e. "animal") model to estimate the quantitative genetic parameters of narrow-sense heritability (h^2), within-sex, and between-sex genetic correlations for two facial coloration traits (red-green opponency and luminosity) and body mass (kg). The model includes sex, age, and dominance rank as fixed effects and the genetic relatedness (A) matrix, maternal ID,

and repeated measure as random effects. Results show moderate, but statistically significant (at $\alpha = 0.05$) heritabilities for all three traits in both sexes. However, this study detected only one significant genetic correlation among traits either within- or between-sexes: between female red facial coloration and body mass. This suggests that the joint evolution of coloration and body mass is constrained in females, but not in males. Results also show a significant environmental (residual) correlation between male red facial coloration and body mass, suggesting correlated selection instead of genetic correlations may be an important mechanism for maintaining sexual dimorphism in these two traits. Future work will incorporate fitness estimates to assess selective hypotheses regarding the evolution of these traits in mandrills.

Innovation or continuation? Development of wet-rice agriculture in Prehistoric Northeast Thailand

JESSICA SCHALBURG-CLAYTON¹, CHARLOTTE KING¹, HALLIE BUCKLEY¹, SIÂN HALCROW¹, CHARLES HIGHAM¹, LOUISE SHEWAN², CHRISTINA STANTIS³, DOUGALD O'REILLY⁴, KATE DOMETT⁵, JANA ZECH⁶ and PATRICK ROBERTS⁶

¹Department of Anatomy, University of Otago, ²Sydney Medical School, University of Sydney, ³Department of Archaeology, Anthropology, and Forensic Sciences, Bournemouth University, ⁴School of Archaeology and Anthropology, The Australian National University, ⁵College of Medicine and Dentistry, James Cook University, ⁶Department of Archaeology, The Max Planck Institute for the Science of Human History

Archaeological evidence in the Upper Mun River Valley (UMRV), Thailand, during the Iron Age (400-900AD) supports the development of social stratification. This social development is hypothesized to be impacted by the intensification of wet rice agriculture contemporaneously. Isotopic analysis is a useful tool for examining prehistoric human diet to test changes in agricultural practices between the Bronze and Iron Age. In this study, new carbon ($\delta^{13}\text{C}$) and oxygen ($\delta^{18}\text{O}$) values have been determined from the Iron Age site Non Ban Jak (NBJ), the best preserved and largest Iron Age skeletal sample in the region, and have been compared with the nearby Bronze Age site, Ban Non Wat. The $\delta^{13}\text{C}$ values demonstrate no significant change between Bronze Age and Iron Age, while the $\delta^{18}\text{O}$ values increase and have a greater range during the Iron Age compared with the Bronze Age. An increase in the monsoon could create more variable $\delta^{18}\text{O}$ values observed, or light isotope evaporation from standing water could cause the increase of values. However, if wet-rice agriculture was being more heavily employed at NBJ, a shift in $\delta^{13}\text{C}$ values would also be expected, as plant values have been shown to increase with rising water usage. By investigating human

ABSTRACTS

diet through isotope analysis, we have tested the model of wet-rice agricultural advancement and the results do not conclusively support its intensification during the Iron Age in the UMRV.

Thank you to the Marsden Fund, the Max Planck Institute for the Science of Human History, and a University of Otago Doctoral Scholarship for supporting this research.

Effects of compliant substrates on gait kinematics in squirrel monkeys (*Saimiri boliviensis*)

NICOLE M. SCHAPKER^{1,2}, BRAD A. CHADWELL³ and JESSE W. YOUNG^{1,2}

¹Department of Anatomy and Neurobiology, Northeast Ohio Medical University, ²School of Biomedical Sciences, Kent State University, ³Department of Anatomy, Idaho College of Osteopathic Medicine

Wild arboreal primates must navigate substrates that vary in size and compliance. In order to understand their strategies to maintain stability, laboratory researchers must endeavor to mimic those conditions. Here, we evaluate kinematic changes in the gait of squirrel monkeys (*Saimiri boliviensis*) due to substrate compliance. Using high speed cameras, we filmed the strides of two juvenile female monkeys as they voluntarily walked across poles of varying diameter (5cm, 2.5cm, 1.25cm) mounted in an enclosed runway. Poles were mounted on either a stiff wooden base ("stable" condition) or foam blocks ("compliant" condition). We scored footfall timings and digitized approximate center of mass displacement to calculate kinematic variables (N = 136 strides). We predicted that on compliant supports monkeys would walk more slowly and – controlling for speed – increase stride lengths and duty factors while decreasing stride frequencies. As expected, stride length was greater on all compliant pole diameters, and stride frequency was significantly decreased on two of the three compliant poles ($p \leq 0.018$). Unexpectedly, the highest speeds were on the largest compliant pole ($p < 0.001$), and otherwise, monkeys did not significantly adjust speed. Compliance had minimal influence on duty factor with little discernible pattern across the three diameters. In short, squirrel monkeys made only minor kinematic adjustments to increases in substrate compliance. These results, while further emphasizing the importance of studying compliance on gait in the lab, also underscore the variability in kinematic adjustments to compliant substrates that have been observed in studies of wild primates.

Supported by NSF BCS-1126790.

Investigating human-pathogen evolution using ancient genomics and proteomics

CHRISTIANA L. SCHEIB¹, MERIAM GUELLIL¹, RICHARD HAGAN², MARCEL KELLER¹, SARAH A. INSKIP³, CRAIG CESSFORD^{3,4}, RUOYUN HUI³,

EUGENIA D'ATANASIO⁵, JENNA DITTMAR³, ALICE A. ROSE³, BRAM MULDER³, PIERS MITCHELL⁶, TAMSIN C. O'CONNELL⁶, ALEXANDER HERBIG⁷, JOHANNES KRAUSE⁷, TINA WARINER^{7,8}, TOOMAS KIVISILD⁹ and JOHN E. ROBB⁶

¹Institute of Genomics, University of Tartu, ²Department of Archaeology, University of York, ³McDonald Institute for Archaeological Research, University of Cambridge, ⁴Cambridge Archaeological Unit, University of Cambridge, ⁵Department of Human Genetics, Katholieke Universiteit Leuven, ⁶Department of Archaeology, University of Cambridge, ⁷Department of Archaeogenetics, Max Planck Institute for the Science of Human History, ⁸Department of Anthropology, Harvard University

A number of factors influence a person's susceptibility to and manifestation of infectious disease including: inherited genes, diet, age, microbiome composition, and the virulence of the pathogen itself. Teasing apart these factors is especially difficult and in archaeogenomic studies, the focus is usually on the phylogeography of the people or the pathogen itself, though recently a few studies have incorporated some functional and/or immune-gene analysis. By layering multiple bioanthropological and geochemical techniques (aDNA, proteomics, lipids, isotopes, radiocarbon dating, histology, morphology, and osteology) per individual on a population-scale, we can attempt to reconstruct a "health landscape" for that population through time and test the relationship between factors and manifestation of disease. I will present preliminary results and the workflow we established for the After the Plague Project (Wellcome Trust) with our collaborators to develop new laboratory and bioinformatic methods as well as novel applications of standard methods to analyse hundreds of ancient individuals. We use shotgun genomic data to combine human demography, kinship, phenotype prediction, oral microbiome diversity, and pathogen presence/strain analysis. We incorporate a method for efficient co-extraction of proteins and DNA (endogenous and exogenous) allowing us to study the diet, pathogen-specific proteins and immune response to infection, whether chronic (e.g. periodontal disease) or acute (e.g. plague). This framework has allowed us to detect unexpected bacterial and viral infections and to start to elucidate the complex interactions between diet, environment, hereditary traits and disease, which have and continue to shape our evolution as a species.

CLS is supported by the Institutional Development Program for R&D Institutions and Higher Education Institutions (ASTRA). The After the Plague project is supported by the Wellcome Trust (Award no. 2000368/Z/15/Z).

Spatial patterning in the evolution and diversity of early modern humans in East Asia

LYNNE A. SCHEPARTZ¹, XIUJIE WU^{2,3} and WU LIU^{2,3}

¹HVIRU, Anatomical Sciences, University of the Witwatersrand, ²Key Laboratory of Vertebrate Evolution and Human Origins of CAS, Institute of Vertebrate Paleontology and Paleoanthropology, ³CAS Center for Excellence in Life and Paleoenvironment, Chinese Academy of Sciences

The patterning of early *sapiens* morphological diversity in East Asia was evaluated through a spatial-temporal analysis of fossils dated approximately 300-20 kya from 34 localities. The fossils were studied using non-destructive morphometric and scanning modalities. Taphonomic, aDNA and environmental data were also incorporated. The results suggest the existence of two general morphotypes that vary spatially with one in the north and one in the south.

Identified Neandertal-like features were primarily cranial attributes (vault form and contours, supraorbital morphology, occipital gracility, suprainion form and bunning, mid-facial breadth, nasal form (Dali, Jinnuishan, Xuchang) and temporal labyrinth form (Xujiayao, Xuchang; but not Liujiang). Neandertal-specific (derived) characters are not seen in the dentition or the limited East Asian postcranial material (Jinnuishan, Liujiang, Tianyuan). Neandertal-like morphology was found to be distributed among the northern sites, raising the question of shared craniofacial climatic adaptations across northern Eurasia in conjunction with gene flow as attested from aDNA.

Similarities to modern *sapiens* morphology were most consistently seen in the dentition (Zhiren, Fuyan, Huanglong, Panxian Dadong, Tongzi and others) and dental development (Xujiayao), although there was non-dental evidence (Tianyuan, Liujiang). The persistence of earlier Asian dental characters in modified form, notably those of the incisor and canine crowns, supports the recognition of a new early modern *sapiens* pattern distinctive to East Asia and lacking the climatic adaptations and gene flow characterizing the northern fossils. Predominance of this morphotype in more southern sites may be a result of current exploration or taphonomic biases.

Support provided by the South Africa National Research Foundation Incentive Funds for Rated Researchers and grants from the National Natural Science Foundation of China and the Chinese Academy of Sciences.

Applied Geometric Morphometrics in Surgery Planning

STEFAN SCHLAGER^{1,2}, MARC ANTON FÜSSINGER², MATHIEU GASS² and MARC METZGER²

¹Biological Anthropology, Faculty of Medicine, University of Freiburg, ²Department of Oral

ABSTRACTS

and Maxillofacial Surgery, Faculty of Medicine, University of Freiburg

Knowing the shape distribution of a biological structure in a healthy population provides crucial information in a clinical settings where surgeons have to deal with deformed or defective versions of that structure. The aim of reconstructive surgery is to repair or replace the missing/damaged parts as close to the original shape as possible. A virtually reconstructed shape can be used to generate patient-specific implants in order to restore the functionality of a defective area.

Geometric Morphometrics is a feasible way to quantify shape variation of a population and PCA-models generated from Procrustes-aligned data are a computationally cheap and straightforward way to create probabilistic shape models. These allow to assess the likelihood of a given shape in respect to a reference population and produce estimations that are as close to the given shape as possible while being guaranteed to lie within the variability of a healthy population. In order to achieve a smooth fit to the surrounding intact tissue, however, usually a deformation that produces shapes outside the model space is necessary.

For the application in a clinical context, very dense surface representations are necessary to capture and ensure a continuous representation of the structure at hand. Therefore, sparse anatomical landmarks are only used as priors to constrain the variability of the shape models to shapes with similar landmark positions. We are presenting use-cases from maxillo-facial surgery and introduce a shape-model-driven thin-plate spline deformation to allow for generating shapes outside the model space.

Dental Microwear Texture Analysis of late Upper Paleolithic Grotta Maritza and Grotta La Punta Adult Males

CHRISTOPHER W. SCHMIDT¹ and RUGGERO D'ANASTASIO²

¹Anthropology, University of Indianapolis,
²Anthropology, Università degli Studi "G. d'Annunzio"

The late Upper Paleolithic sites of Grotta La Punta and Grotta Maritza in Abruzzo, Italy date to approximately 11,800 and 10,500 years ago (Bietti, 1990). Foragers tend to have coarse molar microwear textures, likely from eating hard foods. They also have microwear features oriented in multiple directions that may be related to having heterogenous diets. Additionally, some foragers have smoother microwear textures because they consumed soft foods such as meat. The current study compares dental microwear texture analysis (DMTA) values from two adult males, one each from Maritza and La Punta. It contextualizes their data via comparisons to Upper Paleolithic populations, as well as to a variety of Holocene

foragers. The DMTA followed standard procedures and included the variables complexity, anisotropy, scale of maximum complexity, and textural fill volume. The La Punta male had an elevated complexity compared to Maritza (1.93 vs 1.28) and similar anisotropy (0.0027 vs 0.0030). Its scale of maximum complexity was slightly higher than that of Maritza (0.499 vs 0.344) but its textural fill volume was much lower (24,475 vs 40,575). La Punta has microwear texture that is similar to hard food foragers, especially those thought to rely heavily on wild nuts and seeds. Maritza's microwear texture is more similar to foragers thought to consume more meat or fish. If these two individuals are representative of their respective populations, their dietary differences may indicate a change in natural resource availability and/or exploitation in central Italy at the end of the Paleolithic.

Funded by a grant from the National Science Foundation (BCS-0922930)

Humanization of SRGAP2C expression increases cortico-cortical connectivity and alters neuronal response properties in the mouse brain

EWOUDE SCHMIDT¹, HANZHI (TERESA) ZHAO², ELIZABETH HILLMAN² and FRANCK POLLEUX¹

¹Neuroscience, Columbia University - Zuckerman Mind Brain Behavior Institute, ²Biomedical Engineering and Radiology, Columbia University - Zuckerman Mind Brain Behavior Institute

SRGAP2A plays a critical role in mammalian brain development by limiting density and promoting maturation of both excitatory (E) and inhibitory (I) synapses. In humans, duplication of SRGAP2A led to the emergence of SRGAP2C, which binds and inhibits all known functions of SRGAP2A. Expression of SRGAP2C in mouse cortical pyramidal neurons (PNs) results in phenotypic traits characterizing human cortical PNs, including increased E and I synapse density and delayed synaptic maturation.

We explored how humanization of SRGAP2C expression affects the structural organization of mouse cortical circuits by using monosynaptic rabies tracing from sparse populations of cortical layer 2/3 PNs. Using a novel method for reconstruction and mapping of traced neurons, we found that SRGAP2C expression causes a significant increase in local connectivity and long-range feedback connections from other cortical areas. Interestingly, we did not detect changes for subcortical inputs, showing humanization of SRGAP2C expression selectively increases cortico-cortical connectivity. These results suggest that developmental mechanisms that control synaptic connectivity, like SRGAP2, represent suitable evolutionary substrates through which increased complexity of cortical circuit wiring has emerged during human brain evolution.

We now investigate how increased cortico-cortical connectivity impacts circuit performance related to sensory processing and behavior. Using *in vivo* imaging approaches to examine cortical activity at both a whole-cortex and cellular level, we are testing how SRGAP2C expression alters cortical circuit function. Our work aims to uncover the mechanisms whereby human-specific genetic modifiers altered neuronal circuit architecture and function to allow for the emergence of human-specific features of brain function during evolution.

Support was provided by NIH (R01NS067557)(FP), Roger De Spoelberch Foundation Award (FP), Netherlands Organization for Scientific Research (Rubicon 825.14.017)(ERES), the European Molecular Biology Organization (ALTF1055-2014)(ERES), and NINDS K99 (K99NS109323-01)(ERES).

Expressing the Thrifty Phenotype? Associations between Lifelong Growth Trajectories and Whole Genome Expression Variation in Captive Baboons (*Papio hamadryas*)

CHRISTOPHER A. SCHMITT¹ and ELLEN E. QUILLEN²

¹Department of Anthropology, Boston University,
²Department of Internal Medicine, Section on Precision Medicine, Wake Forest School of Medicine

The thrifty phenotype hypothesis argues that developmental alterations in gene expression change lifelong weight and health. Baboons are a strong model of age-related changes in weight due to their close relationship to humans and similar progression to metabolic syndrome. We use the baboon model to investigate genome-wide changes in gene expression and methylation associated with lifelong patterns of growth. We used weights taken from 552 baboons with full growth trajectories born in the Texas Biomedical Research Institute from 1985 to 1995. Lifetime growth was clustered into two separate trajectories for each sex – resulting in heavy and light adult weights, respectively – using a shape-based k-means longitudinal clustering algorithm. Upon necropsy, total RNA was extracted from white blood cells from 140 females and 58 males. mRNA counts were normalized to read counts per sample and converted to a log-fold scale before performing differential expression analysis between the two trajectories for each sex independently. Results indicate differential expression in both sexes for 25 known loci implicated in obesity and metabolic syndrome, including *RND2/PTGFRN* for which altered expression is implicated in early puberty and subsequent obesity; *RAG1*, implicated in lymphocyte 'memory' maintaining longitudinal obesity; *RGS6/CENPW* which alter fat intake and over-eating; and *ZNF426/TNCC2/7SK*, each hypermethylated in offspring whose mothers had inadequate gestational

ABSTRACTS

weight gain or diabetes, conditions known to alter lifelong growth. This is one example of the many ways that the impacts of environmental and developmental variation on gene expression can be evaluated on a genome-wide scale in captive non-human primates.

This research was funded by NIH P51OD01113, R01AR064244, R01AR060341, K01AG056663.

Hand and foot postures and loading patterns in monkeys and apes: implications for cheiridial design

DANIEL SCHMITT¹, ANGEL ZEININGER¹, JANDY B. HANNA² and ROSHNA E. WUNDERLICH³

¹Evolutionary Anthropology, Duke University, ²Biomedical Sciences, West Virginia School of Osteopathic Medicine, ³Biology, James Madison University

It is widely assumed that cheiridial morphology and posture reflects locomotor loading, but this relationship is rarely tested. Here we describe cheiridial posture as it relates to force distribution using two species—baboons and gorillas—that, unlike many other primates, have forelimb/hindlimb vertical peak (Vpk) force ratios that are close to or equal to one. We collected force and video data on juvenile and adult *Papio anubis* at Stony Brook University (n=2) and Duke University (n=1) and juvenile and adult *Gorilla gorilla* at the North Carolina Zoo (n=7). In both species, forelimb/hindlimb Vpk increases with age (get closer to one) and the elbow and wrist show limited yield compared to other primates. Results show that depending on palm position, young gorillas land with a more flexed or deviated wrist and a more protracted arm compared to adult gorillas, which almost exclusively use extended, knuckle-walking postures and retracted forelimbs. Similarly, juvenile baboons use a more flexed wrist and elbow than adult baboons. The use of a vertical manus appears to moderate hand and wrist joint moments when forelimb forces are relatively high. In the hindlimb, throughout ontogeny, gorillas adopt an extended and non-yielding knee and ankle and heel-strike plantigrady while baboons adopt a semiplantigrade posture, both of which can moderate ankle moments in the first half of stance. Adjusting cheiridial mechanics, especially in the forelimb, a pattern reported in other studies, seem to reflect locomotor loading and may be used to better understand form-function relationships in living and extinct species.

Research supported by the National Science Foundation Grant BCS-1517561

Putting Neanderthal endocranial form into modern context: Comparing Neanderthal vs. modern human differences with respect to differences among modern human populations

P. THOMAS SCHOENEMANN^{1,2,3} and RALPH L. HOLLOWAY⁴

¹Anthropology, Indiana University, ²Cognitive Science, Indiana University, ³Human Evolution, Stone Age Institute, ⁴Anthropology, Columbia University

Although Neanderthal endocrania are not smaller than those of modern humans on average, they are generally longer (anterior-posteriorly) relative to their height (inferior-superiorly), and tend to have a pronounced occipital protuberance. These differences have long been used to suggest Neanderthals might have differed significantly behaviorally from modern humans, such as possibly having less linguistic ability, poorer executive function, and/or smaller episodic and working memory capacity. However, the extent to which these morphological differences are actually large enough to merit meaningful behavioral implications is not clear. To put them into the context of known populational variation in human brain shape, we have compared shape differences between Neanderthal (specifically: LaChappelle, LaFerrassie, LaQuina 5, and Saccopastore 1) vs. modern human endocrania, to shape differences between a standard modern human brain atlas based on American and European subjects (MNI152) vs. one based on 2020 modern Chinese subjects (CHINESE2020). Morphological registration and quantification of localized shape differences was accomplished using Advanced Normalization Tools (ANTs). We find that on average the morphological differences are only slightly greater than that found between the MNI152 and CHINESE2020 atlases. Specifically, the average (root mean squared) Jacobian scaling difference for Neanderthal vs. modern human voxels was 16%, whereas the equivalent for the MNI152 vs. CHINESE2020 was 13%. Given the lack of clear cognitive differences between Chinese and American/European populations, this calls into question the suggestion of significant cognitive differences between Neanderthal and modern humans. The extent to which surface morphology may hide internal morphology will be evaluated.

This research was supported in part by grant 52935 from the Templeton Foundation titled: "What Drives Human Cognitive Evolution?"

Morphological rates of evolution in the *Phenacolemur praecox* - *Phenacolemur fortior* and *Phenacolemur praecox* - *Phenacolemur citatus* lineages in the Bighorn Basin, Wyoming

NAAVA SCHOTTENSTEIN¹, MARK HUBBE² and JOHN HUNTER¹

¹Department of Evolution, Ecology, and Organismal Biology, The Ohio State University, ²Department of Anthropology, The Ohio State University

The plesiadapiform primate, *Phenacolemur fortior*, is hypothesized to have evolved from *Phenacolemur praecox* in the Bighorn Basin, Wyoming, through rapid sympatric speciation, with intermediate stages known stratigraphically between the two species. This evolutionary transition occurred during a faunal turnover event (Biohorizon A) in the Bighorn Basin. *P. fortior* went extinct and was replaced by *P. citatus* before a second faunal turnover event (Biohorizon B). An ancestor-descendant relationship between *P. praecox* and *P. citatus* has been proposed based on similar morphology and size, suggesting that *P. citatus* arose by allopatric speciation. This study tests whether neutral evolution can explain morphological evolution observed during and between each speciation event. We calculate a rate of morphological evolution, based on the ratio between inter- and intra-species variation in height and protoconid height of p4 and length and width of p4, m1, m2, and m3, between early and late individuals of *P. praecox*, *P. fortior*, and *P. citatus* and over both lineages. Results show that changes in height and protoconid height of p4 and lengths and widths of all cheek teeth within and between species are consistent with strong stabilizing selection (rate <0.000001). Moreover, there is evidence of a release of the selective pressure (rate >0.000001) in both lineages associated with the biohorizons, which resulted in increased rates of morphological change for these tooth dimensions. This suggests that changes resulting in species-level divergence can occur under a process of relaxed stabilizing selection and highlights the importance of the biohorizons for their disruptive effects.

Strontium isotope variability (⁸⁷Sr /⁸⁶Sr) in the ancient Nile Valley (Egypt and Nubia): Establishing baseline data and tracking human mobility

SARAH SCHRADER¹, MICHELE BUZON² and ANTONIO SIMONETTI³

¹Faculty of Archaeology, Leiden University, ²Department of Anthropology, Purdue University, ³Department of Civil & Environmental Engineering & Earth Sciences, University of Notre Dame

Previous research of (⁸⁷Sr /⁸⁶Sr) in the ancient Nile Valley has provided compelling evidence for population movement through time. The estimation of local values, based on faunal sampling, has been established at several sites, providing a better

ABSTRACTS

idea of strontium variability across the landscape. While this $^{87}\text{Sr}/^{86}\text{Sr}$ research remains promising, there are also methodological and interpretative issues that must be addressed. We couch this discussion of limitations and future directions with faunal and human $^{87}\text{Sr}/^{86}\text{Sr}$ data for the Third Cataract region of the Nile Valley ($n=61$). New samples from Abu Fatima (2500-1550 BCE), Hannek (1550-656 BCE), and Tombos (1550-656 BCE) were analyzed and the results are presented here.

Results from two faunal samples supported the previously estimated local $^{87}\text{Sr}/^{86}\text{Sr}$ range for the Third Cataract (0.70710-0.70783). Furthermore, 11 of the 59 human samples were found to have $^{87}\text{Sr}/^{86}\text{Sr}$ outside of this local range, suggesting they had migrated from elsewhere. This sheds new light on the scale of migration during the 3rd-1st millennia BCE and, importantly, illustrates the need for further research. There is a distinct need for a better understanding of strontium variability in the region, particularly in Egypt and the Second Cataract region. Additional comparisons of $^{87}\text{Sr}/^{86}\text{Sr}$ values between modern and ancient fauna would also illuminate changes in bioavailable $^{87}\text{Sr}/^{86}\text{Sr}$ through time. A National Science Foundation grant has been awarded to address these issues and further the examination of $^{87}\text{Sr}/^{86}\text{Sr}$ in the Nile Valley.

Howling for food and females: A cross-site comparison of mantled howler monkey (*Alouatta palliata*) howling behavior in Costa Rica

AMY L. SCHREIER¹ and LAURA M. BOLT²

¹Department of Biology, Regis University,

²Department of Anthropology, University of Waterloo

Howler monkey long calls have been explained by several non-mutually exclusive hypotheses including ecological resource defense (howls are used to defend food resources) and mate defense (howls are used to defend females from extra-group males). We investigated the relationship between howling and resource defense in mantled howler monkeys in two Costa Rican rainforests, La Selva and La Suerte. Only ~25km apart and sharing similar wildlife, La Selva is much larger and has bigger, more abundant fruiting trees than La Suerte. Due to greater food resource abundance at La Selva, we predicted that group size would be larger and monkeys would howl at higher rates, for longer durations, with more howls per bout than at La Suerte. We conducted all-occurrences sampling of howling behavior at La Suerte (June-August 2017/2018, January 2019) and La Selva (November 2018-February 2019). Group size was significantly larger at La Selva (12.7 monkeys) than La Suerte (9.1) although there was no difference in number of males/group. Mean howl length and number of howls/bout were both significantly higher at La Selva

(156.6sec; 9.2howls/bout) than La Suerte (121.4; 5.2), but howling rate was significantly higher at La Suerte (1.1howl/hour) than La Selva (0.6). Rate was positively correlated with group size at both sites but number of males/group did not vary, suggesting that howling rate relates to mate defense with differences in operational sex ratio driving how often males howl. In contrast, howl length and number/bout are associated with ecological resource defense, with longer howling bouts occurring in richer habitats.

Coming Apart at the Seams: A Bioarchaeology of Care analysis of 50-59 year old female with tuberculosis from the Middle Archaic Midwest (6000 – 3000 BC)

ALECIA SCHRENK

Anthropology, University of Nevada, Las Vegas

Understanding how prehistoric communities provided healthcare for chronic illnesses is essential to understanding human behaviors surrounding poor health. Here, a Bioarchaeology of Care analysis is presented for a 50-59 year old female with a probable case of tuberculosis from the Middle Archaic (6000-3000 BC) hunter-gatherer community of Carrier Mills, Illinois. Over the course of her illness, she suffered from complete destruction and eburnation of her hip, femur, knee, and humeri which would have resulted in mobility impairments and difficulty completing daily tasks. Despite this, she survived to old age due to the accommodation and direct healthcare provided by members of her community. Initially, she would have needed accommodation for her fatigue and mobility impairments. However, as her disease progressed, she would have gradually required more accommodation of her differences and direct care as the destruction of her joints made traveling long distances increasingly difficult. Additionally, she was given a differential mortuary treatment facing East with a deer bone tube pendant that may have linked her to Southeastern concepts of birth and healing. Possibilities for spiritual healthcare provisioning are also discussed. A Bioarchaeology of Care analysis for this individual provides a more nuanced understanding of the ways that prehistoric Midwestern hunter-gatherers would have perceived, rationalized, and dealt with poor health.

Is the chin a spandrel? Insights from evolutionary quantitative genetics

LAUREN SCHROEDER^{1,2,3}, JILL E. SCOTT⁴, CHRIS A. ROBINSON^{5,6,7} and NOREEN VON CRAMON-TAUBADEL³

¹Department of Anthropology, University of Toronto Mississauga, ²Human Evolution Research Institute, University of Cape Town, ³Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, ⁴Department of Sociology and Anthropology, Metropolitan State

University of Denver, ⁵Department of Biological Sciences, Bronx Community College (CUNY), ⁶Doctoral Program in Anthropology, City University of New York Graduate Center, ⁷The New York Consortium in Evolutionary Primatology (NYCEP)

A recent study of the mandibular symphyseal angle in primates indicated rapid evolutionary change within hominins, suggesting a strong effect of natural selection on symphyseal morphology, potentially leading to the development of a chin in humans. However, it has yet to be explicitly tested whether the chin was under direct selection, or was a product of correlated selection with other traits. To address this issue we used a two-step quantitative genetic approach. First, we estimated evolutionary rates, via Lande's generalized genetic distance, along each branch of a fully-resolved hominoid phylogeny to detect rate-shifts in mandibular form. Second, where directional selection was identified, we reconstructed the pattern of selection acting on specific mandibular traits. Overall, results indicate that much of the diversity in extant hominoid mandibular form can be explained by either genetic drift or strong stabilizing selection; however, a rapid evolutionary rate (suggestive of directional selection) was detected along the branch to humans. Reconstructed selection gradients indicated strong selection acting to decrease alveolar length and anterior corpus width and height, and to increase posterior corpus width and the relative size of the posterior dentition, consistent with selection for a parabolic dental arcade. However, for the majority of traits related to the chin, selection gradients and trait responses occurred either in opposite directions, indicating correlated responses to selection, or selection gradients were not significantly different from zero. Thus, our results provide evidence that the distinct human chin could be an evolutionary by-product of direct selection on other aspects of mandibular form.

Data collection was funded by the Leakey Foundation.

Did infant-laden leaping lead to lullaby, melody, and prosody?

DAVID SCHRUTH

Anthropology, UW

Unlike (litter-birthing) tree shrews, who leave their infants in nests, most (lower-parity) primates carry their infants to avoid predation. Additional avoidance strategies such as inter-tree leaping can create communication gaps—which not only allows primates to avoid scent-tracking by predators but also requires them to develop contact calls that are distinguishable from background noise. The function of acoustic differentiability goes beyond just group confirmation of location and identity, however, as extra-group display can also evoke elaborate acoustic patterning. To help disentangle these selective influences, I explored a collection of 502 calls and contexts, from 46 species, in a causal modeling framework

ABSTRACTS

using the PC-algorithm. I found that contact and foraging contexts had more tonal and repetitive elements while display and territorial contexts were more syllabically diverse. At the species level, diversely reappearing syllabic displays were directly associated with social monogamy and risky locomotion (e.g. leaping and swinging)-indicative of a possible three-way co-evolution. These results are consistent with the theory that parental care in primates could have facilitated the learning of precarious arboreal subsistence strategies that further necessitated highly patterned acoustic signals. While galagos and tarsiers, who park their infants, serve as important exceptions, anthropoids have been synapomorphic in fur-cling carrying for most of the Cenozoic and serve as a plausible parental attachment model underlying the co-evolution between complex limb landing and elaborate note landing in our hominoid ancestors.

2,000-year-old pathogen genomes reconstructed from mummies provide insights into the state of health of ancient Egyptians

VERENA J. SCHUENEMANN^{1,2}, JUDITH NEUKAMM^{1,2,3}, SASKIA PFRENGLE^{1,2}, MARTYNA MOLAK⁴, ALEXANDER SEITZ³, MICHAEL FRANCKEN², PARTICK EPPENBERGER¹, CHARLOTTE AVANZI⁷, ELLA REITER², CHRISTIAN URBAN^{1,2}, BEATRIX WELTE⁸, BARBARA TESSMANN⁹, ALEXANDER HERBIG¹⁰, KATERINA HARVATI^{2,5,6}, KAY NIESELT³ and JOHANNES KRAUSE^{10,2}

¹Institute of Evolutionary Medicine, UZH, ²Institute for Archaeological Sciences, University of Tübingen, ³Center for Bioinformatics Tübingen, University of Tübingen, ⁴Museum and Institute of Zoology, Polish Academy of Sciences, ⁵Senckenberg Centre for Human Evolution and Paleoenvironments, University of Tübingen, ⁶Dept. of Geosciences, University of Tübingen, ⁷Department of Microbiology, Immunology and Pathology, Colorado State University, ⁸Institute of Pre- and Protohistory and Medieval Archaeology, University of Tübingen, ⁹Anthropology, Berlin Society of Anthropology, Ethnology and Prehistory, ¹⁰Archaeogenetics, Max Planck Institute for the Science of Human History

For many decades, ancient DNA analysis of Egyptian mummies was considered highly challenging due to preservation and contamination issues of the extracted DNA. However, recent advances in ancient DNA methods in combination with next-generation sequencing has allowed reliable retrieval of human mitochondrial and nuclear genomic data. Here, the metagenomic content of Egyptian mummies from different time periods was investigated via analysis of the microbial composition of various tissues. The analysis of the dental calculus' microbiome identified Red Complex bacteria, which are correlated to periodontal diseases. From bone and soft tissue, the genomes of two ancient pathogens, a 2,200-year-old *Mycobacterium leprae* strain and

a 2,000-year-old human hepatitis B virus, were successfully reconstructed. Overall, the results show the reliability of metagenomic studies on Egyptian mummies and permit the evaluation of a local ancient Egyptian population's health status through time.

Genetic Diversity in Contemporary Charleston African-Americans: Connecting Ancestral and Descendant Communities

THEODORE G. SCHURR¹, RAQUEL E. FLESKES¹, ADEYEMI ODUWOLE², ADE A. OFUNNIYIN^{3,4} and JOANNA K. GILMORE^{3,4}

¹Anthropology, University of Pennsylvania, ²Biology, College of Charleston, ³Cultural Heritage, The Gullah Society, ⁴Sociology and Anthropology, College of Charleston

The discovery and anticipated genomic analysis of human remains found in downtown Charleston, South Carolina, stimulated African-American community members to examine their own genetic ancestry and possible biological relationships to these 18th century Anson Street Ancestors. Seventy-six Charleston African-Americans provided DNA samples for analysis, with one analyzed using the GenoChip 2.0 at Family Tree DNA, and the other subjected to mtDNA control region sequencing and Y-chromosome STR analysis at the University of Pennsylvania. The resulting data were compared with those from the Anson Street Ancestors and other African and African-American populations. Charleston African-Americans exhibited a wide array of haplotypes from haplogroups F3, L0-L4, T2, and U6, although not sharing any of them. Nearly all of the Y-chromosomes of male participants belonged to African haplogroup E1b1, with A1, E1a2, E2b1 and R1b haplotypes also being present and a number of men sharing a specific E1b1a sublineage. All participants showed significant African autosomal ancestry (83.5% average), with some degree of European, Near East and/or Asian admixture. We evaluated these data in the context of genealogical and historical information, and used them to explore the extent of genetic continuity between Charleston African Americans and the Anson Street Ancestors. Overall, these data illuminated the population genetic history of contemporary African-Americans living in Charleston and their connection to historic African-descended populations from the area. Furthermore, descendent communities were engaged in discussions about the genetic data, African-American ancestry and the history of Charleston in the trans-Atlantic slave trade throughout the study.

This research was funded by awards from the National Geographic Society (#NGS-52378R-18 to A.A.O.; #EC-52936R-18 to A.O.), the University Research Foundation (UPenn) (T.G.S.) and the College of Charleston (A.O.)

Ancient biomolecules reveal ancestry, diet and microbiomes of Upper Palaeolithic hunter-gatherers from Sicily

GABRIELE SCORRANO^{1,2}, SOFIE H. NIELSEN¹, DOMENICO LO VETRO^{3,4}, MEAGHAN MACKIE^{2,5}, PIER FRANCESCO FABBRI⁶, MORTEN E. ALLENTOF¹, FABIO MARTINI^{3,4}, CRISTINA MARTÁNEZ-LABARGA⁷, OLGA RICKARDS⁷, JESPER V. OLSEN⁵, ESKE WILLERSLEV^{1,8}, ENRICO CAPPELLINI² and MARTIN SIKORA¹

¹Centre for GeoGenetics, GLOBE Institute, University of Copenhagen, ²Evogenomics Section, GLOBE Institute, University of Copenhagen, ³Storia, Archeologia, Geografia, Arte e Spettacolo (SAGAS), University of Florence, ⁴Museo e Istituto Fiorentino di Preistoria, Florence, ⁵Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, ⁶Beni Culturali, University of Salento, ⁷Centro di Antropologia Molecolare per lo studio del DNA antico, Dipartimento di Biologia, University of Rome Tor Vergata, ⁸Department of Zoology, University of Cambridge

In recent years, improvements in the recovery and analysis of ancient DNA (aDNA) have given new insights into the evolutionary history of our species. Likewise, recent investigations have shown that ancient dental calculus, a complex and calcified bacterial biofilm formed from dental plaque, is rich in aDNA and proteins, and it is particularly valuable for characterizing diet, oral microbiome, and diseases in ancient populations. Here we present a joint "multi-omics" approach, integrating palaeo(meta)genomics and palaeoproteomics on ancient biomolecules recovered from bone and dental calculus of two Upper Palaeolithic individuals from San Teodoro cave (Sicily, Italy), to reconstruct the lifestyle and post-Last Glacial Maximum (LGM) spread of humans in Southern Europe. Our aDNA results show genetic homogeneity in Sicily, and close affinities of the San Teodoro individuals with other post-LGM hunter-gatherers from southern Europe, such as Villabruna from northern Italy. We further document affinity of San Teodoro to a lineage contributing about a half of the ancestry of a post-LGM individual from El Miron in northern Spain. Palaeoproteomic analysis of dental calculus revealed a hunter-gatherer diet based on mammal and fish meat and plants. Finally, composition of the reconstructed ancient oral microbiomes from San Teodoro was most similar to those from Palaeolithic Neandertals, and clearly distinct from later forager and farmers individuals. Our results demonstrate the power of multi-omics approaches to ancient biomolecules to obtain detailed reconstructions of ancestry, metagenomes and diet of prehistoric human populations.

This project has received funding from the European Union's Horizon 2020 under the Marie Skłodowska-Curie grant agreement No 751349 allotted to G.S. G.S. also received support from the SYNTHESYS Project <http://www.synthesys.info/>

ABSTRACTS

Female Fortitude: Exploring the Pivotal Role of Women at the 18th century Fortress of Louisbourg, Canada

AMY B. SCOTT¹ and SARAH MACINNES²

¹Anthropology, University of New Brunswick,

²Fortress of Louisbourg National Historic Site, Parks Canada

Founded in 1713, the fortified town of Louisbourg played an important role in France's colonial empire. It is not surprising that, with its significant garrison, the community's male to female ratio was as high as 10:1 during its occupation. This imbalance, in addition to other factors, proved to demonstratively impact the lived experiences of women in the colony. During a period where societal roles and expectations based on sex were rigid and strictly enforced in France, physical separation from greater French society provided women in Louisbourg with opportunities that were not readily available to their counterparts in Europe or even Quebec. As a result, women in Louisbourg were able to hold non-traditional positions in society, contributing to the economic and overall success of the colony.

From a bioarchaeological perspective, this female influence at Louisbourg is difficult to ascertain as economic success and societal influence is difficult, if not impossible, to identify in skeletal remains. Despite this, an interesting trend has emerged in the skeletal data from the Rochefort Point cemetery (1738-1760). The female skeletons recovered display a significant amount of pathology, similar, if not more, than some of the males. These pathological changes include indicators of childhood stress, evidence of trauma and infection on the lower limbs, and poor dental health including severe caries and abscesses. These preliminary skeletal findings in addition to the rich historical record suggest a similar lived experience between the sexes at Louisbourg, with female fortitude underpinning this expansive French colonial site.

This research was supported by a SSHRC Partnership Development Grant (# 890-2017-0049)

Mother-offspring proximity maintenance in wild Bornean orangutans (*Pongo pygmaeus wurmbii*) in Gunung Palung National Park

AMY M. SCOTT¹, TRI WAHYU SUSANTO² and CHERYL D. KNOTT^{1,3}

¹Anthropology, Boston University, ²Biology, National University, Indonesia, ³Biology, Boston University

Our previous research showed that the distance between an orangutan mother-offspring dyad decreases when males are present. This change in proximity has been argued to be one aspect of a suite of female infanticide avoidance strategies. Therefore, we hypothesized that mothers are responsible for proximity maintenance in the presence of male conspecifics. In order to

investigate this hypothesis, we examined Hinde Indices and Brown-modified Hinde Indices during full day follows of mother-offspring orangutans in Gunung Palung National Park, West Kalimantan, Indonesia, from May 2018-April 2019. We found that 91% of days (N=34) had a Hinde Index indicating offspring control of proximity and 88% of days (N=34) had a Brown-modified Hinde Index indicating greater offspring responsibility for proximity changes than mother responsibility. There was no difference in the Hinde Index ($N_{\text{male absent}}=32$, $N_{\text{male present}}=14$, $t=0.979$, $df=19.122$, $p=0.334$) or Brown-modified Hinde Index ($N_{\text{male absent}}=32$, $N_{\text{male present}}=14$, $t=0.216$, $df=22.424$, $p=0.831$) when males were present compared to when males were absent. Counter to our hypothesis, offspring, not mothers, were still responsible for proximity maintenance in the presence of males. However, controlling for variation by analyzing the data on a per follow basis, we found that Hinde Indices shifted towards becoming more mother-maintained when males were present for 70% of the follows, but this difference was not significant ($N=10$, $t=1.050$, $df=9$, $p=0.321$). One limitation in interpreting these results is that all offspring included in our study were over three years old and past the age at which they are most vulnerable to infanticide.

AMS supported by Boston University, Leakey Foundation, and National Science Foundation (No. DGE-1247312).

CDK supported by National Science Foundation (BCS1613393), Disney Conservation Fund, and US Fish and Wildlife Service (F18AP00898).

Insights from Tooth Morphology on the Peopling of the Americas, with Special Emphasis on South America

G. RICHARD SCOTT, TATIANA VLEMINCO-MENDIETA and KYRA STULL

Anthropology, University of Nevada Reno

Results from craniometric analyses of early Native Americans are at odds with those from tooth morphology. From craniometric data, authors suggest a two-wave model for the peopling of the Americas with an early Paleoindian or pre-Mongoloid population replaced around 8000 years ago by a northeast Asian Mongoloid population. Excluding Circumpolar and Northwest Coast populations, dental morphological data suggests all Native Americans south of the subarctic shared a single common ancestor dating back some 15,000 years. Adopting a new line of analysis to determine if the two sets of data could be reconciled, South American samples from the C.G. Turner II database were broken down into four groups: (1) late Pleistocene-early Holocene; (2) mid to early Holocene; (3) late Holocene; and (4) recent (past 2000 years). Included in the analysis were other Native American, Asian, and Pacific populations. Using Bray-Curtis with both UPGMA and neighbor joining cluster analyses, two major clusters were evident: all Native Americans and all

Asian/Pacific groups. Within the American cluster, Inuit and Northwest Coast groups branched off first. All American Indians fall in the next cluster, with the mostly highly divergent group being Paleoindian. The four South American groups cluster together with the earliest sample the most divergent. North America and Mesoamerica are closely linked to all four South American samples. Craniometric and dental data remain at odds regarding the peopling of the Americas. Crown and root morphology provide no evidence for a Sundadont ancestor for any Native American group, including South American Indians.

One rate to rule them all? The tempo of trophic evolution in small-bodied primates

JEREMIAH E. SCOTT

Department of Medical Anatomical Sciences, Western University of Health Sciences

As a primary trophic strategy, insectivory is uncommon and unevenly distributed across extant primates. This pattern is partly a function of body mass: insectivory presents metabolic challenges for large-bodied species and is therefore unlikely to evolve or persist in many primate lineages. However, the pattern also holds in small-bodied primates, suggesting the influence of other factors. This study tests the hypothesis that small-bodied lineages differ in their propensity to shift between insectivory and herbivory by examining variation in the rate of transition between trophic strategies. The sample consisted of 307 extant species classified by trophic strategy and body size, creating an ordered three-state character: small-insectivorous, small-herbivorous, and large-herbivorous. The data were analyzed using likelihood and Bayesian methods that allow clades selected a priori to have different transition rates between states relative to the rest of the tree. Evidence for heterogeneity in rates of trophic evolution was strongest when Lorisiformes were partitioned from other primates: small-bodied lorises and galagos have a transition rate between insectivory and herbivory that is 4.7–5.9 times higher than the background rate. The analysis did not provide clear support for trophic rate variation when Anthropoidea were partitioned from other primates, challenging the idea that diurnality constrains trophic evolution in primates. These results support the hypothesis that trophic evolution has been more labile in some small-bodied lineages than in others, indicating that body size is not the only factor involved in structuring the distribution of insectivory and herbivory in primates.

ABSTRACTS

In Search of Linear Enamel Hypoplasia in a Stressed Population of *Propithecus diadema*

MELISSA S. SEABOCH^{1,2}, KAREN E. SAMONDS^{3,4}, JEAN-LUC RAHARISON⁴ and MITCHELL T. IRWIN^{3,4}

¹Anthropology, Salt Lake Community College, ²Anthropology, University of Utah, ³Anthropology, Northern Illinois University, ⁴SADABE, Madagascar

Body size and composition reflect adaptations to local conditions, such as resource availability. Sifakas (*Propithecus diadema*) in degraded fragmented habitats exhibit wasting in adults and stunting in subadults when compared to conspecifics in continuous habitats, likely reflecting reduced resource availability and resulting nutritional stress. Enamel hypoplasia, deficiencies in enamel thickness, can result from stress (e.g. poor nutrition) during tooth crown formation and can provide additional evidence of resource insufficiency. In this pilot study, we visually examined, under lighted magnification, 70 anterior teeth (15 canines and 55 incisors) of eight adult *P. diadema* for linear enamel hypoplasia (LEH). The skeletons were from the Tsinjoarivo Forest, Madagascar with six subjects from fragmented habitats in the Mahatsinjo area. Because this population showed other anatomical signs of nutritional stress, we expected to find LEH on most subjects. Surprisingly, linear enamel hypoplasias were not present on any of the canines or incisors examined thus refuting our hypothesis, though we note our sample size is quite small. The lack of LEH could be related to the rapid dental development of strepsirrhine primates which would be especially true of sifakas. In *Propithecus* species, the adult maxillary dentition (except for the canine) and the toothcomb erupt before weaning. It is possible that dental development occurs too rapidly to interrupt the formation of enamel. Also, it may be that nursing mothers are able to buffer their infants from the effects of nutritional stress. Future research on a larger sample of subjects is needed.

150 years of research on the origins of the Japanese: Colonialism and neo-colonialism

NORIKO SEGUCHI

Faculty of Social and Cultural Studies, Kyushu University, Department of Anthropology, The University of Montana, Missoula

The search for the origins of the Japanese people was initiated by foreign scholars such as F. F. Siebold, E. S. Morse, and E. von Baelz in the 19th century. This work was then continued by Japanese anatomists and physical anthropologists, who had received their medical education mainly from Germany. Subsequently, the origin of the Japanese people has long been a popular topic for speculation and research within Japan. In undertaking the explorations of the origins of

the Japanese, anthropologists of the Japanese Imperial Universities collected human remains of the Ainu and Ryukyu peoples, and later, collected remains from colonized areas of Imperial Japan such as the Korean Peninsula and Taiwan. Thus the origins of this research reveal strong linkages between colonialism and Japanese origins. However, Japanese anthropologists do not typically admit or discuss and reflect upon this strong colonial perspective.

Here, I argue that a colonialist framework has shaped anthropological research on Japanese origins. I explore the history of research on the origins of the Japanese people that took place during the imperial Japanese period, through imperial Japan and World War II, and continuing until the present day with modern technology such as DNA analysis. I will discuss why and how this framework on the origins of the Japanese people is problematic and what pitfalls will exist in future if we “physical” anthropologists continue the research on the origins of the Japanese people without reflecting on Japan’s colonial and imperial past.

This work was supported by JSPS KAKENHI Grant Number JP18KT0005 and JP19H05737.

The evolution of the hominin foot in a phylogenetic context

YEGANEH SEKHAVATI and DAVID S. STRAIT
Anthropology, Washington University in St. Louis

The evolutionary morphology of the hominin foot has recently been comprehensively reviewed. As part of that review, hominin pedal morphology was subjected to phylogenetic analysis, resulting in a cladogram showing that the phylogenetic signal of the foot differs from that of the skull. This is a valuable finding, but there is an alternative, complementary approach to utilizing these cladistic data. Here we use parsimony to examine the pattern by which pedal characters evolve in reference to previously proposed phylogenetic hypotheses. Twelve trees were examined with varying positions of *Au. africanus*, *Au. sediba* and *Au. prometheus*. Character states were reconstructed at three key nodes: the last common ancestor (LCA) of hominins, the LCA of *Au. afarensis* and all later hominins, and the LCA of *Au. africanus*, *Paranthropus* and *Homo*. Certain synapomorphies were recovered in all trees. Ten synapomorphies define the LCA of hominins that are functionally related to stiffening the lateral midfoot, supporting the longitudinal arch, stabilizing the lateral tarsometatarsal joint, propulsion off of the oblique axis of the foot, increasing the efficiency of propulsion, and dorsiflexing the toes. These results point to a major reorganization of the foot at the base of the hominin clade.

The First Annual Human Evolution Summer Teacher Workshop: Evolution Education in the Southeastern United States

MOLLY C. SELBA¹, MICHAEL J. ZIEGLER² and JOHN S. MEAD³

¹Anthropology, University of Florida, ²Geology, University of Florida, ³Science, Saint Mark’s School of Texas

The first annual Human Evolution Summer Teacher Workshop (HESTW) was designed to provide middle school and high school teachers with the educational resources they need to incorporate human evolution into their existing curricula. Nineteen K-12 educators from the southeastern United States were chosen to attend the inaugural workshop on the University of Florida campus. During their time at the workshop, educators received background information on significant paleontology and paleoanthropology research, were given the opportunity to ask questions to practicing paleoanthropologists, paleontologists, and anthropologists both in person and virtually over Zoom, and learned about 3D printing as a potential strategy for the teaching of morphologically-heavy concepts in human evolution. The educators received guidance in how to structure lesson plans (aligned to state-specific science standards) around open-source data and were able to experience firsthand the power of using 3D technology in the classroom. Additionally, issues inherent to evolution education were addressed in a variety of ways. Lectures about the evolution-religion “controversy” and a panel on the obstacles of teaching evolution allowed the workshop participants to ask questions and derive real-world solutions to the problems that might arise in their own classrooms. By directly addressing many previously-identified obstacles to the teaching of evolution, we successfully impacted teacher perceptions of the teaching of evolution and provided educators with the tools necessary to successfully implement human evolution into their existing science curricula.

Funding for this workshop was provided by iDigFossils and the Thompson Earth Systems Institute.

Identification and Implications of Carious Lesions in a Large Sample of Early Eocene Stem Primates from the Bighorn Basin of Wyoming

KEEGAN R. SELIG and MARY T. SILCOX
Anthropology, University of Toronto Scarborough

Caries is a dental disease resulting from the consumption of high levels of carbohydrates, commonly found in non-human primates, and therefore provides insight into patterns of diet. The disease is common among modern populations of humans and some non-human primates and has been identified in primates spanning the Plio-Pleistocene and even the Miocene. However,

ABSTRACTS

very little is known about caries in more ancient primate taxa, particularly during the Eocene, when global and local temperatures fluctuated dramatically. The microsyopid plesiadapiform, *Microsyops latidens*, is a stem primate known from a sample of nearly 1,000 stratigraphically controlled specimens from the early Eocene of Wyoming's Bighorn Basin. Because this sample is large, stratigraphically controlled, and spans a previously identified hyperthermal period, it allows for the characterization of patterns of variation through time in the context of climatic change. Using high-resolution micro-CT data, we identified occlusal caries in over 8% of the individuals in our sample (MNI = 960), which is relatively high compared to modern primates. Moreover, we identified two dramatic spikes in caries prevalence, with as many as 25% of individuals characterized by the presence of lesions. Although there are no climatic data for the period relevant to the latter of these two spikes, the earlier spike coincides with the previously identified period of temperature increase. Our analysis therefore provides a framework for identifying caries in early primates and suggests that changes in climate likely affect patterns of diet, particularly levels of fruit consumption, and dental health in early Eocene primates.

Funding was provided by a NSERC Discovery Grant to MTS and a University of Toronto Department of Anthropology Pilot Funding Grant to KRS

Biomechanical implications of variation in Hunter-Schreger Bands in early hominins

RACHEL S. SENDER¹, ALYSSA S. HILKO¹, GARY T. SCHWARTZ² and DAVID S. STRAIT¹

¹Department of Anthropology, Washington University in St. Louis, ²School of Human Evolution, Institute of Human Origins, Arizona State University

Hunter-Schreger Bands (HSBs) are an optical manifestation of decussation, the varying orientation of enamel prisms that is thought to be a mechanically significant feature of teeth related to arresting crown fractures. HSBs can be easily studied as they can be seen on sectioned or fractured surfaces of enamel. Variation in HSBs in early hominins have been documented, but advances in tooth fracture theory suggest that this phenomenon should be revisited. Photos from a previously published analysis of naturally fractured early hominin teeth were digitally scanned and HSB width, orientation and density were quantified using ImageJ. Our results corroborate the findings of the original study that found differences between the microstructure of early *Homo* and *Paranthropus boisei* enamel. However, measurements of HSB packing density were not evaluated previously but are mechanically important given that catastrophic ribbon fractures traverse the crown from cusp to cervix and vice versa. We found that *P. boisei* had thinner HSBs that occurred at a higher density than in *Homo*.

We suggest this configuration confers greater resistance to fracture, as there would be more opportunity for a developing crack to arrest as it is forced to change direction more frequently. Our results contrast with a previous interpretation that *P. boisei* had weaker crowns than expected given their thickness and suggest that further inquiry into enamel microstructure and fracture mechanics of fossil hominin teeth is warranted.

It's Lit: Campfire Relaxation as a Preadaptation for Television Viewing

ALEX SENTIS, EMI SMITH and CHRISTOPHER LYNN
Anthropology, The University of Alabama

Evolutionary mismatch theory suggests that preadaptation for rare needs in antiquity become problems in the modern world when they are no longer rare. We hypothesize that fire increased the prosocialness of ancestral humans by extending the wakeful day and creating physiological calming responses through sound, smell, and visuals. With the rise of technology, ubiquitous flickering screens have taken the place of flames. Because of the evolutionary sensory predispositions that humans have to fire, there is a similar physiological response to television screens. In a previous study, we found significant relaxation effect for fire with sound. Our sample of 98 undergraduate students were administered a similar randomized crossover experimental design. Conditions included a static picture of a flame as the control, and videos of fire with sound, fire without sound, and anthropological videos as the experimental variables. We measured blood pressure before and after each fifteen minute condition controlling for room temperature, fire exposure, anxiety, absorption, and other factors. Using multiple linear regressions, we found that there are significant differences of systolic and diastolic blood pressure that reflect a relaxed physiological response. Significant changes in blood pressure were seen during variables of video of fire with sound and TV conditions. The most prominent factors that affect these changes include socialness, previous fire and screen exposure, gender, relationship, absorption, state anxiety, prosociality, and socioeconomic status. The implication of these findings is that the current pandemic of cyber-dependence may be linked to our sensory preadaptations.

Mortuary Practices, Body Modification and Identity in the Western Maya Borderlands: Evidence from Late-Terminal Classic (AD 600-1000) Cemeteries at Comalcalco, Tabasco, Mexico

STANLEY SERAFIN¹, RICARDO ARMIJO TORRES² and MIRIAM JUDITH GALLEGOS GÓMORA²

¹Anatomy, University of New South Wales,

²Arqueología, Instituto Nacional de Antropología e Historia – Centro INAH Tabasco

Ossuaries and other forms of large secondary burial in public architecture or on communal lands become much more common at Postclassic Maya sites compared with the earlier Classic period during which household and single, primary burials predominated. Here, we demonstrate that Late-Terminal Classic cemeteries recently discovered on the outskirts of the westernmost Maya site of Comalcalco represent a transitional burial practice. The age-at-death profile suggests that these cemeteries were communal burial places. Differences in mortuary treatment and body modification, however, indicate that individuals continued to signal other aspects of identity, such as age, gender, status and ethnicity. Forty-eight individuals were interred directly in the soil, nearly all in lateral flexed position. Interspersed among them, meanwhile, were 34 individuals who had been placed inside ceramic urns, some of which were large enough to contain fully articulated adults. Tooth filing and dental inlays are significantly more common in urn burials (8/13, 61.5%) compared with direct burials (3/18, 16.7%; Fisher's Exact $P = 0.021$). Cranial modification patterns are similar in the two groups both of which show a predilection for the tabular erect style. This contrasts sharply, however, with elite and royal contexts in the site center where tabular oblique predominates in both art and actual crania. Our results demonstrate the utility of the integrated bioarchaeological analysis of skeletons and their archaeological contexts to provide insights into larger socio-political transformations, in this case the increased focus on more collective forms of identity that characterizes the Classic-Postclassic transition.

Transverse Lines: An Exploration of Bilateral Symmetry in Subadult Remains and a Re-Assessment of Their Utility in Bioarchaeological Studies

MARGOT SERRA

Institute of Archaeology, University College London

Transverse lines (TLs) are radiopaque structures visible at the ends of long bones. Scholars have attributed the formation of TLs to abnormal growth cessation, leading bioarchaeologists to use them as non-specific indicators of stress when studying past populations. However, recent studies have proposed that TLs may simply be a by-product of normal growth fluctuations. Therefore, the present study aimed to re-assess the utility of TLs in bioarchaeological studies by reviewing the existing literature on TLs and critically assessing it by examining the current knowledge on longitudinal growth and bone metabolism. Also, the bilateral symmetry of TLs distribution pattern encountered in radiographs of archaeologically derived subadult remains was researched in order to contribute to the understanding of TLs. It was found that more than half of the bilateral pairs of bone investigated displayed a symmetrical

ABSTRACTS

TLS distribution pattern. However, the proportion was not statistically significant and could simply have been the result of chance. Several suggestions were put forward to explain the results of the bilateral symmetry analysis. Furthermore, the extensive literature review on TLS undertaken by this study revealed considerable disagreements and uncertainties regarding the nature of TLS, their exact mechanism of formation, and their etiological causes; calling into question their utility in bioarchaeological studies.

Sexual dimorphism in the human calcaneus using 3D geometric morphometric methods

MARIA C. SERRANGELI¹, RITA SORRENTINO^{2,3}, MARIA G. BELCASTRO², STEFANO BENAZZI^{3,4} and ROBIN N.M. FEENEY¹

¹Anatomy, School of Medicine, University College Dublin, ²Department of Biological, Geological and Environmental Sciences, University of Bologna, ³Department of Cultural Heritage, University of Bologna, Ravenna, ⁴Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Leipzig

Sex determination of unknown individuals is central to Biological and Forensic Anthropology. Conventionally, sex assessment focuses on scored qualitative and metric features. An increasing number of studies have applied geometric-morphometric (GM) techniques to overcome limits of traditional approaches. With the exception of the skull and pelvis, GM application to the human postcranial skeleton remains limited.

Here the analysis of the degree and nature of sexual dimorphism in the modern human calcaneus, whose value in sex determination is well-acknowledged, is addressed for the first time by means of GM methods.

69 calcanei from two modern (19th-20th) well-documented (for sex and age) collections (Italy) from different geographical environments (Sassari, insular/Bologna, non-insular) were analysed.

Linear Discriminant Analysis returns high-accuracy in PCA form space (95.1% Bologna, 89.6% Sassari, 92.7% pooled sample) and centroid size (92.6%, 86.2% and 89.8%, respectively) but drops using PCA shape space (73.1% Bologna, 72.4% Sassari, 76.8% pooled sample). Overall, regardless of population, differences in calcaneal morphology were due to sexual dimorphism and are mainly related to allometry. This highlights the crucial role of size for sex determination in humans using the calcaneus. This outcome has further implications for inferring evolutionary trajectories.

Future research will incorporate a more comprehensive sample and the GM approach will be tested on virtually damaged specimens. The latter objective aims to evaluate the accuracy

of the GM approach as a tool to cope with fragmented calcanei, which are common in forensic and archaeological settings and often cannot be utilised via traditional linear methods for sex discrimination.

This project is funded by the European Research Council under the European Union's Horizon 2020 Research and Innovation programme (No. 724046 - SUCCESS) and the Medical Trainee Scholarship, Anatomy, UCD.

Reference sample mean age at transition is strongly influenced by sample size

VALERIE SGHEIZA¹ and HELEN M. LIVERSIDGE²

¹Anthropology, University of Illinois at Urbana-Champaign, ²Institute of Dentistry, Barts and the London School of Medicine and Dentistry, Queen Mary University of London

Previous studies have indicated that differences between reference samples for age estimation may be due in part to the small sample sizes within ordinal categories. The effect of reference sample size and composition on age estimation parameters are tested here both directly and holistically. The data consist of Moorrees, Fanning, and Hunt scores of the first permanent incisor through third molar of 2607 London children between 2 and 23 years of age. Scoring was performed on radiographs by the second author. Direct testing is performed by computing the standard error of the difference in mean age at transition between groups, varying group sizes and degrees of admixture. Admixture of ethnic groups for a single sex and admixture of sex for a single ethnic group does not affect standard error, when admixture ranges from 0-50%. Standard error increases with decreasing sample size (100% < 80% < 60%) in both designs. The Akaike information criterion of a multivariate cumulative probit model fit to the full dataset shows a significant effect from sex but not ethnic group. Altogether, these findings suggest that the effect of within-stage sample size on mean age at transition may outweigh the effect of other factors such as sex and ethnic group, even when these factors are significant in the model as a whole.

Variation in primate hunting over a five-year period among Waiwai subsistence hunters in Guyana, South America

CHRISTOPHER A. SHAFFER¹, PHILLIP SUSE², CHARAKURA YUKUMA², ELISHA MARAWANARU², STEPHEN SUSE², ROMMEL SHONI² and MARISSA S. MILSTEIN³

¹Department of Anthropology, Grand Valley State University, ²Masakenari Village, Konashen Indigenous District, ³Veterinary Population Medicine Department, University of Minnesota College of Veterinary Medicine

The hunting of primates is integral to the food security of millions of Amazonians, particularly indigenous groups. However, it is also one

of the greatest threats to primate populations throughout South America. In situations where stopping hunting altogether is not practical or desirable, primate conservationists should work together with indigenous groups toward the shared goal of long-term sustainability. This requires methods for assessing sustainability that are both accurate and tractable for co-management. Unfortunately, most studies of the sustainability of subsistence hunting are limited to a single year of harvesting data, making them highly susceptible to erroneous conclusions due to stochasticity. We studied the subsistence hunting behavior of Waiwai forager-horticulturalists in the Konashen Community Owned Conservation Area (KCOCA), Guyana from 2014-2019. In collaboration with the Waiwai community, we initiated a hunter self-monitoring program in 2014 where hunters collect detailed data on their harvesting behavior including prey choice, movement data, technology, and prey sex, weight, and age. We also conducted over 100 hunter follows to supplement and validate our hunter self-monitoring data. While some primates, particularly spider monkeys (*Ateles paniscus*), were highly preferred in each year of the study, Waiwai hunters showed considerable annual variation in the number of primate individuals harvested. This variation was primarily related to the availability of shotgun shells, which varied from one year to the next, and the movements and corresponding availability of white-lipped peccaries (*Tayassu pecari*) as prey. Our results demonstrate the importance of longitudinal research and long-term hunter self-monitoring for accurate assessments of hunting sustainability.

Funding was provided by the National Geographic Society, Conservation International, the International Primatological Society, Grand Valley State University, and the University of Minnesota - College of Veterinary Medicine

Testing East Turkana bovid mortality profiles using site-specific data

ROWAN M. SHERWOOD¹, ASHLEY S. HAMMOND^{2,3} and FRANCES FORREST^{3,4}

¹Department of Anthropology, The George Washington University, ²Division of Anthropology, American Museum of Natural History, ³New York Consortium in Evolutionary Primatology (NYCEP), ⁴Hall of Human Origins Laboratory for Comparative Genomics and Human Origins, American Museum of Natural History

Hominins have accessed ungulates as meat resources for at least 1.5 million years, but their carcass acquisition strategies are less well-known. Bovid mortality profiles demonstrate that hominins increasingly targeted prime-aged adults through time. A previous study inferred a prime-age signal for bovids in East Turkana between ~1.8-1.4 Ma, but the interpretations were limited because the study assessed broad

ABSTRACTS

subregions rather than specific sites. This study examines hominin mortality profiles at specific sites within East Turkana where there is clear evidence of hominin carnivory.

In 2019, we recovered 64 fossil bovid molars from two sites in Areas 1A (Okote Member) and 8A (KBS Member) to test whether prime-dominated profiles exist at the site level in the presence of hominin butchery. Three age classes were utilized based on molar infundibular occlusal wear: juvenile (little to no wear), prime adult (moderate wear), and old adult (severe wear). Mortality profiles for the two sites were created using triangular graphing software and compared to Kanjera South, FLK-Zinjanthropus, and modern lion- and hyena-killed bovid profiles.

Results support the inference that prime-dominated hunting by hominins occurred at the site-level in the presence of butchery in East Turkana. We approximated 95% confidence intervals around the data points using bootstrapping. Both site profiles were significantly different from the modern carnivore profiles and the Kanjera South Profile. However, the results may have biases due to variability in taphonomic preservation, as fragile bones of younger individuals are less likely to preserve and may be underrepresented.

Research was supported by the National Science Foundation (BCS-1624398, REU supplement 1930719), the National Museums of Kenya, the GWU Luther Rice Undergraduate Research Fellowship, and the William Warren Endowment Fund.

'The forgotten of antebellum Natchez: A bioarcheological case study of the nineteenth century Fort Rosalie burial ground'

BRITTNEY K. SHIELDS

Southeast Archeological Center, National Park Service

In AD 1716, construction began on a French fort located upon the bluffs of the Mississippi River, the future site of strategically important trade routes at Natchez, Mississippi. Christened Fort Rosalie, the site was continuously occupied as a trading post throughout the 18th-19th centuries, and has since become integrated into the Natchez National Historic Park. Despite its clear key impact on the cultural fabric of the developing city, little is known regarding the use of the fort's surrounding grounds as a slave burial ground and a 'potter's field' (for paupers, prisoners, and other stigmatized members of society) beyond that detailed in Audubon's journals during his tour of the South in the early 1820s.

Excavations conducted in 2019 by the National Park Service uncovered seven burials in this oft-forgotten funerary landscape. Osteological and stable isotope analysis conducted on the remains of these individuals revealed that four were adults (two female and two male), two were

adolescents (12-18 years), and one was a child (6-10 years). Strontium, carbon, and nitrogen analysis indicate that the individuals originated within the area directly surrounding Natchez, and subsisted on a diet primarily of grain, typical for the American south at this time.

This study not only reveals the life histories of these individuals, but also considers the experiences of marginalized groups in arguably the most fascinating frontier town of the antebellum South.

Intraspecific Analysis of Chimpanzee Dental Crown and Root Proportions

EMILY SHIPLEY¹ and JAMES D. PAMPUSH^{1,2}

¹Exercise Science, High Point University, ²Physician Assistant Studies, High Point University

While there have been a number of studies to investigate the morphology of dental crowns or dental roots, few studies have assessed the proportional relationships between these fundamental components of teeth. In assessing the hypothesis that crown dimensions correlate to root dimensions, this study presents intraspecific analysis of chimpanzee (*Pan troglodytes*) mandibles. High resolution medical CT-scans of chimpanzee mandibles were imported into Avizo. Six linear measures of dental proportions (i.e., root depth, crown height, root and crown breadth, root and crown length) were made for each tooth position (i.e., I₁, I₂, C, P₃, P₄, M₁, M₂, M₃) from the high-quality scans. Between 12 and 15 individuals were measured for each tooth position. Generally, our results indicate that within Chimpanzees crown heights are not correlated with root-depths, nor are root-lengths correlated with crown-lengths. There is a tendency in the anterior dentition for root-breadth to correlate with crown breadth, but this pattern frays in the post-canine dentition. Within chimpanzees, linear root dimensions are a poor indicator of linear crown dimensions, and should not be inferred from one-another. Considering the lack of relationship between root and crown dimensions within this particular species, future studies should explore this question on an interspecific dataset.

Relationships between sex-biased dispersal and allomaternal care behaviors in 143 mammal species

SOFIYA SHREYER¹, ANDREA L. BADEN², STACEY R. TECOT³ and JASON M. KAMILAR¹

¹Anthropology, University of Massachusetts - Amherst, ²Anthropology, Hunter College- City University of New York, ³Anthropology, The University of Arizona

In polygynous mating systems, patterns of natal dispersal are typically dependent on the sex of the offspring. In many groups, natal dispersal is male-biased and females remain in their natal

groups (i.e., female philopatry). In female philopatric mammals, female group membership is typically stable and altruistic traits are common, particularly among close relatives. This has been explained by kin selection, whereby costly altruistic traits evolve via inclusive fitness benefits. One form of seemingly altruistic behavior is allomaternal care (AMC), infant care provided by group members other than the mother. AMC is relatively unusual in mammals but is observed in a diverse set of lineages across the class. Here, we test the hypothesis that AMC will occur more frequently in groups characterized by female philopatry compared to mammals with female dispersal. To test our hypothesis, we conducted a comparative study of 143 mammal species. We gathered data from eight published datasets and conducted phylogenetic generalized least squares models. We found that mammals with female-biased dispersal are more likely to exhibit allomaternal care such as communal nesting ($p=0.017$) and protection ($p=0.01$). Our study suggests that while kin selection may play a role in highly costly allomaternal behaviors such as allomaternal nursing, less costly allomaternal care is likely to occur in groups even where females are not expected to be related. Our results have important implications for the evolution of mammal behavior and social structure.

The Paradoxical Embodiment of Violence and Injuries on a Colonial Sugar Plantation: Bioarchaeological Evidence from Newton Plantation, Barbados

KRISTRINA A. SHULER

Sociology, Anthropology & Social Work, Auburn University

Caribbean sugar plantations in the 17th-18th centuries are described as the harshest circumstances of enslavement. African laborers worked largely on field gangs, suffering 10-12-hour days, year-round, with inadequate resources and frequent illnesses (Handler 2006) that culminated in the highest mortality and lowest fertility in the western hemisphere (Higman 1984). Archival and ethnographic data for sugar producers predicts widespread injuries, and absenteeism among British owners on Barbadian plantations likely fostered an environment of mistreatment and interpersonal violence (Kiple 1984, Mintz 1985). Skeletons from Newton Plantation, Barbados (ca. 1660-1820) offer direct assessment of the bodies of 49 enslaved sugar producers who were assessed macroscopically for trauma through normalcy of element shape, alignment, and evidence of amputation. Healed fractures were observed on single elements from three adults (one male and two females). Trauma is surprising low at Newton (6%) compared to urban enslaved from American sites such as the African Burial Ground and Catoclin Iron Works (Wilczak et al. 2004). Yet, when contextualized with evidence

ABSTRACTS

including frequent localized periosteal inflammation on lower limbs (41%; n=49), mainly in males, and low mean age at death (19.95 years) (Shuler 2011), and compared to other diasporic bioarchaeological series, a strong pattern of structural violence emerges. Complex osteological findings from Newton Plantation are theoretically situated and discussed with general predictions for captivity and violence (Martin and Harrod 2015) and compared with findings from other diasporic sites in the Caribbean and North America to better understand the variable embodiment of violence in the past.

Osteoarthritis in South American Foragers: A Comparative Analysis

ASHLEY SHULTS¹, SARA JUENGST¹, JOSÉ CAPRILES² and SERGIO CHÁVEZ³

¹Anthropology, University of North Carolina at Charlotte, ²Anthropology, Penn State University, ³Anthropology, Central Michigan University

The study of South American foragers from material remains is well documented in the archaeological record when compared to skeletal material. Bioarchaeological analysis of mobile foraging groups can give us insight into the daily lives and activities of people that may not be available otherwise. The identification of osteoarthritis (OA) in skeletal remains is a helpful indicator in the investigation of mobility in the past. OA affects articular joints and is characterized by changes of appositional bone along the margins. It is complex and involves multiple causes and considerations, however, biomechanical loading associated with repetitive movements is a significant part of OA development. We present a comparative analysis of the prevalence of vertebral osteoarthritis between two archaic foraging populations (4500-3600 BP) from Bolivia as part of a larger mobility study. Lipping, porosity, and eburnation were recorded for each vertebra and defined as osteoarthritic if two or more of these elements were present. A skeletal subsample from the Tarija region of South Bolivia showed evidence of vertebral OA with 7/8 individuals affected, whereas in a subsample from the Lake Titicaca Basin of Bolivia only 4/12 individuals were affected. Removing all individuals over the age of 45 to account for age related changes still leaves 4/5 for the Tarija sample and the Titicaca Basin sample remains the same with 4/12 individuals affected. Both groups were likely foragers engaged in low levels of pastoralism; thus, we interpret these differences as resulting from environmental, genetic, and activity related variables.

Funding provided by the Thomas L. Reynolds Graduate Student Research Award and UNC Charlotte.

Neoplastic Disease in Urban and Rural Contexts, in Medieval Poland: A Paleoepidemiological Investigation

THOMAS SIEK

Institute of Archaeology, University College London

Palaeopathological studies have shown that rates of communicable disease were higher in urban settings than in their rural counterparts, and the same is true for non-communicable diseases, such as neoplasms, in modern contexts. However, it is unclear if the relation between urban or rural settings and neoplastic disease is unique to the modern age. This palaeoepidemiological investigation examines if living in an urban environment was a possible risk factor for neoplastic disease in medieval Poland. Following its transition from a loose association of pagan tribes to a Christian, monarchical state in 966 CE, Poland experienced rapid urbanization and was soon economically, socially and politically at the same level of development as other European countries. This period in Poland's history offers a unique perspective into the potential impact of medieval urban contexts on the prevalence of neoplastic disease. Skeletal material from urban and rural medieval Polish assemblages, ranging from the 9th to 16th centuries, were examined macroscopically and radiologically for evidence of neoplasms, followed by a standardized palaeoepidemiological analysis. The results indicate that, although neoplastic prevalence was higher among the rural assemblages, the medieval Poles did not have a greater chance of having a neoplasm in either an urban or rural setting. This is in stark contrast to modern epidemiological data and suggests the relationship between an urban/rural environment and neoplastic disease has likely changed over time. This study also acts as a starting point for future research to further explore the interaction of environment and neoplastic disease.

Compete, then care: Male baboons' reproductive tactics change with age

JOAN B. SILK^{1,2}, VERONIKA STADELE^{1,4}, LINDA VIGILANT⁴ and SHIRLEY C. STRUM^{3,5}

¹School of Human Evolution & Social Change, Arizona State University, ²Institute for Human Origins, Arizona State University, ³Anthropology, University of California, ⁴Primate Institute, Max Planck Institute for Evolutionary Anthropology, ⁵African Conservation Centre

In polygynous species, there is often intense intra-sexual competition over access to females and evolution has favored greater investment in mating effort than parenting effort. Males that are in prime physical condition out-compete others, and there is often an Γ -shaped relationship between age, condition, and resource holding power. However, there are some polygynous species, like savanna baboons, in which males invest in both mating effort and parenting effort. Male baboons compete for high ranking positions in the group,

and there is an Γ -shaped relationship between male age and dominance. Male dominance rank is generally associated with paternity success, although the extent of skew may vary across time with and between populations. Adult males baboons also form close ties to lactating females ("primary associates"). Males are attentive to their primary associates' distress and buffer them and their infants from harassment. These relationships are thought to be a form of male parenting effort as males are often the sires of their primary associates' infants. Here, we show that male olive baboons are more likely to become the primary associates of lactating females as they become older. This pattern is independent of the effects of paternity, and suggests that males adjust their reproductive tactics over the life course, investing more in mating effort when they are in prime physical condition and more in parenting effort when they have passed their prime.

Sickle cell trait is a young-adult and teenage cause of death.

ARIANA KELLY SILVA¹, HILTON SILVA¹, LARA FIGUEIRAS¹ and LORENA MADRIGAL²

¹Anthropology, Federal University of Para, ²Anthropology, University of South Florida

In 2013, we presented a poster which summarized the number of deaths due to sickle cell trait (SCT) in the USA between 2000-2010 (n=74). De-identified data are not available from the CDC after 2010 because the CDC does not provide information if fewer than 10 people died in a single year. We gathered data on SCT deaths from: Thorgmantin et al., 2011 and Crowder et al., 2018. The total number of SCT-related deaths from these sources is n=19, distributed as follows: 4 under police "care" or due to violence, 3 while playing American football, 7 while playing other sports and 5 from other causes. Since these publications, there have been two deaths of young army recruits thus raising the number of deaths to n=21. In this sample of 21 individuals the mean-age-at-death was 23 years, ranging from 11 to 43. Notably, 14.30% died under 14 and 14.30% died between 15-19 years of age. Twelve out of 21 died between 20 and 24, which is both when they attend college or the armed forces. Stovitz and Shrier (2012) argued that estimates of risk should be presented by ethnicity, since most individuals who died due to SCT in sports were African-American. This may very well be the case. However, a bio-cultural anthropological view of this cause of death demands that we look at it as a young adult and teenage killer. We wonder if the reason it has not received attention before is because most of the dead have unfortunately been African American.

ABSTRACTS

A Dental Revolution? How dietary changes during the British Industrial Revolution transformed masticatory behaviours

CHRISTOPHER M. SILVESTER¹, SIMON HILLSON¹, JAMES STEELE¹ and OTTMAR KULLMER^{2,3}

¹Institute of Archaeology, University College London, ²Department of Palaeoanthropology, Senckenberg Research Institute, ³Department of Paleobiology and Environment, Goethe University

The British diet radically changed during the 18th-19th centuries. Import of new commodities, principally sugar, was accompanied by advancements in milling technology, altering the consistency and physical properties of key dietary staples. This foreshadowed the soft hyper-nutritive diets of 20th/21st century industrialised groups. Differences in dietary consistency will alter the biomechanical demands placed on the masticatory system during oral processing. Masticatory behaviours are reflected in dental macrowear patterns, which represent cumulative tooth use over a substantial portion of an individual's lifetime.

This study examined the impact of dietary changes on the dentition during the Industrial Revolution by comparing the molar macrowear patterns of 104 Industrial-era individuals (c.1700-1900CE) with a sample of 130 individuals from Medieval and Early Post-Mediaeval cemeteries (c.1100-1700CE). The area, inclination and orientation of the wear facets on the occlusal surface of lower second molars were quantified by applying Occlusal Fingerprint Analysis (OFA) to high resolution 3D models. Industrial macrowear patterns were dominated by phase II wear facets and exhibited less well-developed, yet more steeply inclined, phase I facets. This indicates that the Industrial power stroke typically involved a strongly vertically orientated shearing action during the incursive phase I movement. A pronounced crushing action followed, prior to and during maximum intercuspation. The Medieval macrowear pattern was consistent with greater lateral displacement of the mandible during mastication. The diminished lateral component of the power stroke in the Industrial period would have reduced the biomechanical demands placed on the masticatory system with potential implications for its growth and development.

This research was funded by the London Arts and Humanities Partnership.

Accuracy of age estimation through Transition Analysis in the Hamann-Todd Collection

ALLYSON M. SIMON¹ and MARK HUBBE^{1,2}

¹Department of Anthropology, The Ohio State University, ²Instituto de Arqueología y Antropología, Universidad Católica del Norte

Trying to reconstruct the demographic parameters of past populations using skeletal data is challenging for several reasons. First, skeletal traits are proxy to biological age, which does not always reflect chronological age. Second, different parts of the skeleton age at different rates, making age estimation problematic when based on methods that only incorporate a few anatomical features. A proposed solution to address this limitation is transition analysis (TA), a multifactorial method of age estimation that incorporates information from the pubic symphysis, iliac auricular area, and cranial sutures. However, despite its methodological refinement, TA has been shown to have varying degrees of accuracy when applied to different known-age skeletal samples. Here, we contribute to the discussion about TA's accuracy by estimating the age for 221 individuals from the Hamann-Todd Collection. We contrasted the maximum likelihood estimates generated through TA to the known ages, and analyzed the error for the entire sample, as well as according to sex and ancestry. Estimates show an average error of 11.6 (SD=10.3) years, with white individuals' errors (14.1 years) being significantly higher than black individuals' (9.1 years; Independent Samples T-Test $p < 0.001$). There are no significant differences in the errors between sexes (males = 11.2; females = 12.1; Independent Samples T-Test $p = 0.526$). These findings further support that TA accuracy depends on the prior distribution used and that in the case of the Hamann-Todd Collection, the accuracy for white individuals is more influenced by this limitation than when black individuals are analyzed.

Impacts of endocranial shape on middle meningeal arteriovenous pattern in 6-8.0 year old humans

PINA S. SIMONE¹, REBECCA S. JABBOUR² and GARY D. RICHARDS³

¹Molecular and Cell Biology, University of California Berkeley, ²Department of Biology, Saint Mary's College of California, ³Department of Biomedical Sciences, A.A. Dugoni School of Dentistry

The meningeal arteriovenous system supplies or drains blood from the cranial vault bones and dura. In juveniles aged 6-8.0, complexity of middle meningeal patterns varies bilaterally, by developmental age, and by the configuration of the main rami. We employ geometric morphometric analysis to discern potential relationships between the neurovascular bundle and endocranial shape differences.

Forty crania, developmentally aged from 5.8-7.9 years, were CT-scanned. Tooth calcification patterns were employed to determine developmental age. Middle meningeal neurovascular patterns were mapped on isosurfaces and evaluated for complexity, bilateralism, age differences and Adachi types. We collected 33 3D endocranial

landmarks from CT-scans. Principal Component Analysis (PCA) was performed on Procrustes aligned shape variables in Morphologica to assess endocranial shape differences.

We found that individuals with less complex middle meningeal patterns clustered within -PC1 but were randomly distributed on PC2. Bilateral complexity analysis shows that right-dominant complexity clustered around the mean of PC1-PC2, but not in the left. The Adachi types varied in their distribution bilaterally. When Adachi types differ in individuals, one type occurs randomly relative to the side, but the other type tends to cluster within -PC1.

The association between the neurovascular pattern and endocranial shape in relation to complexity is based on endocranial length-breadth differences. Dolichocephalic endocrania exhibit less complex branching. Right-dominated patterns correlate with shape while left patterns are randomly distributed. Although the correlation between the meningeal neurovascular bundle and endocranial shape appears unclear, specific patterns are emerging. Further work is required to elucidate causative factors for pattern differences.

Testing the Giles hypothesis using developmental simulation

EVAN A. SIMONS

Anthropology, University at Buffalo

The Giles hypothesis posits that differences in the cranial morphology of *Pan troglodytes* and *Gorilla gorilla* are largely the result of ontogenetic scaling, indicating that extending the ontogenetic trajectory of a chimpanzee would produce an adult gorilla-like cranial morphology. However, previous support for this aspect of the Giles hypothesis was based on bivariate plots of linear measurements, and has yet to be retested using geometric morphometric methods.

To address this, 43 3D cranial landmarks were collected from a mixed-sex, ontogenetic series of 76 *Pan troglodytes* and 58 *Gorilla gorilla* specimens. Ontogenetic trajectories of cranial shape change were then computed through multivariate regression of Procrustes aligned coordinates against LnCS (growth vector) and molar eruption stage (developmental vector). These two vectors were then used in developmental simulations to extend the ontogenetic trajectories of adult chimpanzees. Differences between simulated chimpanzee and actual adult gorillas were quantified by Procrustes distance between the mean simulation and mean adult configurations, with significance tested using permutation.

All of the simulated *Pan* configurations produced using both the size and developmental vectors significantly differed in shape from actual adult gorillas ($p < 0.0001$). Additionally, the more the *Pan* developmental vector was extended, the more

ABSTRACTS

distinct the simulations became from actual adult gorillas (Procrustes distance for developmental vector: x1: 0.0986; x2: 0.1139; x3: 0.1493). This indicates that neither “growing” a chimpanzee to the size of a gorilla, nor extending a chimpanzee’s developmental shape trajectory will result in a gorilla-like cranial morphology, casting doubt on the validity of the Giles hypothesis.

This research was funded by a National Science Foundation DDRIG (BCS-1751885).

Parallel gene regulatory signatures of social stress and aging in rhesus macaques

NOAH D. SIMONS¹, PAUL L. MAURIZIO², JOAO BATISTA², VASILIKI MICHPOULOS³, LUIS B. BARREIRO² and JENNY TUNG^{1,4}

¹Evolutionary Anthropology, Duke University, ²Department of Medicine, University of Chicago, ³Yerkes National Primate Research Center, Emory University, ⁴Department of Biology, Duke University

In humans and other social primates, exposure to chronic social stress can increase both susceptibility to disease and mortality risk itself. This relationship is thought to be due in part to convergent biological effects of social stress and aging. To investigate this possibility, we used an experimental rhesus macaque model for chronic, social subordination-induced stress to test for a causal relationship between the gene regulatory signature of low social status and the gene regulatory signature of aging. We manipulated dominance rank in 50 adult female macaques (n=10 social groups) and used single-cell RNA-seq to profile peripheral blood mononuclear cell (PBMC) gene expression. We also used scRNA-seq to measure PBMC gene expression in an independent sample of female macaques that spanned the adult age range (n=14, ages 3.5 – 23.5). Our data reveal pervasive, but highly cell type-specific, effects of both age and social status, such that age signatures are enriched in pathways that are also social status-sensitive (e.g., the inflammatory response and cytokine-mediated signaling). Preliminary analyses also suggest that, in monocytes, CD4/CD8+ T cells, cytotoxic T cells, and natural killer cells, advanced age also predicts increased cell-to-cell transcriptional variance. Currently, we are testing the prediction that low status animals thus appear “old-for-age,” either in a baseline state or following immune challenge. Together, our analyses provide insight into whether, and to what degree, social stress recapitulates the molecular signatures of aging—highlighting the many routes through which social adversity gets under the skin to affect primate health and fitness.

National Institutes of Health and the North Carolina Biotechnology Center

Synchrotron X-ray Fluorescence Imaging of Biogenic and Experimentally-Induced Diagenetic Lead Exposure in Modern and Archaeological Bone

RACHEL SIMPSON¹, TAMARA L. VARNEY², TREENA SWANSTON^{3,4}, IAN COULTHARD⁵ and DAVID M.L. COOPER⁶

¹Archaeology and Anthropology, University of Saskatchewan, ²Anthropology, Lakehead University, ³Anthropology, Economics, Political Science, MacEwan University, ⁴Biological Sciences, MacEwan University, ⁵n/a, Canadian Light Source, ⁶Anatomy, Physiology, Pharmacology, University of Saskatchewan

Bioarchaeological trace element analysis of lead (Pb) can provide a window into the industries, socio-economic dynamics, morbidity, and mortality of past human populations. However, difficulties accounting for the effects of element diagenesis, the post-mortem modification of bone’s chemical composition, have plagued this area of research for decades. Lead from the burial environment can accumulate in bone, masking the biogenic uptake of lead that occurred during an individual’s life. Novel techniques such as synchrotron X-ray Fluorescence Imaging (XFI) provide precise spatial data for elements; by assessing the distribution of elements in relation to bone microstructure, it may be possible to discriminate the nature of element exposure. Previous research has used XFI to identify possible examples of biogenic or diagenetic lead exposure from the bioarchaeological record; however, experimental research is required to validate whether there are indeed spatial differences in biogenic and diagenetic exposure. For the present study, we obtained femoral samples from a cadaveric collection and experimentally exposed a portion of each sample to a pseudo-diagenetic lead treatment. We used XFI to map the spatial microdistribution of lead in archaeological bone samples from Antigua and Lithuania representing examples of possible biogenic and diagenetic lead exposure respectively. XFI will also be used to examine the spatial patterns of lead in both the treated and untreated modern cadaveric samples. Through the comparison of the lead distribution maps across bone microstructural features for both biogenic and diagenetic lead exposure, we will expand on the utility of this method for identifying diagenesis in bioarchaeological remains.

This research has been supported by a SSHRC Insight Grant (Dr. Tamara Varney, PI.) and the Canadian Research Chairs Program (Dr. David Cooper).

Genetic portrait of North-West Indian population based on Autosomal and X-chromosomal *Alu* insertion markers

GAGANDEEP SINGH¹, HARKIRAT SINGH, SANDHU², INDU TALWAR¹ and A.J.S BHANWER²

¹Anthropology, Panjab University, Chandigarh, India, ²Human Genetics, Guru Nanak Dev University, Amritsar, India

Alu insertion elements account for the largest family of Short Interspersed Nuclear Elements (SINEs) in the human genome. Polymorphic *Alu* elements are stable and conservative markers that can potentially be applied in studying human origin and relationships as they are identical by descent and known for lack of insertion in ancestral state. In the present study, 25 *Alu* insertions of autosomes and X chromosome were utilized to tabulate allele frequency distributions and compute parameters of forensic relevance in the unrelated healthy individuals belonging to five diverse ethnic groups (Bania, Brahmin, Khatri, Jat Sikh and Scheduled Caste) of North-West India. The D_A and F_{ST} values of pairwise inter-population differentiations, multidimensional scaling and Bayesian structure clustering analyses were also computed to probe the genetic relationships between present studied populations and other regional and global reference populations. Overall, uniform allele frequency distribution patterns, high average heterozygosity values, and a small degree of genetic differentiation suggest genetic proximity among the selected populations. A low level of genetic differentiation was observed in the studied population groups indicating that genetic drift might have been small or negligible in shaping the genetic structure of North-West Indian populations.

None

Heightened AMC is not correlated to self-reported maternal stress in a WEIRD sample in Tucson, AZ

BRITT SINGLETARY

School of Anthropology, University of Arizona, Crane Center for Early Childhood Research & Policy, The Ohio State University

Humans use extensive allomaternal care (AMC: care from individuals other than the mother) to help raise their young. AMC can offset the mother’s energetic load, supplement the infant’s nutritional needs, and create opportunities for improved early cognitive and language learning outcomes in infants. AMC might also play a role in mediating a mother’s experience of stress by lightening her care-load. If this is the case, we might expect to see that a mother reports lower parenting stress and depressive symptoms when using heightened AMC. As part of a larger study, data was collected from 102 mothers and their typically developing infants aged 13-18 months in Tucson, AZ. AMC variables were collected

ABSTRACTS

using questionnaires, daily diaries, and interviews to create a holistic picture of current and past AMC utilized by the mother for her participating infant since birth. Principle Component Analysis was used to generate four multidimensional AMC components: Highly Involved Familial AMC, Household AMC, Formalized AMC, and Overall AMC Network Extent. Maternal stress was measured using the sub-scale and total scores from the Parenting Stress Index 4 Short Form (PAR, Inc) and the total score for the Center for Epidemiological Studies Depression Scale Revised. Pearson's correlation coefficients were used to determine if AMC and maternal stress are correlated. Across all AMC components and measures of maternal stress, there were no significant correlations ($p > 0.1$ in all cases). As clinically significant levels of stress were low in this sample (<4%), future studies in more vulnerable populations may yield different results.

Funding received from the National Science Foundation (BCS-1752542), International Chapter of the P.E.O. Sisterhood, and University of Arizona's School of Anthropology, SBSRI, GPSC, and Conflucenter for Creative Inquiry.

Biomechanical correlates of zygomatic surface shape in papionin monkeys

MICHELLE SINGLETON^{1,2}, DANIEL E. EHRLICH¹ and JUSTIN W. ADAMS^{3,4}

¹Department of Anatomy, College of Graduate Studies, Midwestern University, ²Department of Anatomy, Chicago College of Osteopathic Medicine, ³Department of Anatomy & Developmental Biology, Biomedicine Discovery Institute, Monash University, ⁴Palaeo-Research Institute, University of Johannesburg

Extant African papionins are distinguished from macaques by the presence of excavated facial fossae; however, facial excavation differs among taxa. Mangabeys (*Cercocebus*, *Lophocebus*, *Rungwecebus*) exhibit maxillary fossae that invade the zygomatic forming pronounced sub-orbital fossae (SOFs). Larger-bodied *Papio* and *Mandrillus* have shallower maxillary fossae with minimal/absent SOFs. Because prior studies have shown that mangabeys exhibit adaptations to anterior dental loading (e.g., facial retraction), it is plausible that mangabey SOFs represent structural accommodation to masticatory geometry rather than facial allometry, as commonly hypothesized. We analyzed covariation between zygomatic surface shape and masticatory geometry in 141 adult crania of *M. fascicularis*, *P. kindae*, *Cercocebus*, and *Lophocebus*. Selected taxa provide a range of SOF expression while minimizing allometric variation. Masticatory landmarks ($p=39$) were selected to register palate shape, bite points, muscle attachments, and the TMJ. Semilandmarks ($p=450$) were used to capture zygomatic surface shape bilaterally. Following Procrustes superimposition with semilandmark sliding and exploratory PCA,

2B-PLS was used to examine covariation. PCs 1–2 (73.4% and 10.8% variance) and PLS1 (94% squared covariance) separate mangabeys from *Macaca* and *Papio*. Notably, PC1 is uncorrelated with centroid size across species ($r = 0.16$, $p = 0.057$). PLS1 shows a linear relationship between zygomatic shape and masticatory geometry ($RV = 0.871$, $p < 0.001$). Negative PLS1 scores in mangabeys reflect anterior displacement of the lateral malar (deep SOF), posterior displacement of bite points (palatal retraction), and anterior displacement of adductor muscles and TMJ. These results support a relationship between zygomatic shape and masticatory geometry independent of size.

This research was supported by the Australian Research Council (DP170100056), The Leakey Foundation, and by Midwestern University Department of Anatomy, ORSP, and Core Facility.

Exploring the impact of evolutionary forces on Japanese cranial and dental traits

CASSIE E. SKIPPER and MARIN A. PILLOUD
Anthropology, University of Nevada, Reno

Japanese history includes periods of migration and isolation, which would allow the evolutionary forces of genetic drift and gene flow to shape phenotypic differences. This initial pilot study employs biotaxonomy analyses to investigate how this population history shaped the skeletal phenotype in a Japanese skeletal collection. Data were collected on craniometrics, cranial nonmetrics, and odontometrics from a modern Japanese skeletal sample ($n=33$). These data were compared to published data on various global skeletal reference samples. The impact of evolutionary processes and the degree of variation in the Japanese sample were analyzed using R-matrix r_{ii} and F_{ST} values using RMET and tetra-choric Mahalanobis distances (TMD).

Comparative reference samples from the Howells dataset (craniometrics), the Forensic Anthropology Data Bank (cranial nonmetrics and craniometrics), and the dataset in Pilloud et al. (2014) (odontometrics) were used in analyses. The craniometric and odontometric unbiased F_{ST} values demonstrated that 12.2% and 1.8% of variation exists among the populations, respectively. These results indicate more influence of genetic drift on cranial metrics than odontometrics. In the TMD analysis using cranial nonmetric data with American White, American Black, and Hispanic reference samples, the Japanese sample aligned most closely with the Hispanic sample, which was expected as these two groups share common ancestry and therefore phenotypic similarity due to gene flow. Expanding the Japanese sample and increasing reference samples and sample sizes

will further illuminate how evolutionary forces have impacted Japanese skeletal morphology and metrics and further our understanding of modern human variation.

Selection of human immune response genes as a product of ancestral *Yersinia pestis* exposure

CARLY SLANK
Department of Anthropology, Wayne State University

Yersinia pestis, or plague, has been a powerful selective pressure among many human populations throughout history. Recent research has revealed positive selection for several immune-related genes as a result of historical plague exposure among Roma and Romanian populations. The present study examines 12 additional populations ($N=1,147$) with known patterns of historical plague exposure for signatures of positive selection in three toll-like receptor genes. Pairwise F_{ST} values are a useful indicator of trends in selection; ranging from 0-1, this value indicates the amount of variation in a sample resulting from differential genetic structure. Genetic data was sourced from the publicly-available 1000 Genomes Project, and F_{ST} values were produced using DnaSP v6.

Prior to analysis, populations were assigned qualitative scores based on known historical plague exposure and mortality. Populations with similar exposure histories, and therefore similar scores, should produce low pairwise F_{ST} values; disparately scored populations should produce high pairwise F_{ST} values, indicating greater difference in genetic structure at these loci as a result of plague exposure. Results follow the expected pattern but with some caveats. The lowest F_{ST} values occurred between populations with the closest exposure scores, and the highest between populations with contrasting scores. Deviations from the predicted pattern may be a result of missing historical data, selective pressure of extraneous diseases, or the ambiguous nature of relating modern individuals and genomes to historical populations. Resolving relationships between pathogens and human immunological evolution is essential to understanding our evolutionary history and the potential for future outbreaks of infectious disease.

Monkeys in the Middle: Modeling ecological flexibility and niche construction in African cercopithecoid primates

IRENE E. SMAIL
School of Human Evolution and Social Change, Arizona State University, Institute of Human Origins, Arizona State University

Niche construction is broadly defined as an organism's influence over its environment, ranging from the depletion of local resources to the intentional

ABSTRACTS

modification of landscapes and ecosystems. While modern humans excel at the latter, the exact timing and nature of our transition to being complex cultural niche constructors remains to be determined. Here I use methods taken from community ecology to develop a baseline model of minimal niche construction within a group of primate generalists. This serves as an important comparison for interpretations of the hominin fossil record and broader paleontological record to determine when and how our hominin ancestors began to diverge from this pattern.

Dental metric data were used in principal components analysis to reconstruct the dietary ecomorphological niches of a sample African cercopithecoid primates from the Plio-Pleistocene to today. Potential niche construction is identified through the displacement of co-occurring species indicating that the focal taxon has excluded potential competitors through resource depletion. Overall, fossil taxa are shown to occupy a more restricted niche than their extant relatives, but otherwise exhibit similar patterns of dispersion and overlap within and across communities. The lack of consistent trends within the Plio-Pleistocene sample – either through time or in response to potential confamilial competition – supports the idea that these generalized primates are not exerting a significant influence over their local environments. I conclude with some suggestions on expanding these analyses to look for evidence of niche construction in other paleontological and paleoanthropological contexts.

This research was funded by the National Science Foundation (NSF BCS 1926163), The Leakey Foundation, and ASU's School of Human Evolution and Social Change.

Interspecific variation in hominid mandibular biomechanics

AMANDA L. SMITH¹, CHRIS ROBINSON², ANDREA B. TAYLOR³, CAROL V. WARD⁴, WILLIAM H. KIMBEL⁵, ZERESENY ALEMSEGED¹ and CALLUM F. ROSS¹

¹Department of Organismal Biology and Anatomy, University of Chicago, ²Department of Biological Sciences, City University of New York Bronx Community College, ³Department of Basic Science, Touro University, ⁴Department of Pathology and Anatomical Sciences, University of Missouri, ⁵Institute of Human Origins and School of Human Evolution and Social Change, Arizona State University

Mandibular morphology varies across hominid species. Corpus thickness, ramus height and orientation, tooth row orientation, and symphyseal depth and inclination have all been hypothesized to be related to feeding function, but how these features affect mechanical performance remains unclear. These features could serve either to reduce bone strain magnitudes, increase biting efficiency, or both, but whether they function in concert to produce species-specific patterns of deformation or strain patterns has not yet been

explored. Previous work has shown that strain and deformation regimes in chimpanzee finite element models (FEMs) broadly match those reported for *in vivo* and *in silico* feeding experiments in macaques. Here, we examine the biomechanical implications of mandibular shape variation in three additional species, expanding our taxonomic scope across extant apes.

Female and male specimens for each of four extant hominid species (*Pan troglodytes*, *Pongo pygmaeus*, *Gorilla gorilla* and *Homo sapiens*) representing mean mandibular shape were selected for modeling using geometric morphometric methods. Eight total models were constructed from CT scans, assigned material properties of bone, loaded with equivalent muscle forces and constrained to simulate biting at multiple locations across the tooth row.

Results indicate common regions of low and high strain across all models with broad similarities in deformation regime in the balancing and working-side corpora, including sagittal bending and shear, and axial twisting. Notable differences in strain pattern are observed at the symphysis, suggesting that interspecific differences in symphyseal shape may be related to interspecific differences in strain regimes.

This research was funded by NSF BSC 1515270 and 1723041.

Variation in Mindreading “On the Ground”: Comparing Patterns of Mental State Talk in Two Societies

ANDREW M. SMITH, H. CLARK BARRETT and ERICA A. CARTMILL

Anthropology, University of California, Los Angeles

A fundamental feature of human social cognition is the capacity to read others' minds. Despite social cognition being mediated by language, no studies have examined whether language communities vary in their mental-state talk. We measured mental-state language in a small-scale society with implicit norms against attributing mental states to others. A simple response-elicitation task was administered in Spanish to bilingual Shuar / Spanish speakers in a small-scale, hunter-horticulturalist society in Amazonian Ecuador (N=40) as well as in English to a sample of American undergraduates (N=26). Participants were shown a set of nine short videos after which participants were asked to describe what had happened in the scene. Verbal responses were transcribed and coded according to a scheme adapted from earlier literature that categorized mental-state terms as affective, perception, desire, or epistemic. Word counts in each category were scaled to control for differences in description length. Hierarchical Poisson Regression models of word counts were run with culture and video as fixed factors and participant as a random factor. American participants used perception, affective,

and epistemic words to describe characters in the videos significantly more often than Shuar participants did ($p < 0.001$). In contrast, Shuar participants used desire words more frequently ($p < 0.001$). Data on cross-cultural differences in mental state talk are important for a complete understanding of the evolution of language as they may illuminate the extent to which human language is constrained or free to vary in terms of how mental states are conceptualized and communicated.

A multifactorial approach to the developmental origins of infectious disease: comparing results from dental histology, paleopathology, and stable isotope analysis

APRIL K. SMITH¹, LAURIE J. REITSEMA¹, ANTONIO FORNACIARI² and LUCA SINEO³

¹Anthropology, University of Georgia, ²Division of Paleopathology, Department of Translational Research on New Technologies in Medicine and Surgery, University of Pisa, ³Department of Science and Biological, Chemical, and Pharmaceutical Technologies, University of Palermo

Bioarchaeological approaches to the Developmental Origins of Health and Disease (DOHaD) hypothesis are confounded by several variables, including cultural context and methodology. This research compares different methodological approaches that assess early childhood stress in skeletal populations and explores the influence of cultural context on bioarchaeological research using the DOHaD hypothesis. We investigate the role of early childhood stress on mortality from infectious disease by comparing cholera victims from Alia (PA) and Benabbio (LU) to contemporaneous, general populations from Badia Pozzeveri (LU) and Pieve dei Monti di Villa (LU), Italy. We compare the results of paleopathological assessments, dental histology, and age-at-weaning estimates between cholera victims and the general population. Pathological markers and demographic characteristics are assessed using the standards outlined in Steckel et al. (2006). Dental histology and incremental stable carbon and nitrogen isotope analysis is performed on canines from a maximum of 30 individuals per site. We find cholera victims exhibit significantly lower prevalence of cribra orbitalia ($X^2 = 6.857$, $df = 1$, $p = 0.009$) and an older average age-at-defect ($t = 5.047$, $df = 367.5$, $p < 0.001$, 95% CI [0.26, 0.60]) compared to the general population, but we also find significant differences between the four sites, including differences in average age-at-defect ($X^2 = 48.905$, $df = 5$, $p < 0.001$). No statistical differences in age-at-weaning are found between cholera victims and the general population or between sites. Our research demonstrates

ABSTRACTS

that early childhood stress markers vary between cholera and non-cholera individuals, but cultural context and methodological approach are influential factors that explain part of this variation.

This research is supported by the National Science Foundation [grant number 650930].

Dietary intake and digestibility of frugivorous and insectivorous diets in captive *Otolemur garnettii*

B. KATHERINE SMITH¹, SYDNE BIANCHI¹, MEAD KROWKA², JAMES E. LOUDON³, ANDRES M. GOMEZ⁴, OLIVER C.C. PAINE⁵ and MATT SPONHEIMER⁵

¹Anthropology, The University of Southern Mississippi, ²Anthropology, The University of North Carolina-Wilmington, ³Anthropology, East Carolina University, ⁴Animal Science, University of Minnesota, ⁵Anthropology, University of Colorado, Boulder

Examining dietary intake and digestibility of the foods consumed by a primate has provided insights into their morphological and physiological adaptations. To date, only two studies have examined the dietary intake of the Northern greater galago (*Otolemur garnettii*) (Harcourt and Nash, 1986; Masters et al., 1988). Harcourt and Nash (1986) found that *O. garnettii* consumed a diet consisting of ~50% insects and ~50% fruit, with supplements of some invertebrates, vertebrates, and gums. In this study, we examined the intake and dry matter digestibility (DMD) of two diets (one frugivorous and one insectivorous) in a colony of captive *O. garnettii* (females = 5, males = 6) over the course of 6 weeks. For each diet we analyzed the crude protein (CP), crude fat (CF), acid detergent fiber (ADF), and neutral detergent fiber (NDF) of each food item provided to the galagos. To estimate digestibility, we analyzed the same nutritional properties in the fecal matter of each individual. Preliminary results show that *O. garnettii* digested higher levels of NDF and CP during the insectivorous diet and showed significantly higher rates of DMD during the insectivorous diet compared to the frugivorous diet ($P < 0.0001$). These data may be useful for understanding the food choice and dietary challenges faced by wild galagos which are difficult to observe given their nocturnal activity patterns, small size, and dynamic locomotory behavior.

This project was supported by a grant from the National Science Foundation (RAPID Award #1840977).

A comparison of dental microwear texture across hunter-gatherer sites in South Australia

CAITLIN B. SMITH¹, SARAH KARSTENS¹, RACHEL M. SCOTT^{1,2} and JUDITH LITTLETON¹

¹Anthropology, University of Auckland, ²Department of Anatomy, University of Otago

Differences in the patterning of macro and microwear have been noted between and within groups of Aboriginal hunter-gatherers. These differences are thought to reflect heterogeneity in diet and activity. More recently, dental microwear texture analysis (DMTA) data from South Australia have indicated that local environment and the presence of grit or sand may play a significant role in the production of microwear complexity values. A comparative analysis of dental microwear texture was conducted on individuals from three hunter-gatherer sites in South Australia, Roonka, Yorke Peninsula and the Gillman Mound ($n=55$). These sites span 3 very distinct ecological zones within South Australia (riverine, coastal, and estuarine).

Four measures of microwear texture were analysed; textural fill volume (Tfv), area scale fractal complexity (Asfc), scale of maximum complexity (Smc) and anisotropy (ePLsar). Analysis of Asfc and Smc demonstrate significant differences between the sites ($F(2,52)=4.858$, $p=0.012$); ($F(2,52)=12.180$, $p<0.005$) respectively. The complexity of the microwear texture is highest at the coastal site, followed by the riverine site, and then the estuarine site, indicating different amounts of abrasives were consumed with foods. However, there is also an indication that the nature of the abrasives is not consistent across sites. The riverine site shows the highest Smc values, while the coastal and estuarine site show comparatively low Smc values. We interpret these results in relation to environmental, food preparation, and dietary variation across these three sites.

The research is funded by the Royal Society of New Zealand Marsden Fund (14-UOA-19).

Does the sex difference in upper body strength explain the sex difference in depression?

CAROLINE B. SMITH and EDWARD H. HAGEN
Anthropology, Washington State University

Depression is a cross-cultural, burdensome disease which occurs more often in women than men. Physical assault specifically, and conflict more generally, are some of the most potent predictors of depression. One evolutionary model of depression proposes that depression occurs when a person is at risk of a fitness cost either imposed by social partners or exacerbated by their lack of support. Physically stronger individuals can protect themselves from assault or otherwise induce partners to change their behavior, whereas others might rely on bargaining by withdrawing from usual activities, the core feature of depression. Therefore, according to this model the sex difference in depression is due to the dramatic sexual dimorphism in physical formidability. Previous research found that grip strength, a measure of upper body strength, mediates most

of the effect of sex on depression. The current study extends this finding by ruling out chronic disease and partner status as confounds and by replicating the study with new data.

Using data from the 2011-2012 phase of the National Health and Nutrition Examination Survey (NHANES), a large representative sample of US households ($N=4192$), the current study found that although chronic disease and partner status are risk factors for depression, they do not explain the effect of strength or sex on depression. Finally, these results were replicated in the 2013-2014 ($N=4384$) phase of NHANES albeit with reduced effect sizes. The sex difference in depression might be explained in part by the sex difference in physical formidability.

Stress Chronologies in a Mass Burial, Charterhouse Warren Farm Shaft, United Kingdom: Microstructural Reconstruction of Environmental Interactions at the Precipice of Violent Death

EMILY M. SMITH¹, DANIEL H. TEMPLE¹ and RICK SCHULTING²

¹Anthropology, George Mason University, ²Archaeology, University of Oxford

This study examines the occurrence of accentuated striae at the site of Charterhouse Warren Farm Shaft (CWFS) individuals, dated to the Early Bronze Age (EBA, ca. 2000 cal BC), Mendip Somerset, England. Previous documentation concluded that these individuals were victims of violent deaths, defleshing, and conceivably cannibalism before internment within a deep natural fissure instead of the normative practice of burial under an EBA round barrow. Histological methods were used to identify the presence and estimate the chronology of accentuated striae in 19 permanent first, second, and third molars and canines ($n = 11$). Accentuated striae were identified as large, dark striae of Retzius that were visible over 75 percent of the region between the enamel-dentine junction and tooth surface. Chronology of accentuated striae was estimated based on distance from the neonatal line and matches of accentuated striae between teeth. Defect timing ranged between 1.1 and 11.0 years. Average age-at-defect for each tooth type included M1 ($\bar{x} \pm \text{SD} = 2.2$ years), M2 ($\bar{x} \pm \text{SD} = 5.4$ years), and M3 ($\bar{x} \pm \text{SD} = 10.7$ years). The greatest frequency of accentuated striae accumulated around the average age-of-first-defect in the M1 ($\bar{x} \pm \text{SD} = 2.0$ years). Accentuated striae were not found in canine teeth. The high frequency of M1 defects in the mid-crown formation time (range, 1.1-2.9 years) may correspond to the weaning process. These findings of metabolic stress during permanent enamel development provide insight into the subsequent violent deaths and postmortem defleshing of the Charterhouse Warren individuals as environmental stress might explain the violent episode at this site.

ABSTRACTS

Qualitative and quantitative variation within the antebrachial musculature of Callitrichidae and Lemuridae

MADISON R. SMITH¹, ISABELLA HERTZIG¹, MARISSA L. BOETTCHER^{1,2}, EDWIN DICKINSON¹ and ADAM HARTSTONE-ROSE¹

¹Biological Sciences, North Carolina State University, ²College of Medicine, Medical University of South Carolina

The antebrachial muscles of primates contribute to several key parameters of manual and wrist function, including grip strength and dexterity. Recently, several attempts have been made to describe the anatomy of these muscles across the primate order using large, interspecific samples. However, the breadth of such studies often obscures potentially interesting trends relating to variation on lower taxonomic levels, such as variation between species within a genus, or genera within a single family. In an effort to better contextualize our understanding of anatomical variation within closely-related taxa, this study explores both qualitative and quantitative forearm muscle variation in broad samples within two representative families: the Callitrichidae (30 specimens of 11 species) and Lemuridae (15 specimens of 7 species). Following previous protocols, muscles were divided into one of four functional groups (wrist flexors, wrist extensors, digital flexors and digital extensors). For each compartment, qualitative data on the presence/absence of each muscle, and the degree of integration between related muscle portions, were first noted. Subsequently, quantitative architectural variables (muscle mass, fascicle length, and physiological cross-sectional area) were collected. Callitrichids universally demonstrated a greater frequency of qualitative variation across each compartment than lemurs. This included the variable presence of distinct accessory extensor muscles, and alternating degrees of fusion between muscle bellies (particularly between flexor digitorum superficialis and profundus). Among architectural variables, fascicle lengths vary most substantially both within and between taxa (relative to body mass), while muscle mass scaled more consistently with overall body size.

This research was funded in part by the National Science Foundation (IOS-15-57125 and BCS-14-40599).

Antemortem tooth loss in Late Prehistoric west-central Tennessee: are there subsistence corollaries?

MARIA O. SMITH¹ and TRACY K. BETSINGER²

¹Sociology and Anthropology, Illinois State University, ²Anthropology, SUNY, Oneonta

The prehistory of the Kentucky Lake Reservoir (KLR) in northern west-central Tennessee is poorly understood. The material cultural and human remains were recovered during a large salvage archaeological project (i.e., 1938-1944) prior to

the completion of Kentucky Dam. There are few site reports and little assessment of the material culture. Bioarchaeological assessments are the primary archaeological problem-solving tool. The later prehistoric subsistence-settlement pattern in the KLR is of particular interest as human occupation inexplicably terminates circa AD 1450. Although the settlement pattern is indicative of the Middle Mississippian (~AD 1100-1300) period (i.e., aggregated village, central plaza, quadrilateral mounds), it is unclear whether these peoples cultivated the cariogenic carbohydrate, maize.

Previous research evaluating Middle Mississippian period KLR caries prevalence by tooth type yielded conflicting results. Compared to three unequivocal maize-intensive Late Mississippian agriculturalist samples from East Tennessee, the Gray Farm sample is maize intensive. However, the caries in Link and Slayden resembled KLR Late Woodland samples. Adding confusion to the comparisons, Gray Farm exhibited patterns of caries location and lesion size more congruent with the Late Woodland pattern. Given the distinct possibility that antemortem tooth loss introduced sampling bias in the sample comparisons, the sites are re-examined, with the addition of the Middle Mississippian KLR site of Thompson, for age-at-death and subsistence-associated patterns of antemortem tooth loss. Despite the fact that antemortem tooth loss is multi-factorial, it clearly distinguishes Middle Mississippian KLR samples from Late Woodland samples (particularly for the posterior teeth) and their congruence with East Tennessee maize-intensive samples.

From Kin to Kind: Becoming Molecular in the Time of American Settler Colonialism

RICK W. A. SMITH

Anthropology, Dartmouth College, Neukom Institute for Computational Science, Dartmouth College, Indigenous Science Technology and Society Laboratory, University of Alberta

As biological anthropologists turned to populations as units of evolutionary analysis during the latter half of the 20th century, Marxist political theorists began to identify populations as sites of social control. While Sherwood Washburn worked to redirect biological anthropology away from questions of types towards those of populations, Michel Foucault, and later Donna Haraway and Achille Mbembe, showed how populations became the governing logic of inequality, shaping who lives and dies in modern nation states. Using two demographic case studies, I will read theoretical developments in evolutionary anthropology and Marxist political thought through one another. In doing so, I consider the ways that population thinking in science has produced concepts of Indigeneity that further colonization.

First, I reanalyze a cryopreserved blood collection to evaluate the role of population genomics in defining Indigeneity as a biological category. Previous studies with this collection analyzed only a subset of tribal members who had solely Indigenous ancestors and excluded tribal members with non-Indigenous ancestors. By conducting a genetic analysis of 54 previously excluded samples, this reanalysis shows that measures of genetic diversity significantly change and rejects the idea that Indigenous peoples are biologically discrete groups. Therefore, population genomics has often undermined Indigenous sovereignty by disaggregating the complex kin relations of Indigenous peoples and reassembling Indigeneity as a biological type. Finally, tracing the history of land allotment in Texas, I analyze the evolutionary and molecular ecological consequences of population governance and its role in reproducing settler life and Indigenous death in the colony.

This work was supported in part by a grant from the Norman Hackerman Advanced Research Program.

Developmental and elemental records in orangutan teeth reveal a complex interplay between primate behavior, physiology, and seasonal climate variation in the tropics

TANYA M. SMITH¹, CHRISTINE AUSTIN², MANISH ARORA², DANIEL R. GREEN³ and IAN S. WILLIAMS⁴

¹Australian Research Centre for Human Evolution, Griffith University, ²Department of Environmental Medicine and Public Health, Icahn School of Medicine at Mount Sinai, ³Department of Human Evolutionary Biology, Harvard University, ⁴Research School of Earth Sciences, The Australian National University

Our 2017 study of calcium-normalized barium (Ba/Ca) patterns in four wild orangutan dentitions demonstrated a novel phenomenon of increased nursing on an approximately annual basis, which may relate to seasonal cycles of resource availability. Here we explore this further in their first molar tooth enamel by measuring oxygen isotope compositions ($\delta^{18}\text{O}$), which vary with milk consumption, temperature, precipitation, and evaporation cycles during an animal's development. We characterized molar development and developmental stress histologically, followed by trace element distributions and oxygen isotopes measured in situ on a weekly-basis over 3–5 years per tooth. Both Ba/Ca and $\delta^{18}\text{O}$ increased during the first year of life, consistent with field reports of exclusive nursing. Postnatal increases in $\delta^{18}\text{O}$ ranged from 3 to 10 ‰, in excess of reported isotopic enrichment in human infants. $\delta^{18}\text{O}$ began to cycle before Ba/Ca, decreasing overall after the first year in three individuals. It is likely that these approximately annual $\delta^{18}\text{O}$ cycles reflect meteoric water variation in plants consumed by infants, as Ba/Ca and $\delta^{18}\text{O}$ are rarely in phase after the first year of life, when orangutans typically begin to

ABSTRACTS

supplement their mother's milk with solid foods. Subtle accentuated lines were observed on an approximately annual basis over 1–2 years, but there was no consistent relationship with trends in Ba/Ca or $\delta^{18}\text{O}$, underscoring the multifactorial nature of developmental disruptions in teeth. Studies of juveniles with concurrent environmental and dietary records are needed to further clarify the enigmatic pattern of prolonged cyclical nursing in Bornean and Sumatran orangutans.

Funded by the Australian Academy of Science, the Australian National University, Griffith University, Harvard University, and the Icahn School of Medicine at Mount Sinai.

Ontogenetic differences in the midline cranial synchondroses of primates

TIM D. SMITH¹, BRODY WOOD¹, LANRE OLADIPUPO¹, NANAMI MANO¹, JANE TAYLOR², HAYLEY CORBIN³, ALEXANDER UFELLE⁴, EMILY DURHAM⁵, CHRISTOPHER J. VINYARD⁶, JAMES J. CRAY² and VALERIE B. DELEON⁶

¹School of Physical Therapy, Slippery Rock University, ²Division of Anatomy, The Ohio State University, ³Department of Biology, Slippery Rock University, ⁴Department of Public Health and Social Work, Slippery Rock University, ⁵Department of Anatomy and Neurobiology, NEOMED, ⁶University of Florida, University of Florida, ⁷Department of Anthropology, Pennsylvania State University

Five synchondroses have been described in the midline of the mammalian basicranium. They exist at interfaces between basicranial bones (spheno-occipital, intrasphenoidal, and spheno-ethmoidal) and between basicranial bones and the unossified septal cartilage (prespheno-septal, and ethmo-septal). Midline synchondroses have been implicated as having a potential role in the angularity observed in the adult primate basicranium. However, few studies have examined them histologically. Using histological and immunohistochemical methods, we studied these basicranial joints in serial sagittal sections of newborn heads from ten genera of primates (seven anthropoids, three strepsirrhines). Each synchondrosis was examined for characteristics of active growth plates, including the zones of chondrocyte proliferation and hypertrophy, as well as corresponding changes in matrix characteristic (i.e., density and organization of type II collagen). Results reveal three synchondroses (spheno-occipital, intrasphenoidal, and prespheno-septal) possess attributes of active growth centers in all species. One additional synchondrosis (ethmo-septal) was present with growth center characteristics in newborn *Papio anubis* and *Galago moholi*, but not in the other species. The sphenoethmoidal synchondrosis (SES) varies at birth. In the catarrhines and *Galago*, it is a suture-like joint at birth (collagenous tissue between the two bones). But in most species, the jugum sphenoidale is ossified while the ethmoid remains cartilaginous. No species possesses a SES that has the organization of a

growth plate. Thus, only four midline synchondroses have the potential to actively affect basicranial angularity and facial orientation during the perinatal timeframe. In contrast, we hypothesize the SES essentially transitions toward a "suture-like" function, permitting passive growth postnatally.

This study was funded by NSF grant numbers BCS-1830894, BCS-1830919 and BCS-0959438

The effects of climate change on the ecology and health of indigenous Arctic populations

J. JOSH SNODGRASS
Anthropology, University of Oregon

Climate change in the Arctic is occurring faster than in other global regions and has already led to decreased permafrost and glacial and sea ice melting. This paper systematically reviews the health effects of climate change on contemporary indigenous populations in the Arctic, with attention to regional variation and vulnerabilities, as well as cultural strategies to mitigate the consequences of climatic change. Indigenous Arctic populations are already experiencing the effects of rapid regional economic development and pollution, and are uniquely vulnerable to the effects of climate change. The health effects of climate change among Arctic populations are complex and difficult to predict; however, key issues include: higher sea level, which threatens coastal communities; shifts in weather patterns and ecological conditions; altered access to traditional lands and foods, with effects on diet and psychological well-being; disruption of water supplies, with concomitant increases in infectious disease burden; and, northern range expansion of parasitic zoonoses. Results of this review indicate that climate change has already altered Arctic lifeways and health, including precipitating food insecurity among Inuit populations in Greenland and Canada, and damaging community water access among rural Alaskans thus leading to increased burden of respiratory and skin infections. Arctic populations are serving as the bellwethers of global climate change.

Reconstructing life histories using strontium isotope ratios of cremated human remains

CHRISTOPHE SNOECK^{1,2}, MELANIE M. BEASLEY³ and DAWNIE W. STEADMAN⁴

¹AMGC, Vrije Universiteit Brussel, ²G-TIME, Université Libre de Bruxelles, ³Dept of Anthropology, Purdue University, ⁴Dept of Anthropology, University of Tennessee-Knoxville

The high temperature reached during cremation destroy all organic matter present in bone, limiting the amount of information that can be obtained. Still, other signals, such as strontium concentrations and isotopes, are preserved

during cremation, and can be used to assess the geographical origin of cremated individuals. Here, we measured these proxies on fourteen recently deceased cremated individuals of known age and sex and residential history from the *Forensic Anthropology Center*, Knoxville, Tennessee, US. By measuring the various proxies on different bones with different turnover rates, we investigate the possibility to reconstruct life histories of burned people.

The strontium isotope ratios measured go from 0.7086 to 0.7145, while the concentrations go from 55 to 190 ppm. The difference in strontium isotope ratios between the petrous part (minimal turnover) and ribs (maximal turnover) can go up to 0.0032, highlighting a change in food source, likely linked to moving from one place to another. One ought to keep in mind, however, that a change in diet might also have a significant impact on these results and need to be taken into account. The difference between ribs and femur (intermediate turnover) are minimal in ten out of fourteen individuals (≤ 0.0001) and remain small in the four other (≤ 0.0005). These trends are also observed in the strontium concentration measurements. These results demonstrate the power of strontium concentrations and isotope ratios to reconstruct the movements of burned individuals throughout their lives.

Using aDNA and Archaeological Data to Explain Migration in the Casas Grandes Region of Northern Mexico

MERADETH SNOW
Anthropology, University of Montana

Migration as an archaeological topic has addressed huge distances, such as the colonization of the Americas, as well as smaller regions, such as the peopling of specific sites. The use of genetics as a medium to enhance our understanding of population movement can be an asset. There are potential pitfalls, however, such as the misrepresentation of DNA ranging across the landscape without human vectors or motivations. Genomic data must be interpreted through the lens of all available data from the site and surrounding region in order to understand how the data fit into the potential for human migration. These ideas will be discussed with mitogenome data accumulated from the site of Paquimé in Casas Grandes, Mexico, which has long been tied to hypotheses of migration from the south and north. How such migrations could be identified genetically and fit into the larger understanding of the site will be discussed, particularly in respect to the cultural transformation and fluorescence that marks the transition from the Viejo to Medio periods. While mitogenome data points to *in situ* population growth, our genetic evidence aligns with the archaeological record that individuals were migrating into the region from both the north

ABSTRACTS

and south. Our data points to the potential of individuals being brought to the site from elsewhere in what is now Mexico for sacrificial purposes, as well as regional migrants attracted to the site for reasons that may be associated with other cultural factors.

This work was supported by NSF funding [grant number 1821483].

High altitude adaptations in gelada monkeys (*Theropithecus gelada*)

NOAH SNYDER-MACKLER^{1,2}, KENNETH L. CHIOU¹, MAREIKE C. JANIAK³, AMANDA D. MELIN³, JACINTA C. BEEHNER^{4,5}, THORE J. BERGMAN^{4,5} and AMY LU⁶

¹Psychology, University of Washington, ²Center for Studies in Demography and Ecology, University of Washington, ³Anthropology, University of Calgary, ⁴Psychology, University of Michigan, ⁵Anthropology, University of Michigan, ⁶Anthropology, Stony Brook University

Life at high altitude is associated with myriad stressors, including hypoxia. These stressors challenge core physiological processes and have been strong selective forces throughout the course of evolution. In humans, for instance, Andeans and Tibetans adapted to high altitude exhibit divergent physiological adaptations: Andeans have increased hemoglobin concentrations, while Tibetans increase their respiratory rates. With this in mind, we investigated genomic and physiological adaptations to high altitude in a novel catarrhine model, the gelada monkey (*Theropithecus gelada*)—one of the most extreme obligate high altitude primate species. To do so, we generated a high-quality, chromosome-level *de novo* genome assembly using a combination of 10x Chromium linked-reads and Hi-C. We then sequenced RNA from gelada fibroblasts to generate a high-quality reference annotation. To identify signatures of high-altitude adaptation in the gelada lineage, we compared our genome to a dataset of 39 publicly available reference genomes and identified significantly expanded gene families and accelerated protein evolution in genes related to hypoxia response, angiogenesis, and embryonic development. Interestingly, coding changes in hemoglobin protein did not alter the oxygen-binding affinity of gelada hemoglobin—an adaptation found in some high altitude birds and rodents. Lastly, we resequenced 90 papionin genomes to 10x coverage in order to reconstruct gelada population histories and identified a handful of strongly differentiated variant sites in gelada populations. Together, these results significantly advance our knowledge of genotype-phenotype relationships underlying high-altitude adaptations in a comparative primate model.

NSF SBE-1848900; UW Royalty Research Foundation

Endocrine-epigenetic mechanisms of disease induced by pregnancy exposure to endocrine disrupting chemicals

MARISSA SOBOLEWSKI

Environmental Medicine, University of Rochester

Maternal exposure to endocrine disrupting chemicals (EDCs) is ubiquitous, as nearly 100% of reproductive aged women in the United States have measurable levels of EDCs, including plasticizers (like phthalates and bisphenol-A (BPA)) and perfluoroalkyl substances (like PFOA). Further, 90% of children have BPA and PFOA in their blood at birth. Our work previously identified that reproductive aged Tsimane' women have higher urinary phthalate levels with increased global market integration. Since pregnancy is a critical window of susceptibility to EDCs and disease, research is needed to understand how EDC exposure increases health risks for pregnant women and infants, informing unique health risks of women and developmental origins of adult disease. To address these questions, mouse dams were exposed to a representative EDC mixture (atrazine, BPA, PFOA, and dioxin) to understand lifelong consequences for metabolic maternal health and developing infant nervous systems. Mothers developed glucose intolerance, insulin insensitivity, and elevated LDL and total serum cholesterol levels. Male offspring increased testosterone at birth reprogramming adult behavior: altering attention, impulsivity and social deficits. Early testosterone exposure also decreased serum testosterone and decreased striatal methylation profiles along estrogen receptor-alpha and imprinted genes in adulthood. These data provide mechanistic plausibility for human research on pregnancy exposure and increased risk to develop Type II diabetes in mothers and children's neurobehavioral disorder risk in infants. Research is needed on how endocrine modulation reprograms epigenetics and lifelong health. Anthropologists and health scientists are uniquely suited to understand how low-dose EDC exposures impact health and development for mothers and children.

Supported by National Institutes of Health P30 ES001247 and T32 ES007026-3

Dynamic factor analysis as a dimension reduction technique for shape trajectory data

K. JAMES SODA

Department of Mathematics and Statistics, Quinnipiac University

Despite advances in geometric morphometrics (GM), most common GM methods still assume that every specimen has a single, static shape. Yet, an individual body can assume many shapes through locomotion or aging, such that a temporally ordered set of shapes, or shape trajectory, better represents the system. Vector

autoregressive (VAR) models are one methodology to represent and analyze shape trajectories when the interrelationship between shapes in the trajectory is the main focus. However, the high dimensionality of GM data makes model estimation difficult without dimensional reduction.

Here I compare the efficacy of dimensional reduction through principle components analysis, which is a common method in GM, to that of dynamic factor analysis, which, to the best of my knowledge, has not yet been applied to GM data. Dynamic factor analysis represents a shape trajectory as a linear transformation of a lower dimensional, latent time series, which serves as a dimension-reduced trajectory. It also simultaneously estimates a latent process, here a VAR model, which describes the interrelationship between observations in the latent series and thus between shapes in the original trajectory. To compare these two reduction techniques, I reduced the dimensionality of simulated shape trajectories using each method, estimated a VAR model for the reduced dataset, and used the resulting VAR model to simulate new trajectories. A comparison between the original trajectory and the model-based trajectory then assessed the fidelity of each reduction. Despite its computational complexity, dynamic factor analysis provides a promising new option for dimensional reduction in temporally dynamic systems.

A pilot study examining gunshot radiating fracture pathways using virtual methods

TESSA SOMOGYI, ELIZABETH A. EVANGELOU and ELIZABETH A. DIGANGI

Anthropology, Binghamton University

Radiating fractures are commonly observed in cases of gunshot trauma and radiate outwards from an entrance or exit defect. Cranial vault architecture and buttressing are thought to influence fracture pathways. Here we present a pilot study utilizing computed tomography (CT) scans to analyze the pathways of gunshot radiating fractures by mapping cranial vault thickness. This study is part of a larger project focusing on gunshot fracture patterns. For this pilot study, we selected 10 skulls with easily observable radiating fractures. Computer software programs Mimics and 3-Matic were used to map cranial vault thickness and measure fracture length. We measured cranial vault thickness at the origin, termination, and redirection points (where the fracture changed direction) of the fractures, as well as immediately beyond the redirection point. These measurements were used to characterize the vault thickness along the fracture pathways. A Pearson Product correlation test was used to assess the relationship between cranial vault thickness at the recorded points on the fractures and fracture lengths. Correlation results found a moderate negative correlation between thickness

ABSTRACTS

at the origin point and fracture length ($R=-0.577$), associating thicker bone at origin points with shorter radiating fractures. A paired samples T-test was used to compare the redirection point vault thickness to the vault thickness immediately beyond the redirection. T-test results indicated that cranial vault thickness is greater beyond the redirection point than it is at the redirection point ($p=0.05$), demonstrating that the fracture had redirected to an area of thinner bone.

This project was supported by award number 2016-DN-BX-0155 from the National Institute of Justice.

Exercise and postural effects on trabecular and subchondral bone properties in the medial femoral condyle

HYUNGGWI SONG¹, MARIANA E. KERSH¹ and JOHN D. POLK^{2,3,4}

¹Mechanical Science and Engineering, University of Illinois, ²Biomedical and Translational Sciences, University of Illinois, ³Anthropology, University of Illinois, ⁴Kinesiology and Community Health, University of Illinois

Properties of subchondral and trabecular bone are commonly used to infer joint loading patterns and differentiate behaviors used by living and fossil primate and hominin species. However, the specific ways that bone responds to altered load magnitude and position remains uncertain. Furthermore, there remains uncertainty about which subchondral and trabecular properties best reflect joint loading history. This experimental study tests the hypotheses that (i) exercise increases the amount and density of trabecular and subchondral bone and (ii) the distribution of bone across the joint surface is explained by differences in joint posture. Thirty juvenile sheep were randomly assigned to flat exercise ($n=11$), inclined exercise (15% grade; $n=11$) and non-exercised control groups. Exercise was conducted on motorized treadmills twice daily for 20 min at 1.12m/s for 60 days. Distal femora were micro-CT-scanned at 50 μ m resolution. Trabecular thickness, apparent density, bone volume fraction anisotropy, as well as subchondral thickness and apparent density were measured using custom algorithms in AMIRA, ImageJ and MATLAB. This analysis focuses on the medial side of the medial femoral condyle. Subchondral thickness was the only property that showed significant, consistent and interpretable effects of exercise and postural differences among the treatment groups, with thicker bone found in both exercise groups and posteriorly-positioned on the condyle in the inclined group, compared to non-exercised controls. Trabecular properties, and subchondral density differed significantly between flat-exercised and controls, but not between incline-exercised and controls

confounding simple explanations. These results suggest that subchondral thickness responds to exercise during development supporting behavioral interpretation.

This research was funded by National Science Foundation 1638756

Bioarchaeological insight into subsistence of Alborz highlanders, northern Iran, during the Parthian period (c. 200 BCE – 226 CE)

ARKADIUSZ SOŁTYSIAK

Department of Bioarchaeology, Institute of Archaeology, University of Warsaw

Parthians were mobile herders from Central Asia who gradually gained control over Iran and Mesopotamia during the 2nd and 1st centuries BCE. The economy of their state is still not well known, especially in the Iranian mountainous provinces that are believed to have been inhabited by the transhumant pastoralists. Some insight into subsistence of the population living in that time in the Alborz mountains is possible thanks to stable isotope research. Human remains from two cemeteries: Liarsangbon (Guilan province) and Vestemin (Mazandaran province), were analyzed using collagen $\delta^{13}C$, $\delta^{15}N$ and enamel $^{87}Sr/^{86}Sr$ values. Average $\delta^{13}C$ values at both sites are similar (Vestemin: -18.1‰, s.d. 0.58, $N=10$; Liarsangbon: -17.7, s.d. 0.67, $N=17$) and they suggest diet with some indirect share of C_4 plants, likely through the uptake from products of animals that grazed at C_4 -abundant pastures. Average $\delta^{15}N$ differ between the sites (Vestemin: 8.7‰, s.d. 0.54; Liarsangbon: 9.3‰, s.d. 0.66) due to more arid conditions around Liarsangbon. At Liarsangbon most $^{87}Sr/^{86}Sr$ values are within the local range, but at Vestemin a bimodal distribution of $^{87}Sr/^{86}Sr$ suggests exploitation of two different zones, perhaps due to transhumance. Negative correlation between $\delta^{15}N$ and $\delta^{13}C$ values ($r=-0.59$, $p<0.02$) at Liarsangbon seems to be the consequence of a relatively wide spectrum of subsistence models from intensive high-manure farming in the valleys (high $\delta^{15}N$, low $\delta^{13}C$) to herding in the low-manure pastures abundant in C_4 plants (low $\delta^{15}N$, high $\delta^{13}C$). Available data suggest higher diversification of subsistence strategies in more arid areas of the Alborz Mountains.

National Science Centre (NCN) in Poland, grant No. 2016/22/M/HS3/00353.

Body mass estimation in modern juveniles using postmortem computed tomography

LAURE SPAKE, JULIA MEYERS and HUGO FV. CARDOSO

Department of Archaeology, Simon Fraser University

Skeletal estimation methods for juveniles have largely focused on age at death to the exclusion of other aspects of the biological profile. The recent accrual of anthropological data from computed tomography (CT) scans of children allows for the exploration of these aspects. This study explores the association between measurements of the femur and body mass in children. CT scans of 131 children aged birth through 12 years at death were consulted. These scans were taken between 2011 and 2016 at the Office of the Medical Investigator in Albuquerque, New Mexico, USA. The sample was divided into life history stages as per Bogin (1999). Body mass was estimated from the femur using equations from Robbins Schug et al. (2010) and two measures: J taken at midshaft, and distal metaphyseal breadth. Residual and absolute residuals were calculated for the overall sample and for life history stage groups separately. Body mass was consistently underestimated when using metaphyseal dimensions (mean residual -5.11), and overestimated when using J (mean residual = 3.70). This was especially the case for children over 7 years of age (mean residuals = -11.90 and 12.20 for metaphyseal breadth and J respectively). The original population used to develop these methods was studied between 1941 and 1967. Secular trends in height and weight of children could contribute to these results, especially in older children. Body mass estimation in juveniles is not free of the problems associated with age estimation, namely calibration of methods on appropriate reference samples.

Natural Sciences and Engineering Research Council of Canada (NSERC); Social Sciences and Humanities Research Council of Canada (SSHRC)

A little more conversation, a little more action, please: The potential of bone-muscle cross-talk for mapping skeletal markers of neurodegenerative disorders

NIVIEN SPEITH

School of Human Sciences, College of Life and Natural Sciences, University of Derby

Due to the complex differential diagnosis in the living and their multidimensional aetiology, cases of neurodegenerative disorders such as Amyotrophic Lateral Sclerosis (ALS) remain in the dark when it comes to their palaeopathological appraisal and presence in the bioarchaeological record. Yet the clinical presentation of these types of chronic conditions, marked by severe muscle degeneration and wasting ensued by continuous loss of movement, is well-established and accompanied by an increasing body of substantial evidence indicating imbalances in bone health and metabolism.

This study presents the results of a metadata analysis exploring the rich archives emerging from conversations between clinical and

ABSTRACTS

biomedical sciences and palaeopathology, providing major insights regarding the complex bone-muscle interactions at entheses and associated novel approaches for tracing neurodegenerative disorders in the human skeleton. Reviewing pathophysiological pathways and the effects of inhibited neuron-to-muscle signalling indicates a distinct role of oxidative stress in the formation of enthesal changes as an effect of allostatic disturbances. It is hypothesised that the combination of biochemical and neurological factors with biomechanical stressors not only delivers a potential explanation for a well-described yet relatively poorly understood phenomenon, but facilitates enhanced comprehension of disease mechanisms and particularly the analysis of neurodegenerative disorders from the skeleton, as this synthesis of clinical and skeletal data allows for a first mapping of skeletal manifestations of ALS in the palaeopathological record. Engaging bone-muscle cross-talk effectively connects clinical and palaeopathological perspectives and creates new directions in palaeopathology towards a holistic understanding of rare diseases and their experience in bioarchaeological frameworks.

Body Composition and Skeletal Acquisition in a Model of Chronic Stress

TAYLOR M. SPENCER¹, REBECCA TUTINO² and MAUREEN J. DEVLIN¹

¹Anthropology, University of Michigan,
²Epidemiology, University of Michigan

In industrialized humans, skeletal robusticity has declined and obesity has risen globally, but urban communities are disproportionately affected. Similarly, age at menarche has declined globally, while happening earlier for Black girls. Although higher body fat, earlier menarche, and lower bone density are seen in children of all socioeconomic statuses, children of color in urban environments bear a higher cumulative allostatic load, for which the biological effects have largely been ignored. We hypothesize that high allostatic load in subadults causes interrelated physiological and metabolic changes that lead to obesity, earlier age at menarche, and reduced skeletal acquisition. We examined the effects of chronic stress on body mass, body fat, bone mineral density (BMD), and bone mineral content (BMC) in a mouse model. We predicted that chronic stress would increase body mass and body fat and decrease skeletal acquisition. Female C57BL/6J mice were subjected to varying stressors (S) or were not stressed (N) (n=8/group) from 3-6 wks of age. Stressors included exposure to music or mouse distress sounds, dim light during sleep, social isolation, and frequent group changes. Results indicated no significant differences in body mass, BMD, or BMC. S mice gained less body fat (48%) than N mice (64%) (p<0.05 for all). Food intake increased by 46% for S mice and 123% for N

mice (p<0.001). These findings don't support the hypothesis that chronic stress increases body fat. This short-term study shows that stress can affect food intake, but longer studies are needed to understand how chronic stress impacts skeletal acquisition.

The effect of clothing on decomposition in the cooler months in Cape Town, South Africa

MAXIMILIAN J. SPIES¹, DEVIN A. FINAUGHTY², LOUISE J. FRIEDLING¹ and VICTORIA E. GIBBON¹

¹Faculty of Health Sciences, Department of Human Biology, University of Cape Town, ²School of Anthropology and Conservation, University of Kent

No clear, universal effect of clothing on decomposition has been established, with conflicting results from research conducted in various habitats across the world. Little data are available from South Africa, especially the Western Cape where many victims of the province's high murder rate remain unclaimed and unidentified. Better methods of estimating the post-mortem interval (PMI) will narrow the search window for police and improve chances of correct identification of the deceased. Currently, no known PMI method explicitly accounts for clothing's possible effect on decay rate, therefore, this study assessed the influence of common, seasonally-appropriate clothing on porcine decomposition in the forensically-significant thicketed Cape Flats Dune Strandveld habitat, Cape Town. The clothes were tailored to ensure an appropriate fit, preventing unrealistic access by biotic agents of decay. The initial trial consisted of four ~60 kg domestic pig carcasses (*Sus scrofa domestica*) as proxies for human decomposition, two of which were clothed and two unclothed. Since clothing limits the use of visual decomposition scoring methods, daily weight loss was used as a quantitative measure to track decomposition progression. Weight loss was closely linked with scavenging activity by the Cape grey mongoose (*Galerella pulverulenta*). Clothing caused a notable decrease in decay rate, possibly mediated by scavenger preference for unclothed carcasses. Since scavengers targeted unclothed carcasses and multiple decedents at scenes are rare, the influence of clothing on decay may be more accurately and realistically assessed with only a single clothed carcass in environments where scavengers play a substantial role in the taphonomic process.

South African National Research Foundation

It's elementary: Extending the teaching of anthropology to elementary schools

JULIA G. SPONHOLTZ, CHRISTOPHER D. LYNN and AVERY MCNEECE

Anthropology, University of Alabama

Anthropology is usually confined to college classrooms, limiting to the subject. Anthropology is important for all humans to understand because it fosters understanding of human differences and similarities. We attempt to challenge this norm in the Tuscaloosa community with our program Anthropology is Elemental (AiE). Through the program, anthropology students have been teaching local elementary schoolers the basics of anthropology for the past 9 years. Through a service-learning course, undergraduates learn from doctoral students how to team teach. For each topic, one of the undergraduate students plans and teaches a lesson to elementary students in local schools and guides a group activity inspired by the lesson. All of the resources are uploaded to the AiE website for open access. To determine the effectiveness of the approach for the elementary children, we collect free-listing responses from them about main ideas relating to the lesson and the previous lessons. As well as providing feedback on the program, this also helps to reinforce the new ideas for the students. Projects like this can help foster a greater understanding of the nuances of anthropology, including controversial topics like evolution, from a young age when kids are more accepting of new ideas, allowing students to develop critical thinking skills and a greater appreciation for science and culture at an earlier age.

From the Bay to Belize: changes in genetic diversity over time

LAUREN C. SPRINGS¹, JAMES F. GARBER² and DEBORAH A. BOLNICK³

¹Anthropology, University of Texas at Austin,
²Anthropology, Texas State University,
³Anthropology, University of Connecticut

European colonization during the 17th and 18th centuries significantly altered the population demography of the Bay of Honduras (now Belize) as Spanish and British colonists formed permanent settlements, displacing or subjugating Indigenous populations and bringing enslaved Africans to the region to labor in agricultural industries. Today, the population of Belize is considered a creole society with cultural and genetic roots in Indigenous, African, and European populations. In 2009, the St. George's Caye (SGC) Archaeological Project was established to learn more about a prominent British colonial settlement located on one of the nation's cayes. Ten years of archaeological excavations at the British cemetery at SGC have identified 76 burials in varying states of preservation. When possible, osteological and genetic analyses were undertaken for each burial to explore the demographic makeup of the settlement's inhabitants. A total of 54 individuals were sampled for ancient DNA analysis of mitochondrial haplotypes and estimation of genetic ancestry based on genome-wide SNPs. In addition, to assess changes in genetic diversity

ABSTRACTS

over time, we collected saliva samples from 43 contemporary residents of Belize who have genealogical ties to the early settlement. For these individuals, we determined mitochondrial and Y-chromosome haplotypes and genotyped over 600k SNPs to generate genetic ancestry estimates for each person. We illustrate changing genetic diversity patterns in the historic population and in their contemporary descendants and discuss the implications of this data for understanding the genetic effects of British colonization in Belize and the formation of a creole society in the colony.

This work was funded in part by grants from the National Science Foundation (1826656) and the Wenner-Gren Foundation (9631).

Bronze Age *Y. pestis* genomes from the Lake Baikal region

MARIA A. SPYROU¹, HE YU¹, RITA RADZEVICIUTE¹, GUNNAR U. NEUMANN¹, SANDRA PENSKE¹, JANA ZECH², PETRUS LEROUX³, MARINA KARAPETIAN⁴, PATRICK ROBERTS², ALEXANDRA BUZHILOVA⁴, COSIMO POSTH¹, CHOONGWON JEONG^{1,5} and JOHANNES KRAUSE¹

¹Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Jena 07745, Germany, ²Department of Archaeology, Max Planck Institute for the Science of Human History, Jena 07745, Germany, ³Department of Geological Sciences, University of Cape Town, Rondebosch 7701, South Africa, ⁴Research Institute and Museum of Anthropology, Moscow State University, Moscow 125009, Russia, ⁵School of Biological Sciences, Seoul National University, Seoul 08826, Republic of Korea

The Bronze Age in Eurasia was a period of intense human mobility that transformed the genomic landscape of this entire region. In recent years, metagenomic analyses of human remains dating between 5,000 and 3,500 years before present (BP) revealed a number of human-associated pathogens that accompanied and potentially influenced these population movements. One such example is the plague bacterium, *Yersinia pestis*. Previous studies have shown that Late Neolithic and Early Bronze Age (LNBA) *Y. pestis* genomes formed a putatively extinct phylogenetic lineage that paralleled human mobility across Eurasia. Here, we present the metagenomic screening of Neolithic and Bronze Age remains from the Lake Baikal region in Siberia and show the presence of *Y. pestis* infections in two individuals. Subsequent whole-genome enrichment and comparison against a panel of ancient and modern-day *Y. pestis* genomes revealed their analogous phylogenetic placement and genomic contents to published LNBA isolates from Europe and Central Asia. Their further analysis alongside newly generated human genome-wide and isotopic data shows high mobility within Siberia during the Bronze Age, through the identification of genomic outliers. Moreover, we present a novel

age estimation approach, using molecular dating of bacterial genomes, and show a large offset in the radiocarbon dates of *Y. pestis*-positive individuals, likely influenced by a regional freshwater reservoir effect. Collectively, our results suggest that *Y. pestis* spread into the Lake Baikal region within the context of human expansions across the Eurasian steppe during the 5th millennium BP, also affecting individuals whose genomic makeup was not impacted by such migrations.

This research was supported by the Max Planck Society and the European Research Council (ERC-CoG 771234 PALEORIDER).

GaJ17: A Middle Stone Age site at Koobi Fora, East Turkana (Kenya)

CHRISTOPHER SSEBUYUNGO¹, SILINDOKUHLE MAVUSO², DEBRA COLAROSSO³, TAMARA DOGANDZIC^{3,4}, KAEDAN O'BRIEN⁵, EMMANUEL NDIEMA⁶, DAVID R. BRAUN^{7,8}, JOHN W.K. HARRIS⁶ and KATHRYN L. RANHORN⁹

¹Museums and Monuments, National Museum of Uganda, ²School of Geosciences, University of the Witwatersrand, ³Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ⁴Department of Anthropology, University of Pennsylvania, ⁵Department of Anthropology, University of Utah, ⁶Department of Earth Sciences, National Museums of Kenya, ⁷Department of Anthropology, Center for the Advanced Study of Human Paleobiology, George Washington University, ⁸Archaeology Department, University of Cape Town, ⁹Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University

The Omo-Turkana Basin boasts an extended and detailed Pleistocene chronological record, including some of the earliest known modern human remains. Since 2013, the Koobi Fora Middle Stone Age Project has conducted archaeological survey and excavation at multiple localities, stratigraphically above to the Koobi Fora Formation, with an interest in understanding the context of the rare MSA archaeological deposits in the Koobi Fora region. Specifically, we investigate site formation processes. Despite limited sample sizes, taphonomic analysis indicate some post-depositional processes. A high proportion of small finds suggests little evidence of winnowing of artifacts at GaJ17. Fabric analysis and other indications suggest a lakeshore occupation in a primary context. Optically stimulated luminescence age estimates range from ~70-30 Ka. Stone artifacts recovered include convergent Levallois points made on volcanics (basalt and ignimbrite) and small retouched tools, fashioned predominantly on cryptocrystalline silicas. Aquatic taxa such as fish and hippopotamus are the most abundant component of the faunal assemblage. Micromorphological evidence implies GaJ17 formed via aeolian processes. A capping caliche deposit buffered this site from subsequent Holocene high lakestands. GaJ17

provides the first evidence of modern human occupation in East Turkana Basin in association with radiometric age estimation. These finds are important in relation to modern human fossils, such as KNM-ER 3884 and KNM-ER 999, which were found in Ileret. (Additional geological research is needed to connect the GaJ17 locality in Koobi Fora to fossil discoveries in Ileret, and additional localities throughout northern Kenya.

This work was supported by the National Science Foundation IRES 1358178 and 1358200, REU 1930719, ARCH 1624398 and the Leakey Foundation.

Variation in masticatory muscle attachment areas: exploring potential relationships to dental wear and allometry in *Otolemur* and *Saimiri*

ELIZABETH M. ST CLAIR and JONATHAN MG. PERRY

Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Primates show considerable variation in the attachments of the masticatory muscle adductors on the skull. Results from some apes show that features such as sagittal crests can increase across adult ontogeny, suggesting that variation in muscle size might compensate for molar wear. Here we investigate variation across a range of wear stages in adults of *Saimiri sciureus* (n=10) and *Otolemur monteiri* (n=9). Dental wear was assessed from degree of enamel wear and dentine exposure in the permanent molars. Temporalis origin (TO) and the combined attachment area for masseter and temporalis on the lateral surface of the mandibular ramus (LMR) were measured on 3D models from microCT data, and the square root was calculated (SQRT-TO, SQRT-LMR) for allometric analyses. Mandible length was used as a proxy for overall size.

Both species showed positive allometry in the regressions of areas on mandible length (R^2 0.81-0.89): Ln SQRT-TO slope: *Otolemur* 2.154, *Saimiri* 1.684, Ln SQRT-LMR slope: *Otolemur* 1.67, *Saimiri* 1.38. Of these comparisons, only the slope of LMR on mandible length in *Saimiri* has confidence limits that include isometry. While a significant relationship exists between dental wear score and muscle attachment areas for *Otolemur*, this result was reduced or absent when the areas are considered relative to mandible length. No significant relationship between tooth wear and muscle attachment area was seen in *Saimiri*. In these species, individuals do not seem to compensate for greater tooth wear by increasing muscle mass or attachment area, but do show strong effects of variation in overall size.

CT scans used in this study are publicly available on MorphoSource and were funded by a Trinity College of Arts and Sciences grant from Duke University to C E Wall.

ABSTRACTS

Death and Fire: Characterising the burning process and the cremation environment using archaeological burned human remains from Belgium.

ELISAVET STAMATAKI^{1,2}, CHRISTOPHE SNOECK^{1,3,6}, IOANNIS KONTOPOULOS¹, MARTA HLAD^{1,2}, KEVIN SALESSE², BARBARA VESELKA¹, AMANDA SENGELØV², RICA ANNAERT¹, MATHIEU BOUDIN⁷, GIACOMO CAPUZZO², SARAH DALLE⁴, GUY DE MULDER⁴, CHARLOTTE SABAU⁴, EUGÈNE WARMENBOL⁵, MARTINE VERCAUTEREN² and DRIES TYS¹

¹Art Sciences and Archaeology, Vrije Universiteit Brussel, ²Biology of Organisms and Ecology, Université Libre de Bruxelles, ³Chemistry, Vrije Universiteit Brussel, ⁴Archaeology, Ghent University, ⁵History, Arts, and Archaeology, Université Libre de Bruxelles, ⁶G-Time Laboratory, Université Libre de Bruxelles, ⁷Royal Institute for Cultural Heritage, Brussels

Burned human bones are commonly found in archaeological contexts. Due to the high temperatures reached during burning (up to 1000°C), organic components of bone disappear and significant structural, chemical and isotopic changes to the inorganic fraction (bone apatite) take place. Despite these changes, burned bones play an increasingly important role in our understanding of societies in which cremation was practiced. The application of new micro- and macroscopic techniques to archaeological cremated bone collections enables new inferences on pyre technology, pyre management and specialization concerning the use of fire in funerary rituals.

The aim of this project is to investigate inter- and intra- site differences in burning conditions (temperature of the fire, duration, size of the pyre, amount and quality of the fuel, position of the body, fire extinguishing), pre and post-cremation treatment of body at several Belgian Late Bronze Age, Iron Age and Roman sites. In addition to osteological analysis, carbon and oxygen isotope analysis, infrared spectroscopy (FTIR), and X-Ray diffraction (XRD) were conducted in order to extract information from the burned bones. The results obtained on different skeletal elements (diaphysis, cranial bones, ribs) from different sites indicate that both the temperature and the position of the body on the pyre vary between different sites and time periods. This variability adds to our understanding regarding the specialization of pyre technology and management at the studied sites.

Life Course Perspective of the Elite Burials of Early Bronze Age Umm el-Marra, Syria

CHRIS STANTIS¹, GLENN M. SCHWARTZ², GEOFFREY NOWELL³, ERNEST K. BATEY⁴, NINA MAARANEN¹ and HOLGER SCHUTKOWSKI¹

¹Department of Archaeology and Anthropology, Bournemouth University, ²Department of Near Eastern Studies, Johns Hopkins University, ³Department of Earth Sciences, Durham University,

⁴Department of Social Sciences, Lower Columbia College

This research combines funerary archaeology, paleopathology, and stable isotope data to investigate the life courses of individuals from Umm el-Marra (MNI=35). The archaeological site of Umm el-Marra (in the Jabbul plain, western Syria), is a large, fortified urban center. Excavations have uncovered ten tomb structures built during the Early Bronze Age (ca. 2500–2200 BCE) that possibly containing royalty as evidenced by lavish grave goods, and paleopathological evidence suggesting sociocultural buffering from the harsh social and physical environments of agricultural urban centers in the Bronze Age Near East. Interred inside adjacent brick installations are animal (primarily equid) skeletons interpreted as sacrifices as part of ceremonies honoring the entombed, as well as infant remains, which might be sacrifices or later deposits.

Although much of the assemblage is currently inaccessible due to the political unrest in the wider region, some samples were available for isotope analyses ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$, $\delta^{18}\text{O}$, $\delta^{34}\text{S}$, $^{87}\text{Sr}/^{86}\text{Sr}$). All analyzed individuals display local values; this is in contrast with comparative contemporaneous sites to the east along the Levantine coast and to the west in the Khabur Basin where individuals moved much more frequently. Dietary isotopes in conjunction with animal baseline data suggest a heavy reliance on cereal grains and ovicaprines in line with ancient subsistence practices. After abandonment of the burial site for almost three centuries, a monumental platform was constructed above the tombs, perhaps for ritual activities of ancestor veneration. Evidence of how these elites lived and died is integrated into the concept of 'social memory' and discussed.

This project receives funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation program (grant agreement No 668640).

Hip trauma and convalescence: The case for care at Ghazali

ROBERT J. STARK¹, JOANNA CIESIELSKA² and ARTUR OBLUSKI²

¹Department of Anthropology, McMaster University, ²Polish Centre of Mediterranean Archaeology, University of Warsaw

Part of the medieval Kingdom of Makuria (ca. 6th–14th c. CE), the settlement of Ghazali is located within the Wadi Abu Dom region of the Bayuda desert in northern Sudan. Occupied between ca. 680-1275 CE the coenobitic monastery at Ghazali was inhabited by an unknown number of lay individuals and up to 70 monks at any one time. A large cemetery (Cemetery 2) along the southern limit of the monastery was the final resting place for the resident monks.

During excavations in Cemetery 2 an adult male (Ghz-2-036), ~35-45 years old, with a drastic hip fracture was recovered. Macroscopic and radiographic observation identified an extracapsular basicervical fracture of the right femur with complete separation along the intertrochanteric line at the femoral neck (a type 31B.3 fracture according to the AO/OTA classification), resulting in non-union and the development of a pseudarthrosis.

The presence of significant osteoblastic response and evident wear around the pseudarthrosis indicate substantial healing and suggest this individual may have been mobile to some degree following hip fracture healing. Hip fractures can have severe, and in many cases life threatening, implications and typically require extended periods of immobility and attendant care, bringing into question the nature of recovery and convalescent care of this identified individual. This paper engages with the bioarchaeology of care and broader archaeological and textual materials to examine the nature of the hip fracture experienced by individual Ghz-2-036 and the possibility of having been cared for at the Ghazali monastery during the recovery phase.

the Qatar-Sudan Archaeological Project (QSAP); the Polish Centre of Mediterranean Archaeology (PCMA), University of Warsaw; the De Brzezie Lanckoronski Foundation in association with the Polish Academy of Arts and Sciences.

Ethical Considerations and Stewardship of Contemporary Donated Human Remains

DAWNIE W. STEADMAN¹, MARY C. DAVIS¹, JOANNE B. DEVLIN¹, HELI MAIJANEN², LEE M. JANTZ¹ and GIOVANNA M. VIDOLI¹

¹Anthropology, University of Tennessee, ²Archaeology, University of Oulu

The mission of the Forensic Anthropology Center (FAC) is to promote research, training and public outreach in forensic anthropology. At the heart of this mission is our whole body donation program, active since 1981. This program is distinct from medical schools in that donations are not part of a state anatomical gift program, donors are placed at the Anthropology Research Facility (or "Body Farm") for decomposition training and research, and the skeletons are accessioned into the Bass Donated Skeletal Collection. The Bass Collection currently holds nearly 1800 skeletons and approximately 5000 living persons are registered to become donors ("predonors").

The FAC must constantly negotiate an influx of research requests that often challenge us to re-evaluate our mission, balance the spirit and intent of the donors with the scientific discoveries and abilities, and protect the privacy and dignity of the donors and their families in the face of technologies that may reveal identities. Since

ABSTRACTS

the donors are well-documented and families are living, privacy issues and ethical treatment of remains are at the forefront of all decisions made concerning research requests.

The purpose of this paper is to outline the scientific needs that prompted the development of the FAC body donation program and to discuss how previous ethical dilemmas have been addressed. Moreover, we will provide some insight on current and potential future challenges that require thoughtful negotiation in order for stewardship of contemporary skeletal collections to continue to serve the living but protect the dignity of the deceased and their descendants.

Red-tailed monkeys (*Cercopithecus ascanius*) employ both behavioral and physiological strategies to overcome seasonal hardship

RONNIE STEINITZ¹, MELISSA EMERY THOMPSON² and MICHELLE BROWN¹

¹Anthropology, University of California, Santa Barbara, ²Anthropology, University of New Mexico

A pervasive ecological constraint faced by all wild animals is the need to find food, and the ability to use acquired food energy to maximize reproductive fitness. Despite its importance to individual fitness and to population growth and viability, little is known about the way non-human primates acquire and allocate energy towards different life history strategies during food scarcity. Assessing primate energy balance—energetic input minus energetic expenditure—can reveal patterns in energy allocation under varying environmental conditions. To tease apart how seasonality in food availability shapes primate energy usage, we examine the relationship between ambient temperature, precipitation, and fruiting of key plant species and urinary C-peptide of insulin (UCP), a by-product of sugar breakdown, collected non-invasively from six groups of free-ranging red-tailed monkeys (*Cercopithecus ascanius*) in Kibale National Park, Uganda. We found that while monkey energy balance decreased when food was scarce in the forest (adj. $R^2 = 2.25 \times 10^{-5}$, $F = 8.16$, $df = 953,410$, $p < 0.0001$), it increased with the abundance of ripe fruits of specific food items, especially in the periphery of the home range (Est = 3.44×10^{-1} , SE = 8.08×10^{-2} , $t = 4.264$). Additionally, short bursts of low night-time temperatures did not initiate intensive thermoregulation, though prolonged cold spells did (Est = -2.31 , SE = 1.07 , $t = -2.15$). These findings highlight adaptive seasonal behavioral and physiological responses to short- and long-term hardship. Our results further expand our understanding of drivers of primate foraging patterns and population growth and contribute to species conservation efforts.

This study was funded by the National Science Foundation (award #1103444 to MB), Leakey Foundation (to MB), and UC Santa Barbara Regents Fellowship (RS).

Machine Learning in Anthropology: A Regularized Deep Network for Osteological Micro-CT Image Segmentation

NICHOLAS B. STEPHENS¹, AMIRSAEED YAZDANI², VENKATESWARARAO CHERUKURI², LILY J. D. DEMARS¹, VISHAL MONGA² and TIMOTHY M. RYAN¹

¹Department of Anthropology, The Pennsylvania State University, ²Department of Electrical Engineering, The Pennsylvania State University

Micro-computed tomography (μ CT) is often used in Anthropology and Paleontology to quantify osteological features of extant and extinct species. One of the most critical and time-consuming aspects of such analyses is the accurate identification and thresholding of bone from non-bone. Traditional thresholding relies on bone being the densest material in a μ CT scan. In archaeological and palaeontological contexts, fossilization, differential preservation, and matrix infill result in heterogeneous densities that match or exceed bone density. There have been many (semi)automatic approaches proposed to overcome these issues but researchers often resort to laborious manual segmentation. Here we present a regularized deep network model (RDN-CS) that incorporates expert knowledge and combines a data-adaptive representation layer, which is sensitive to bone structures, with a U-net image segmentation network. 30 challenging μ CT (30-50 μ m) images of extant human, non-human, and fossil bones were manually segmented. 15 were used for training and 15 for testing. DICE overlap comparisons of the 15 test images found RDN-CS to be more accurate with than segmentations using BoneJ's optimise threshold (0.60), the MIA-clustering algorithm (0.88), a multiple layer perception network (0.89), and a typical U-NET (0.92). When RDN-CS was trained with 5 images, DICE overlap dropped less dramatically (0.92) than the typical U-NET (0.90). Because RDN-CS is trained with TensorFlow, it can easily be retrained with additional images that contain complexities not present in the initial training set. This is an advantage over methods that are static, which require specialized hardware and a lot of training data.

BCS-1719187

Phenotypic plasticity and adaptability in the genus *Homo*: implications from studies of modern human diversity

JAY T. STOCK^{1,2,3}, MANUEL WILL⁴ and JONATHAN CK. WELLS⁵

¹Department of Anthropology, University of Western Ontario, ²Department of Archaeology, Max Planck Institute for the Science of Human History, ³PAVE Research Group, University of Cambridge, ⁴Department of Early Prehistory and Quaternary Ecology, University of Tübingen, ⁵UCL Great

Ormond Street Institute of Child Health, University College London

Phenotypic plasticity is common among meta-zoans. We have previously argued that enhanced phenotypic plasticity is a characteristic of the hominin lineage (Wells and Stock, 2007). This hypothesis remains challenging to test as phenotypic correlates of environmental variation may result from either natural selection or plasticity. Recent evidence suggests that some modern human variation previously attributed to natural selection shows developmental plasticity. Here we explore evidence for phenotypic variation among modern hunter-gatherers and fossil hominins to provide a preliminary assessment of whether phenotypic diversity within our genus is driven by developmental plasticity. We compare body size estimates of adult and subadult foragers from a globally representative dataset ($n=828$) with a comprehensive dataset of Pleistocene size variation within the genus *Homo* ($n=180$). The results demonstrate that: a) the range of body size within modern foragers corresponds to the entire range of size variation in the Pleistocene fossil record; b) ecogeographic variation among adult foragers differs regionally relative to local ecology; c) this variation is differentially expressed during somatic growth, consistent with developmental plasticity; and d) the earliest members of the genus *Homo* demonstrate early evidence of intraspecific differences in phenotype that correlate with local ecology. If similar patterns of intraspecific variation are reflective of phenotypic plasticity in modern humans, it is parsimonious to interpret the observed patterns of variation within early *Homo* as reflective of increased developmental plasticity in response to environmental variation. Increased phenotypic variation within *Homo sapiens* suggests the evolution of even further developmental plasticity within our species.

This study was funded by the European Research Council, ADaPt Project, grant number 617627 to JTS.

Functional morphology of the auditory periphery of humans, common chimpanzees and bonobos and evolution of human auditory capacities

ALEXANDER STOESSEL^{1,2,3}, STEFFEN OSSMANN⁴, MATTHIAS BORNITZ⁴, NIKOLOZ LASURASHVILI⁴ and MARCUS NEUDERT⁴

¹Institute of Zoology and Evolutionary Research, Friedrich Schiller University Jena, Germany, ²Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Jena, Germany, ³Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, ⁴Otorhinolaryngology, Carl Gustav Carus Faculty of Medicine, TU Dresden, Germany

Humans differ from chimpanzees and other catharrines in a number of derived auditory characteristics, some being potentially related

ABSTRACTS

to speech perception. Since distinct anatomical differences in the auditory periphery of humans and chimpanzees exist we assume that this morphological disparity relates to differences in middle and outer ear function which might influence auditory capacities. To test our assumption we experimentally measured the transfer function of the middle ear (METF) on cadavers of four common chimpanzees, three bonobos and 15 humans and also determined the outer ear canal (EAC) transfer function. We recorded stapes footplate vibrations using Laser-Doppler Vibrometry after gaining access to tympanic cavities. Middle ears were excited acoustically through the EAC and the investigated frequency bandwidth ranged between 0.1-10 kHz.

Below 1 kHz the magnitude of the METF of *Pan* is greater compared to that of humans which relates to a lower stiffness of the larger eardrum of *Pan*. *Pan* and humans show a decrease in magnitude of the METF after 1 kHz. While the METF in humans continuously decreases until the end of the measuring range, it slopes upwards around 4-5 kHz in *Pan*, progressing above the human curve. However, after adding the pressure gain of the EAC, the human transfer function exceeds the one of *Pan* around 4-5 kHz, a frequency range humans also show better hearing sensitivity. This demonstrates differences in the functional morphology of human and chimpanzee ears, likely also affecting auditory capacities and opening up new avenues for studying the evolution of human hearing.

The study was funded by the Max Planck Society

Strontium isotope variability in the Palauan archipelago: Preliminary results from the Chelechol ra Orrak site

JESSICA H. STONE¹, SCOTT M. FITZPATRICK^{1,2}, GEORGE D. KAMENOV³ and JOHN KRIGBAUM⁴

¹Department of Anthropology, University of Oregon, ²Museum of Natural and Cultural History, University of Oregon, ³Department of Geological Sciences, University of Florida, ⁴Department of Anthropology, University of Florida

Initial settlement of Remote Oceania represents the last major wave of human dispersal into previously uninhabited environments. Comprehension of this process is critical to understanding how humans adapted to island environments, as these small and remote landmasses presented unique adaptive challenges, including the development of inter- and intra-island movement and interaction. The Chelechol ra Orrak rockshelter in Palau contains one of the oldest and largest cemeteries in Remote Oceania and has great potential to elucidate these processes; however, it is currently unknown where these individuals resided during life.

A number of isotopic proxies may be used to identify the local origins of individuals buried at the site. Here, we focus on strontium isotope ratios from tooth enamel and environmental plant samples. With regards to the human samples, at least two different molars were analyzed for 11 individuals resulting in 23 discrete ⁸⁷Sr/⁸⁶Sr values. Background results for the archipelago will be presented based on forthcoming plant and soil leachate ⁸⁷Sr/⁸⁶Sr data, however, current ⁸⁷Sr/⁸⁶Sr values average 0.70889 (±0.000003). Overall, the sample has low heterogeneity, however, three samples representing two individuals fall outside two standard deviations of the mean ⁸⁷Sr/⁸⁶Sr value. Trace element analyses indicate low levels of diagenetic alteration in some of the enamel samples, which is not expected to affect the Sr isotopic compositions. The addition of environmental baseline sample results, collected from around the archipelago, will aid in establishing local baseline values and placing these individuals in more localized context.

This research was supported by a Wenner Gren Foundation Dissertation Fieldwork grant (Gr. 9104), NSF DDRIG (BCS-1848513), the Edna English Foundation for Archaeological Research, and the UO Global Studies Institute.

DNA methylation patterns in children maternally exposed to extreme drought

BILINDA STRAIGHT¹, GEORGIANA FISHER², BELINDA NEEDHAM³, JAESEONG HWANG², CHARLES E. HILTON⁴, CHARLES OWOUR OLUNGAH⁵, AMY NAUGLE⁶, STEPHANIE M. HAFT⁶, CAROLINE S. KELEMPU⁵, SAMAN LESEELA¹, DANIEL LESEELA¹ and CELINA JESKA¹

¹Gender & Women's Studies, Western Michigan University, ²Statistics, Western Michigan, ³School of Public Health, University of Michigan, ⁴Anthropology, University of North Carolina Chapel Hill, ⁵Institute of Anthropology, Gender, & African Studies, University of Nairobi, ⁶Psychology, Western Michigan University

A growing multi-disciplinary literature links famine exposure in utero to metabolic, cognitive, and emotional outcomes across the life course, including evidence that DNA methylation plays a mediating role. Studies to date typically examine the effects of singular moments of extreme nutritional deprivation (e.g., Dutch Famine of 1944-45 or Chinese Famine of 1959-1961) that contrast sharply with the usual diets and everyday lived experiences of individuals in those populations. Yet, climate change is increasing the frequency of extreme drought events in regions prone to them. Thus, understanding the human experiential and broad health impacts of extreme drought in conditions of chronic, rather than singular, resource scarcity is important on humanitarian grounds in addition to its value for anthropology and other disciplines. In 2009, an extreme drought in northern Kenya decimated livestock, creating hunger that attracted international attention. Here

we report findings of our multi-disciplinary study comparing Samburu pastoralist children exposed to the 2009 drought in their first trimester of gestation to unexposed same-sex siblings. Previously we reported qualitative dimensions of mothers' 2009 experiences and child anthropometric outcomes. For this paper, we report our first EWAS (epigenome-wide association study) results: In comparing drought-exposed children (N=105) to same-sex sibling controls (N=108) (adjusting for age, sex, and cell type covariates), we found significant differences in DNA methylation at 1,309 CpG sites after correction for multiple testing. We consider how the ethnographic and molecular signatures of extreme drought mutually reinforce one another and ask how to distinguish between coping, adaptation, thriving, and failure.

National Science Foundation Award #1728743, "A Bio-Cultural Investigation of Intergenerational Epigenetic Mechanisms" and Western Michigan University Faculty Research & Creative Activities Award

Tool specialization in human cultures: modeling the effects of demography and environmental change on cultural repertoire size

SARAH SAXTON STRASSBERG¹, OREN KOLODNY² and NICOLE CREANZA³

¹Biological Sciences & Medicine, Health, and Society, Vanderbilt University, ²Department of Ecology, Evolution, and Behavior, A. Silberman Institute of Life Sciences at the Hebrew University of Jerusalem, ³Biological Sciences, Vanderbilt University

For millennia, behaviorally modern humans have participated in task specialization for biological, socioeconomic, and cultural reasons. However, humans are not alone in this regard; Neanderthals likely specialized, and some bees, ants, fish, and spiders delegate tasks to certain groups of individuals. Many studies suggest that specialization is a crucial aspect of technological advancement. However, if tools or skills known by few individuals are more likely to be forgotten, specialization also creates a paradox in which innovation is more common but specialized innovations may have a higher probability of being lost. In this study, we build on a computational model (Creanza, Kolodny, Feldman J. Roy. Soc Interface 2017) to examine the varying levels and types of task specialization in human populations (guild-like groups, division of labor by sex, etc.). We then assess when these types of specialization are beneficial, neutral, or deleterious to a population's overall tool repertoire size in relation to the output of generalist populations. We find that environmental change is detrimental to tool repertoire complexity, regardless of level of specialization, but when there are one or more specialized subpopulations present, environmental change inhibits tool accumulation more than it does in a generalist population. In addition, we find that

ABSTRACTS

increased relative size of specialized subpopulations leads to decreased overall tool repertoire size. A high tool loss rate is also detrimental to specialized populations' productivity, whereas a high tool innovation rate is critical to specialized subgroups' success. These results elucidate the mechanisms of the evolution of specialization in human populations.

The Contributions of Eric Delson before NYCEP

M. ELIZABETH STRASSER

Anthropology, CSU, Sacramento

During the first segment of his career as a vertebrate paleontologist Eric Delson set the current paradigm for our understanding of the Old World monkey fossil record and their evolution, laying the foundation for most of the current debates on the subject, including the larger geological and environmental contexts around the origins of their major subclades.

He also was among the first to directly study material from both eastern and southern Africa and synthesize them into a coherent continent-wide biozonation for Africa that is still in use today. Less well-known was his influence in organizing the *Ancestors: the hard evidence* symposium at the American Museum of Natural history in 1984 that brought nearly all the then known hominid fossils together in one place.

Motif and occlusal fingerprint analyses reveal sex-specific molar wear patterns in western chimpanzees

JULIA STUHLTRAEGER^{1,2}, ELLEN SCHULZ-KORNAS^{1,2,3}, OTTMAR KULLMER^{4,5}, MARCEL JANOCHA⁵, ROMAN M. WITTIG^{6,7} and KORNELIUS KUPCZIK^{1,2,8}

¹Max Planck Weizmann Center for Integrative Archaeology and Anthropology, Max Planck Institute for Evolutionary Anthropology,

²Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology,

³Department of Cariology, Endodontology and Periodontology, University of Leipzig, ⁴Department of Palaeoanthropology, Senckenberg Research Institute, ⁵Department of Paleobiology and Environment, Institute of Ecology, Evolution, and Diversity, Goethe University Frankfurt,

⁶Department of Primatology, Max Planck Institute for Evolutionary Anthropology, ⁷Tai Chimpanzee Project, Centre Suisse de Recherches Scientifiques Côte d'Ivoire, ⁸Departamento de Antropología, Facultad de Ciencias Sociales, Universidad de Chile

Dental topography and macroscopic tooth wear have been shown to distinguish between the various feeding ecologies and behaviors in primates. However, it remains unclear whether intraspecifically males and females with distinct dietary preferences can also be separated based on the above.

Here, we investigated the molar occlusal surfaces in young adult male (n=5) and female (n=8) western chimpanzees (*Pan troglodytes verus*) from the Ta-ó National Park population (Ivory Coast). On 3D models generated from μ CT-scans of moderately worn upper first and second molars we used motif analysis (MA) and occlusal fingerprint analysis (OFA) to quantify the cusp geometry and the inclination of wear facets, respectively.

MA revealed that females had larger hypocone tip-radii on the upper first molars than males, while there were no geometric differences between the sexes in the other cusps. OFA showed that the laterorotative (lingual phase I) and mediotrusive (phase II) wear facets of the power stroke have a steeper inclination in males compared to females.

Due to reported dietary preferences between the sexes our results suggest that females are exposed to higher molar wear rates than males. It is possible that this may be related to a higher amount of abrasive particles in the diet of females and/or distinct chewing movements. Moreover, higher nutritional needs during pregnancy and lactation might require higher chewing rates.

We conclude that MA and OFA provide insights into sex-specific dietary behavior within this particular chimpanzee population, and therefore are promising tools for studying intraspecific variation within extant and extinct primates.

This research was funded by the Max Planck Society.

Dental Occlusal Form and Function in *Equus capensis*: Evaluating a Controversial Taxonomic Status

DEANO D. STYNDER, MEGAN M. MALHERBE and REBECCA R. ACKERMANN

Archaeology, University of Cape Town

The extinct Giant Cape Zebra *Equus capensis* is characterised as a relatively long-lived species that persisted throughout the Middle-to-Late Pleistocene in South Africa, covering an important time in hominin evolution. This large equid is recorded at a variety of sites relevant to hominins; understanding these palaeoenvironments provides a framework for understanding human ecosystems. *Equus capensis* is typically described as a large-bodied equid with an occlusal enamel morphology that distinguished it from other contemporary equids. It is important to understand the taxonomic status of *E. capensis*, and especially whether multiple, unrecognized, and potentially ecologically diverse species are represented. Here we investigate occlusal enamel form and function to evaluate the taxonomic status of *E. capensis*, and explore its associated palaeoenvironmental conditions across South African sites (Elandsfontein, Swartkrans, Makapansgat, Gladysvale, Cave of Hearths, and more).

Geometric morphometric analysis was used to quantify occlusal enamel pattern in 117 fossil equid cheek teeth. A sample subset was also used to evaluate levels of enamel complexity to determine habitat preference and palaeo-vegetation. Additionally, a total of 550 dental specimens encompassing eight equid taxa were measured using linear measurements to evaluate overall dental size variation. Finally, mesowear analysis was performed to evaluate dietary regimes, and by extension site palaeoenvironments. No significant morphological or functional differences were found between teeth identified as *E. capensis* and those identified to other fossil equid species, placing the taxonomic status of *E. capensis* in doubt (as in aDNA studies), and suggesting that palaeoenvironmental reconstructions of these hominin sites may be flawed.

This project was funded by the National Research Foundation, the University of Cape Town and the UCT Vice-Chancellor's Research Scholarship.

Potential for extended paternal investment in a polygynadrous primate (*Papio anubis*)

VERONIKA STÁDELE¹, EILA K. ROBERTS^{1,4}, LINDA VIGILANT³, SHIRLEY C. STRUM^{5,6,7,8} and JOAN B. SILK^{1,2}

¹School for Human Evolution and Social Change, Arizona State University, ²Institute of Human Origins, Arizona State University, ³Department of Primatology, Max Planck Institute for Evolutionary Anthropology, ⁴Department of Integrative Biology, Michigan State University, ⁵Department of Anthropology, University of California San Diego, ⁶Uaso Ngiro Baboon Project, ⁷Kenya Wildlife Service, ⁸African Conservation Centre

It is unclear how pair-bonds and paternal care may emerge evolutionarily from non-pair-bonded societies. In the polygynadrously mating multi-male-multifemale groups of savanna baboons, adult males form special bonds (primary associations, friendships) with lactating females. These associations are preferentially formed with the sires of the females' infants and likely benefit infants via protection from infanticide or harassment. However, not all sires become primary associates of their infants' mothers and not all primary associates are sires of the females' infants. It has been suggested that these mismatches might represent kin recognition errors and that cues of paternity are somewhat unreliable. We collected behavioural data on 26 adult females and genetically determined paternity for 55 of their infants. We found that sires interacted more with the mother during her conceptive cycle than non-sires but whether these males later became primary associates or not was independent of their behaviour around the likely time of conception. This suggests that males are not mistaken about paternity but become primary associates for other reasons. We further found that being the sire of the female's previous infant strongly increased a male's probability of

ABSTRACTS

being the female's primary associate independent of whether he was also the sire of the current infant. However, the effects were additive; males who were sires of the previous and the current infant were most likely to become primary associates. Our findings are consistent with prolonged paternal investment indicating that paternal care could lead to extended pair-bonds in this polygynandrously mating species.

This research was supported by Arizona State University, the Humboldt Foundation, the Max Planck Society, the African Conservation Centre and the Dutch Ministry of Foreign Affairs (DGIS).

Accelerated epigenetic ageing and altered stability of DNA methylation detected in adult British-Bangladeshi women exposed to elevated infectious disease loads in childhood

REINHARD STÄGER¹, GREGORY LEEMAN¹, MINSEUNG CHOI², RICHARD D. EMES³, KHURSHIDA BEGUM⁴, PHILIPPA MELAMED⁵ and GILLIAN R. BENTLEY⁴

¹School of Biosciences, Nottingham University, UK, ²Neurosciences Program, Stanford University, USA, ³Advanced Data Analysis Centre, Nottingham University, UK, ⁴Department of Anthropology, Durham University, UK, ⁵Faculty of Biology, Technion-Israel Institute of Technology

Adult British-Bangladeshi females consistently show variation in their reproductive phenotype, depending on where they grew up: Bangladesh or the UK. A childhood spent in Bangladesh, exposed to elevated infectious disease loads, is associated with a shortened reproductive life span. In contrast, childhood in the UK is associated with an earlier age at menarche, increased adult levels of reproductive hormones, and a later age of menopause. We used buccal swab DNA to investigate if the childhood developmental environment is reflected by age-estimates of epigenetic clocks. Women who grew up in Bangladesh (n=15) had a mean epigenetic age of 35.6 years, significantly older than their mean chronological age (30.5 years, Pearson $r=0.61$, $p=0.02$). In contrast, women who developed in the UK (n=11) had a mean epigenetic age of 25.6 years, making them 1.5 years younger, on average, than their mean chronological age of 27.1 years. We further investigated the stability of epigenetic information at the luteinizing hormone receptor (*LHR*) locus, containing one of the CpG sites contributing to Steven Horvath's multi-tissue epigenetic clock. Our data suggest that a childhood in Bangladesh leads to increased stability of DNA methylation at the *LHR* locus. This CpG 'clock' site has diminished capacity to respond to current and future environmental information in buccal cells of women who grew up in Bangladesh. Our study indicates that

the childhood environment influences the tick-rate of the epigenetic clock. It also demonstrates the suitability of the buccal cell methylome for epigenetic age estimates using cross-sectional studies.

Supported by an ESRC-BBSRC Grant to GB, PM and RS (MR/T017007/1).

Cultural Change, Stress, and Mental Health in Palau, Micronesia.

ROGER SULLIVAN

Anthropology, California State University, Sacramento

Men in the Republic of Palau, Micronesia, experience high rates of mental illness. Extensive research has shown that biological markers of illness are comparable to those elsewhere, ruling out a biological etiology particular to the indigenous population. This study tests a hypothesis that economic transformation from traditional subsistence to a money economy have upended gendered cultural roles, and have been particularly stressful for young men.

A sample of 69 Palauans (47 men and 22 woman) with a major mental illness diagnosis were assessed for symptoms, and were self- and externally-rated as to their gendered "role identity" and "role performance" in Palauan cultural practices and duties. Non-parametric ANOVA showed significant negative correlations between ratings of cultural performance and symptoms of mental illness, and were most pronounced among young men.

Indigenous Palauan life includes rule-bound participation in material reciprocity through structured cultural activities and events. Contemporary social status for young men follows from successful participation in customary reciprocity and in the "new" money economy. An inversion of occupational status has accompanied economic transformation such that formerly high-status roles like "fisherman" are now only practiced by those without money employment. Men experiencing mental illness are more likely to be engaged in the subsistence economy, and to struggle with the social and material demands of traditional reciprocal obligations. Our results indicate that high social competence required to satisfy customary obligations, coupled with a recent inversion in traditional male occupational roles has been particularly stressful for young men vulnerable to mental illness.

Funded in part by the Stanley Medical Research Institute (Bethesda MD)

Mitogenome analysis of the elite individuals interred in the House of the Dead complex at Paquimé (Casas Grandes), Mexico

RACHEL SUMMERS-WILSON MA¹, DR. MERADETH SNOW¹ and DR. MICHAEL SEARCY²

¹Anthropology, University of Montana, ²Anthropology, Brigham Young University

This research project investigates the elite population interred in The House of the Dead at the archaeological site known as Paquimé (Casas Grandes), Mexico during the Medio Period (1200 - 1450 A.D.). The subfloor tomb contains the remains of at least 12 individuals, as well as possibly two high ranking individuals. The nature of some of the burials suggests they may be sacrifices of non-locals. Whole mitogenomes have been extracted from many of the individuals from the Paquime site. Haplogroups were determined for several of the individuals, and the results revealed several of the Amerindian mitochondrial lineages A, B, and C. By combining mortuary treatment, archaeological and whole mitogenome analysis to this rich and elaborate burial is not only a means of looking at the maternal relationship that exist between the different interments, but it will also give us a better understanding of various elements of past social organizations, and may mark inequality including prestige, rank and power, and how this was expressed in Mesoamerican and Southwestern elites.

This project is funded by a National Science Foundation Grant

Foot-binding women skeletons from the Qing Dynasty Xifengbu cemetery, Hongtong, Shanxi Province, China

XIAOFAN SUN¹, XINGYU MAN¹, XUEZHU LIAO¹, TING GAO¹, YE FEI¹, LINGYU AN¹, QUANCHAO ZHANG¹ and QIAN WANG²

¹School of Archaeology, Jilin University, ²Department of Biomedical Sciences, Texas A&M University College of Dentistry

Foot-binding, lasting around 1,000 years in China, was an infamous custom of the Han Chinese people used to modify the size and shape of feet in women. Binding started at a very young age and gradually deformed the natural growth of the feet, which was not only a painful process but also a lifetime source of inconvenience and morbidity. In this study, we report numerous skeletons with signs of foot-binding bones excavated from the Xifengbu cemetery, located in Hongtong County at the Shanxi Province in China. Funeral goods and epitaphs indicate that this cemetery belonged to the Qing Dynasty (1644-1911 CE). A total of ninety-three female individuals at Xifengbu who came from two feudal families were found, out of which seventy-four had foot-binding while nineteen were free of the tradition. All foot-binding was identified by type as *Talipes Calcaneus*.

ABSTRACTS

Compared to the non-foot-binding group at Xifengbu, the overall size and robustness of the bones in the leg of the foot-binding group were smaller, indicating a weaker leg musculoskeletal system affecting locomotion and physical activities, as well as an increased risk of fall and injuries. Even though the practice was prevalent, this is for the first time a large group of foot-binding skeletal remains was found in an archaeological site. An in-depth study will not only enrich our knowledge of the foot-binding practice in ancient China, but also shed light on how this gender-biased custom might have compromised the health and quality of life for women in pre-modern societies.

Microbial communities as mediators of disease, malnutrition, and growth in Highland Peru

CLARE SUPER¹, MORGAN K. HOKE¹, SAHANA KUTHYAR² and KATHERINE AMATO²

¹Anthropology, University of Pennsylvania,

²Anthropology, Northwestern University

Early researchers of infant growth in the Peruvian Highlands posited that reduced growth represented an adaptation to chronic hypoxia. Subsequent research has demonstrated the role of disease and malnutrition, both consequences of socioeconomic inequality. Malnutrition stemming from reduced gut function has been distinguished as a mechanism of growth stunting, with focus on intestinal morphology shifts from oral/fecal contamination. New data suggests that altered microbiomes, caused by undernourished diets, chronic diarrhea, and/or disrupted paths of acquisition may also be a factor in stunting. This study uses microbiome data collected from infants (n= 19) in the high-altitude site of Nuñoa, Peru in association with data on growth, nutrition, and infectious symptoms to examine the role of the microbiome as a mediator of the effects of diet and disease on growth. Beta diversity was assessed with unweighted Unifrac distances (UUF) in QIIME. Differences in sample clustering patterns and microbial community composition were evaluated with variables using permutational analysis of variance. Significant or close to significant differences were detected in association with infant age ($R^2 = 0.2$, $P = 0.001$ ***), type of milk consumed ($R^2 = 0.104$, $P = 0.042$ *), infectious symptoms ($R^2 = 0.124$, $P = 0.016$ *), diarrhea frequency ($R^2 = 0.117$, $P = .02$ *), and height-for-age z-scores (HAZ) ($R^2 = 0.123$, $P = 0.05$). These associations suggest that consideration of the role of the microbiome may be necessary to truly understand the determinants of growth in this population. Microbiomes may be key to understanding energy allocations lost to both metabolic dysfunction and combating infection, as opposed to growth, that result in stunting.

Funding was provided by the Anthropology Department and The Penn Museum of Archeology and Anthropology at the University of Pennsylvania.

Distinct early growth trajectory among Daasanach pastoralists of Northern Kenya

ZANE S. SWANSON¹, HILARY BETHANCOURT², JESSICA SAUNDERS¹, ROSEMARY NZUNZA³, ASHER Y. ROSINGER^{2,4} and HERMAN PONTZER^{1,5}

¹Evolutionary Anthropology, Duke University,

²Biobehavioral Health, Pennsylvania State University,

³Kenya Medical Research Institute, (KEMRI), ⁴Anthropology, Pennsylvania State University,

⁵Global Health Institute, Duke University

Dependence on growth references derived primarily from industrialized populations often ignores variation in growth patterns that exists in small-scale populations. Here we used weight and height measures collected by local health workers to estimate growth trajectories among a cross-sectional sample of 899 male and 856 female pastoralist Daasanach children (ages 0-5yrs) living across nine communities in northern Kenya. We tested whether growth velocities vary across different Daasanach communities or differ from WHO (2006) standards. Compared to WHO standards, 63% of male and 58% of female Daasanach children are deemed to be "wasted", having a z-score < -2.0 weight-for-height. Prevalence of "underweight", a z-score of < -2.0 for weight-for-age, is $\sim 41\%$ for males and $\sim 31\%$ for females. Rates of "stunting", a z-score of < -2.0 for height-for-age, are lower at $\sim 11\%$ for males and $\sim 4\%$ of females. Notably, height velocities for 2-4 yo Daasanach males (1.03 cm/month) and females (1.02 cm/month) are nearly twice those of WHO standards of 0.67 and 0.70 cm/month, respectively. Daasanach weight velocities among this age range are also elevated (Daasanach males = 0.22 kg/month, WHO males = 0.17 kg/month | Daasanach females = 0.21 kg/month, WHO females = 0.19 kg/month), but weight-for-height is not. Additionally, weight-for-height was 1.1 z-scores higher for males ($p > 0.001$; $SE = 0.24$) and 0.49 for females ($p = 0.03$; $SE = 0.23$) between the most distinct communities. Together, these results indicate a distinct growth pattern among Daasanach children. We discuss the implications of these findings for understanding variation in human life history strategies and growth responses to local ecology.

NSF ARCH #1624398; NSF REU #1930719; This work was funded by the PSU SSRI Human Health and Environment Seed Grant, and the Triangle Center for Evolutionary Medicine (TriCEM) Graduate Research Grant.

Craniodental correlates of feeding within *Papio* and the interpretation of hominin behavior

LARISSA SWEDELL^{1,3,4}, SHAHRINA CHOWDHURY^{2,3,4}, LUKE D. FANNIN⁵, DAVID J. DAEGLING⁶ and W. SCOTT. MCGRAW⁷

¹Anthropology, Queens College, CUNY,

²Anthropology and Archaeology, Brooklyn College,

CUNY, ³Anthropology Program, City University

of New York Graduate Center, ⁴New York

Consortium in Evolutionary Primatology (NYCEP),

⁵Anthropology, Dartmouth College, ⁶Anthropology, University of Florida, ⁷Anthropology, The Ohio State University

Members of the genus *Papio* have long been used as models for hominin evolution. Although our understanding of the behavioral and ecological diversity within *Papio* has grown dramatically in recent years, most scholars still tend to rely on "savanna" (olive, yellow, and chacma) baboons for their hominin analogs. Here we offer new data on the lesser-known hamadryas baboon (*Papio hamadryas*) and examine the extent that craniodental features routinely used to reconstruct diet and feeding in hominins covary with ecology. The dry and low-quality habitats of hamadryas are argued to have selected for numerous behavioral (large home ranges, increased travel) and physiological (enhanced ability to cope with water deprivation) adaptations to aridity. Here we extend this line of inquiry and hypothesize that hamadryas foods, in addition to being sparsely distributed, present significant mechanical challenges. We explore potential morphological correlates of the hamadryas foraging context via a comparative analysis of tooth proportions, mandibular dimensions, and enamel chipping in several papionin taxa. Our results indicate, firstly, that hamadryas females have more molarized premolars than other baboon females, but males do not. Secondly, initial comparisons reveal narrower mandibular arch widths and larger symphyses in hamadryas, which plausibly reflect greater bite force capacity. Finally, a 15% frequency of chipped teeth in hamadryas is lower than other papionins, but similar to australopithecines, suggesting comparable dental trauma. These results highlight the importance of considering the breadth of variation within *Papio* – including ecological outliers such as *P. hamadryas* – when using baboons to infer hominin behavior.

Estimating hip muscle forces during walking using musculoskeletal modeling

ADAM D. SYLVESTER¹, STEVEN G.

LAUTZENHEISER^{2,3} and PATRICIA A. KRAMER^{2,3}

¹Center for Functional Anatomy and Evolution,

The Johns Hopkins University School of Medicine,

²Department of Anthropology, University of

Washington, ³Department of Orthopaedics and

Sports Medicine, University of Washington

Critical in evaluating the structural capacity of femora is a well-supported understanding of lower limb forces, including forces generated by muscles during locomotion. Earlier analyses within anthropology relied heavily on a model of walking that was based on single-limb standing and used to represent all of stance phase. The present study compares these earlier estimates of hip muscle forces to those generated using a musculoskeletal model of walking.

ABSTRACTS

An eight-camera Qualisys system with four Kistler force plates were used to collect kinetic and kinematic data from 10 unshod participants walking at a self-selected normal speed. Using an established OpenSim model (LowerLimb2010), we estimate forces for muscles that span the hip through the stance phase of walking. First, the model was scaled based marker data (segment lengths) and the mass of each subject. Inverse kinematic and dynamic analysis were used to generate model motion based on measured gait variables. We used the static optimization algorithm to estimate muscle forces. To make our values comparable to earlier estimates, we calculate the sum of the hip abductor muscle forces in anatomical planes.

We find that while earlier estimates for vertical and mediolateral hip forces during midstance are similar to those produced by the model, hip forces are higher at points earlier and later in the stance phase. Further, the anteroposterior component of hip muscle forces is of equal magnitude (~300N) to the mediolateral component. Our results mandate a reevaluation of the impact of hip mechanics on femoral morphology across hominin evolution.

Mental Health is Biological Health; why tackling 'diseases of the mind' is an imperative for biological anthropology in the 21st century

KRISTEN L. SYME and EDWARD H. HAGEN
Anthropology, Washington State University

During the 20th century, biomedicine rapidly reduced the global burden of infectious disease. In the 21st century, non-infectious diseases, including mental disorders, are responsible for most of the disease burden. The causes of mental disorders, however, are mysterious, and many pharmacological treatments have only moderate to weak efficacy, lack precision in targeting biological systems that underlie symptoms, and/or induce debilitating side effects. Critics from within psychiatry are calling attention to the failure of psychiatric research to improve public health and to rampant conflicts of interest that bias the research. There is an urgent need for a broader, more integrative approach to the study and treatment of mental disorders that incorporates cross-cultural data and evolutionary theory.

Anthropology, especially biological anthropology, can offer critical theoretical and empirical insights to combat mental illness globally. Biological anthropologists are unique in that we take a panhuman approach to human health and behavior and are trained to address each of Tinbergen's four levels of analysis as well as culture.

Using Brainstorm data, we present a provisional schema for conceptualizing mental disorders based on population prevalence, heritability, age of onset, and evidence for dysfunction. Highly heritable and rare conditions, such as schizophrenia, are likely the product of mutational load; common conditions with low heritability, such as anxiety and depression, are likely adaptive defenses; conditions of old age are likely best explained by evolutionary theories of senescence.

This presentation corresponds to a paper currently in revision for the 2019 Yearbook of Physical Anthropology.

Does sexual dimorphism in the gorilla scapula vary with altitude?

MAYA SZAFRANIEC¹ and REBECCA S. JABBOUR²
¹Anthropology, University of California, Santa Barbara, ²Biology, Saint Mary's College of California

Gorillas live at a wide range of altitudes, with taller trees and more tree fruits at lower altitudes. Observations suggest that lower-altitude gorillas are more arboreal and female gorillas spend more time in trees than males. Our previous work identified altitude-related variation in the gorilla scapula, which includes attachments for muscles used in climbing. In this study, we tested the hypothesis that sexual dimorphism in scapula shape is greater at lower altitudes. We collected 3D landmarks from the scapulae of 174 gorillas, including *Gorilla beringei graueri* (low and high altitude), *G. b. beringei* (very high altitude), and *G. gorilla gorilla* (low altitude). Linear measurements of the coracoid process, acromion process, supraspinous fossa, and infraspinous fossa were calculated, size-adjusted, and analyzed using univariate and multivariate statistics. Within *G. beringei*, discriminant function analysis found sexual dimorphism to be greatest within low-altitude *G. b. graueri* and least within *G. b. beringei*, as predicted; however, separation between male and female *G. g. gorilla*, at low altitude, was between that of high-altitude *G. b. graueri* and *G. b. beringei*. In univariate analyses, the acromion process was consistently dimorphic and showed greater dimorphism at lower altitudes, but it was relatively larger in males, although males are less arboreal. The supraspinous fossa showed a similar pattern in *G. beringei*. Sexual dimorphism in scapula shape varies across altitudes and taxa in gorillas, but this variation may reflect factors other than habitat and locomotion. These findings have implications for interpreting variation in the hominoid fossil record.

Wenner-Gren Foundation, Leakey Foundation, Sigma Xi, City University of New York, New York Consortium in Evolutionary Primatology, and Saint Mary's College Faculty Research Grant.

Rudimentary and non-rudimentary metapodials differ in developmental constraint in length

ROBERT G. TAGUE

Geography and Anthropology, Louisiana State University

Rudimentary structures are hypothesized to be more variable in size and shape than non-rudimentary homologues. Among primates, *Colobus guereza* either lacks a pollex or has a non-functional nubbin. Correspondingly, its first metacarpal (mc1; metatarsal=mt) is rudimentary in length compared to its non-rudimentary mc2-mt5. This study considers whether the correlation in length between left and right mc1s in *Co. guereza* is lower than the correlations between the bilateral pairs for mc2-mt5. Six other species with functional pollices are included in the study. Species and sample sizes are *Co. guereza* (12 mc, 16 mt), *Chlorocebus aethiops* (12 mc, 12 mt), *Hylobates lar* (18 mc, 16 mt), *Lagothrix lagotricha* (11 mc, 12 mt), *Pan troglodytes* (20 mc, 25 mt), *Papio cynocephalus* (24 mc, 27 mt), and *Pongo pygmaeus* (11 mc, 12 mt); samples include wild caught and captive specimens. Maximum length of metapodials was measured. Results show that Spearman's correlation coefficient between lengths of left and right mc1 is 0.752 in *Co. guereza*, which is significantly lower than the correlations for the bilateral pairs of mc2 and mc4-mt5, and is non-significantly lower than the correlation for mc3. Among the 70 correlations between bilaterally paired metapodials among the seven species, the lowest correlation is for mc1 in *Co. guereza*; extreme values for the other 69 correlations are 0.876 (mt1, *H. lar*) and 1.000 (mt4, *Ch. aethiops* and *Po. pygmaeus*). Results suggest less developmental constraint in length between the bilateral pair of a rudimentary metapodial compared to its non-rudimentary homologues.

Putting it on display: The musculoskeletal consequences of large gapes in male Old World monkeys

ANDREA B. TAYLOR¹, CLAIRE E. TERHUNE², MARK F. TEAFORD³, CALLUM F. ROSS⁴ and CHRISTOPHER J. VINYARD⁵

¹Basic Science, Touro University, ²Anthropology, University of Arkansas, ³Basic Science, Touro University, ⁴Organismal Biology and Anatomy, University of Chicago, ⁵Anatomy and Neurobiology, NEOMED

Old World monkeys (OWMs) are sexually dimorphic and engage in intrasexual competitive displays involving relatively large jaw gapes. Based on previous findings for catarrhines, we hypothesize that male OWMs should have musculoskeletal features of the masticatory apparatus that facilitate wide-mouth gape display behaviors. To test this hypothesis, we evaluated correlations among jaw length, maximum jaw gape, canine height and gape-related musculoskeletal variables

ABSTRACTS

(jaw-adductor fiber lengths and TMJ curvature) in a sample of 22 OWM species. We predicted that these features would be i) significantly correlated in males, and ii) more strongly correlated in males compared to females.

PGLS analyses demonstrate that in males, jaw gape, canine height and jaw length are highly and significantly correlated with each other (r ranges between 0.85-0.91; $p < 0.001$) and with superficial masseter and temporalis fiber lengths (r ranges between 0.82-0.90; $p < 0.01$). In females, only gape and jaw length are significantly correlated ($r = 0.80$; $p = 0.0001$). Alternatively, estimates of glenoid and condylar AP arc lengths (TMJ curvature) are highly and significantly correlated with jaw length and gape in both males and females. However, in all cases these features are more strongly correlated in males. Thus, overall, males show higher and more frequently significant correlations than females. As pertains to canine display behavior, several of these features are also correlated with canine height, more so in males than females. Collectively, these findings suggest that sexual selection for gape and canine-display performance in male OWMs have significantly impacted feeding-system musculoskeletal morphology in this clade.

This work was supported by grants from the NSF (BCS 0452160, BCS 0962677 and BCS 0752661) the NIH (R24 HD050837-01) and the Leakey Foundation.

Phenotypic covariance in modern human limbs

CATHERINE E. TAYLOR and MARIANNE F. BRASIL
Integrative Biology, University of California, Berkeley

The evolution of modern human limb proportions is an area of much interest in biological anthropology. Researchers have identified numerous sources of variation in limb length and relative inter- and intra-limb proportions, including nutrition, sexual dimorphism, thermoregulation, geographic ancestry, and locomotion. Additionally, researchers have approached the many questions about human limb proportions by utilizing analyses of correlation matrices, variance-covariance matrices, inter- and intra-limb indices, and simple linear measurements. In this study, we investigate the limb proportions of 232 modern human individuals from five different populations (South Africa, Jordan, Egypt, Portugal, and Native California). Specifically, we explore the bones of the shoulder girdle, stylopod, zeugopod, and autopod. This study analyzes correlation and covariation to explore relative limb proportions and sexual dimorphism in these five populations of modern humans. Results show a stronger correlation between adjacent limb bones in the leg than in the arm, and stronger inter-limb correlation between proximal limb segments when compared to distal limb segments. There

is some variation between populations, with the Portuguese sample exhibiting relatively shorter radii and longer humeri, resulting in a notably lower brachial index than the other populations. The sample also exhibits statistically significant ($p < .05$) levels of sexual dimorphism in relative hand size and brachial index, but not in relative foot size or crural index. These results support the hypothesis that decreased integration between the arms and legs and reduced constraint within the arms results in greater variation of arm proportions within and between populations.

Data collection was supported by NSF DDRIG-1732221 and the Portuguese Studies Program at UC Berkeley.

Orange is the Old Black: A Bayesian Phylogenetic Analysis of Primate Natal Coats

PARKER M. TAYLOR¹ and CHRISTOPHER OPIE²
¹Department of Anthropology, University of Arkansas, ²Department of Archaeology and Anthropology, University of Bristol

Primate pelage is thought to reflect the importance of sociological functions in regard to sex rather than avoiding predation. It is still unknown whether natal coat colors are involved in sexual selection or if they have their own socioecological role in primate groups. Using Bayesian phylogenetic comparative methods in order to determine the evolutionary driver behind primate natal coats, the goal of this study is to test three hypotheses: the allomothering hypothesis, the infant defense hypothesis, and the paternity cloak hypothesis. Primate natal coat data was collected using digital photographs of mother-infant pairs for 167 species of primates. Additional trait data, such as infanticide, allomothering, and mating system were collected from the literature. Ancestral states for each trait were estimated and then trait pairs were tested using discrete phylogenetic analysis in order to determine which traits, if any, experience correlated evolution. The results of this study show that allomothering and polygyny, the mating system that best supports the infant defense hypothesis, evolved after natal coats had arisen in the primate order. This means that natal coats could not have evolved to signal any individual for extra care or protection. There is, however, strong support for correlated evolution between natal coats and infanticide as well as between natal coats and polygyny. This gives credence to the paternity cloak hypothesis and suggests that infantile coloration in primates plays a role in sexual selection by obscuring paternal heritage, thus reducing paternity certainty and infanticide risk.

Navigating identity: The intersection of social and biological identity from the World War II Battle of Tarawa

REBECCA TAYLOR¹ and BRIANA NEW^{1,2}

¹Scientific Analysis, Defense POW/MIA Accounting Agency, ²Anthropology, SNA International

The 1943 Battle of Tarawa resulted in approximately 6,000 casualties (~1000 U.S. Marines and Sailors, ~4000 Japanese combatants, and ~1000 Korean laborers) on, or around, Betio Island. Of the ~1000 U.S. losses, ~400 service members are still unaccounted for and are the focus of the Defense POW/MIA Accounting Agency's (DPAA) identification efforts. Anthropologists encounter many challenges in the identification of these decedents including vastly commingled remains, as well as incomplete and inconsistent historical documentation. Thus, multiple lines of evidence, both biological and historical, are important for solidifying identifications. Inconsistency between modern definitions of identity and those prescribed during the 1940s create an additional layer of complexity when scientifically derived biological lines of evidence and historical documentation are incongruent.

This presentation explores the complexities of identity through three case examples in which skeletal and genetic analyses present conflicting results, associated material evidence indicates a cultural affiliation that is inconsistent with the historical documentation, and where complex indicators of identity are not represented in historical documentation. The demographic (e.g., biological profile, geographical origin, and/or genetic) data for Battle of Tarawa losses (both unidentified and identified) highlight the difficulties of identification when relatively homogenous indicators of identity (98% "Caucasian" and 78% 17-23 years old) are the basis for analysis, as well as serves to demonstrate how the DPAA has navigated these issues. The identification process, like all anthropology, is inherently context specific and it is imperative for anthropologists to consider historical perceptions of identity when working in military, cold case, and humanitarian contexts.

Functional relationships between estradiol and paternal care in wild red-bellied lemurs

STACEY R. TECOT^{1,2}, MADALENA BIRR^{2,3} and ANDREA L. BADEN^{4,5,6}

¹School of Anthropology, University of Arizona, ²Laboratory for the Evolutionary Endocrinology of Primates, University of Arizona, ³Department of Ecology and Evolutionary Biology, University of Arizona, ⁴Department of Anthropology, Hunter College, ⁵The Graduate Center, City University of New York, ⁶New York Consortium in Evolutionary Primatology

The mechanisms facilitating paternal care are not as well understood as they are in mothers. A growing body of research suggests that several

ABSTRACTS

hormones change as males transition into parenthood, first in response to his partner's pregnancy, then in response to interacting with the newborn. Estradiol increases in expectant men and tamarin fathers, and is higher in fathers than non-fathers. But, it is unknown whether short-term changes are associated with individual behavioral variation. Pair-living red-bellied lemurs have facultative paternal care. We predicted 1) estradiol metabolites (E2) elevate in expectant fathers, and 2) E2 varies with paternal behavior. We collected fecal samples and behavioral data from 9 fathers from conception-weaning, and ran generalized linear mixed-effect models in R (lme4 package) including E2 as the dependent variable, individual nested within year as random effects, and infant age and measures of paternal care as fixed factors. We ran models with five paternal care behaviors, and with a composite measure (Total Care). E2 increased four-fold in expectant fathers. Paternal care did not predict E2; only infant age did (with care behaviors: $\beta=-89.15$, $SE(\beta)=29.45$, $z=3.03$, $p<0.001$; with Total Care: $\beta=-82.49$, $SE(\beta)=32.74$, $z=2.159$, $p=0.011$), reflecting a decrease in E2 once infants were born. Red-bellied lemur fathers respond to their mate's pregnancy with E2 elevations which begin returning to baseline after parturition. These changes could prepare males for fatherhood, but short-term changes are not associated with behavior. Because adipose tissue produces estradiol, weight gain associated with Couvade Syndrome (as in humans and tamarins) might mediate these changes.

Supported by The Leakey Foundation, AAPA Professional Development Grant, Rowe/Wright Primate Fund, Hunter College, NYCEP, and the University of Arizona Social and Behavioral Sciences Research Institute and School of Anthropology.

Hominin introgression in Island Southeast Asia and Sahul

JOAO C. TEIXEIRA

Australian Centre for Ancient DNA, The University of Adelaide

As the ancestors of modern non-African human populations left Africa around 65-50ka and dispersed across the world, they met and interbred with multiple hominin groups. The signatures of these events are preserved in the genomes of modern populations, and provide an eloquent record of the sequence and timing of these early migrations, with Asia proving a particularly complex area. In this study, we perform the most comprehensive genomic survey of modern-day human populations across Island South East Asia (ISEA) and Sahul, and provide a detailed picture of the admixture events taking place when so-called anatomically modern humans arrived in the area. At least three different Asian hominin groups appear to have been involved, including Denisovans. Several interbreeding events are inferred east of Wallace's Line, the

major biogeographical barrier in ISEA. Our results are consistent with archaeological evidence of widespread and early hominin presence in the area and suggest that isolated Denisovan groups inhabited different islands across ISEA, likely as a result of sea-level fluctuations during interglacial periods. Interestingly, of the currently known hominin fossils in the area, none has been associated with the Denisovans, who remain the most elusive member of the recent human family.

João C. Teixeira is supported by the Australian Research Council Indigenous Grant (IN180100017)

The human stress response, deep homology, and paleoanthropology: opportunities to study context, plasticity, and constraint in the ancient past

DANIEL H. TEMPLE

Department of Sociology and Anthropology, George Mason University

Concepts of ancestor-descendent relationships and the recognition of new species is of great interest to paleoanthropologists charged with reconstructing the human evolutionary lineage. Even studies of life history in hominines privilege matters of phylogeny over questions of plasticity, context, and constraint. This approach removes the process-oriented paradigms that stemmed forth from the New Physical Anthropology and Modern Synthesis in evolutionary biology. Teeth provide one solution to this problem. Teeth are a plentiful component of paleoanthropological research and provide a faithful record of development including, diet, climate, and stress experiences, while estimations of age-at-death in fossil remains provide a semblance of information regarding demography in the past. Building on research done with prehistoric hunter-gatherers, this study provides an outline for reconstructing survival of stress events in the past, placing these events in a life history framework. This work focuses specifically on prehistoric hunter-gatherers from Japan and Siberia, where age-at-defect formation, infant dietary behavior, and age-at-death all demonstrate the ways in which humans survive stress events through adaptive plasticity, while future responses to environmental challenges may be inhibited through physiological constraint and exacerbated through local contexts including socioecological systems. These findings include elevated frequencies of accentuated striae during the cessation of breastfeeding, reconstruction of stress experiences during changes in local climates, and diminished capacity for survival in response to surviving early life stress events. Building on these findings, this

study discusses how early life environment may be of great interest to paleoanthropologists, particularly when parred with high resolution data from fossil sites.

Funded by the National Science Foundation, Japan Society for the Promotion of Science, and Social Sciences and Humanities Research Council of Canada

Violent Death: paleo-forensic study of a case of multiple sharp-force trauma from medieval Lombardy (Italy)

CHIARA TESI¹, STEFANO RICCI², JACOPO CREZZINI², PAOLA BADINO¹, ROBERTA FUSCO¹, CHIARA ROSSETTI¹, OMAR LARENTIS¹, ILARIA GORINI¹ and MARTA LICATA¹

¹Department of Biotechnology and Life Sciences, University of Insubria, ²Department of Physical Sciences, Earth and Environment, University of Siena

Skeletal remains occasionally provide traces of traumatic injuries, shedding light on the degree of interpersonal violence in a past society. Putting together the pieces of a violent act, through the analysis of the marks left on bones, physical anthropologists can challenge history in the reconstruction of certain episodes and dynamics of violence from the past. Here we describe a case of traumatic perimortem injuries observed in the skeleton of an individual recovered during archaeological excavation at the medieval cemetery of San Biagio in Cittiglio (Varese, northern Italy). Evidence of multiple sharp-force trauma was observed in the skull of a young adult (T.13), which constitutes a unique case of raw violence in the past within this rural population, as it represents the only case of violent death ascertained in the entire skeletal sample investigated so far. The analysis of multiple lesions displayed on the skull required a systematic multi-analytical approach, combining classical macroscopic examination, computer tomography, photographic three-dimensional modelling and three-dimensional digital microscopy, in order to study in-depth the marks and verify their nature and aspect. The principal aim is to reconstruct the dynamics of this event, biologically archived on bones, applying a modern scientific approach such as digital microscopic methodology, not frequently used in the osteoarchaeological field, but which has been revealed by previous studies able to provide computable data and to overcome many technical limitations of macroscopic assessment.

This work was supported by the Fondazione Comunitaria del Varesotto [http://www.fondazionevaresotto.it/]; the Fondazione Cariplo [http://www.fondazione.cariplo.it/it/index.html]; and the Regione Lombardia [https://www.regione.lombardia.it] who Ó:Ananced the excavation and the Research work.

ABSTRACTS

Graph theory applied to dental topography helps isolating and comparing the sharpest tools of primate molars

GHISLAIN THIERY¹, FRANCK GUY¹, VINCENT LAZZARI¹ and SEBASTIAN O. SOSA²

¹PALEOVPRIM UMR CNRS 7262, Université de Poitiers, ²IPHC UMR CNRS 7178, Université de Strasbourg

Dental topography can now graphically detect multiple elements, akin dental tools, which compose complex teeth such as molars. Still, comparisons are usually based on average values, which may conceal meaningful local variations of the topography. Here we propose to assimilate dental surface to a polygon graph, and dental tools to subgraphs of adjacent polygons, in order to isolate dental elements using network analysis tools. To test whether sharp dental tools are correctly identified, we use two network variables: (i) subgraph count and (ii) the sum of subgraphs' Bacon indices. They are expected to correlate with dental complexity and sharpness, respectively.

Upper and lower second molars from 11 primate species were converted into uniformly meshed surfaces of 10,000 polygons, then into polygon graphs. Sharp tools were defined as subgraphs of more than 10 adjacent polygons with a curvature exceeding the 80th percentile of polygon curvature values. Tooth complexity was measured as occlusal patch count rotated (OPCR) and tooth sharpness as Dirichlet normal energy (DNE).

Subgraphs were found to overlap with the sharpest elements: shearing crests, cutting blades and a portion of crenulations. Subgraph count was significantly correlated to OPCR ($r=0.71$; $p<0.001$) and sum of subgraphs' Bacon indices was significantly correlated to DNE ($r=0.64$; $p<0.001$). More importantly, sharp dental tools were isolated from the bulk of dental surface not only graphically, but as virtual objects as well. Future comparisons of sharp tools, but also other kinds of subgraphs, will greatly enhance our ability to break down the multiple functions of primate teeth.

This work was supported by the Agence Nationale de la Recherche (ANR-17-CE02-0010-01) and a Research Grant from the International Primatological Society.

Pedigree sequencing shows that life history plays a major role in mutation rate variation in primates

GREGG W.C. THOMAS^{1,2,3}, RICHARD J. WANG², R. ALAN HARRIS^{4,5}, MUTHUSWAMY RAVEENDRAN^{4,5}, JEFFREY ROGERS^{4,5} and MATTHEW W. HAHN^{2,3}

¹Division of Biological Sciences, University of Montana, ²Department of Biology, Indiana University, ³Department of Computer Science, Indiana University, ⁴Human Genome Sequencing Center, Baylor College of Medicine, ⁵Department of Molecular and Human Genetics, Baylor College of Medicine

Mutations are a fundamental molecular process that can affect the fitness of an individual and introduce novel genetic variation into a population. Whole genome sequencing of individuals within a pedigree is now possible, allowing mutation rates to be measured by comparing the sequences of parents and their offspring. Pedigree studies in humans have consistently observed an average single nucleotide mutation rate of 1.2×10^{-8} per site per generation, with the number of mutations passed to offspring largely dependent on the age of the father. To test whether these patterns are general to primates, we sequenced parent-offspring trios of owl monkeys (*Aotus nancymaae*) and rhesus macaques (*Macaca mulatta*). We find that the mutation rate for both species is lower than humans, with owl monkeys having a rate of 0.81×10^{-8} and rhesus macaques having a rate of 0.37×10^{-8} mutations per site per generation, and that both species have a strong paternal age effect. We develop a model of mutation rates based on the paternal age effect and find that shorter lifespan and lower puberty ages explain much of the observed rate variation. This suggests life history as the main determinant of mutation rates per generation across primates. We further demonstrate that changes in life history can explain much of the variation in substitution rates among primate species. In contrast to single-nucleotide mutations, we find very similar rates of copy-number variation between rhesus macaques and humans, implying a different model underlies the accumulation of these types of mutations.

This work is funded by the Precision Health Initiative at Indiana University.

Automated and Semi-Automated Rapid Morphological Phenotyping using Geometry Processing

OSHADE O. THOMAS¹, PATRICK J. DEPRET-GUILLAUME², RYAN L. RAAUM^{3,4,5}, WILLIAM E.H. HARCOURT-SMITH^{3,4,5,6}, MARK A. HASEGAWA-JOHNSON⁷ and JOHN D. POLK^{1,8,9}

¹Department of Anthropology, University of Illinois at Urbana Champaign, ²Department of Library and Information Science, The iSchool at Illinois, ³Department of Anthropology, Lehman College CUNY, ⁴Department of Anthropology, CUNY Graduate Center, ⁵Department of Vertebrate Paleontology, American Museum of Natural History, ⁶NYCEP, New York Consortium in Evolutionary Primatology, ⁷Department of Electrical and Computer Engineering, University of Illinois Urbana-Champaign, ⁸Department of Biomedical and Translational Sciences, University of Illinois Urbana-Champaign, ⁹Department of Kinesiology and Community Health, University of Illinois Urbana-Champaign

Capturing bony shape variation with both efficiency and adequate detail is fundamental to studies of organismal form. This study applies the functional mapping techniques of geometry

processing, initially developed for computer vision, to the analysis of bone morphology. Here we compare the accuracy and computational feasibility of four specific methods for rapid non-rigid 3D shape matching of human and ape cuboids and medial cuneiforms. Bijective Continuous Iterative Closest Point (BCICP) and 'ZoomOut', implemented in MatLab, yield highly accurate functional and point-to-point maps between pairs of bone represented as Riemannian manifold triangle meshes. The third and fourth approaches seek to learn better, non-linear, descriptors of bone shape. Both are self-supervised, using Siamese ResNet Neural Network architectures but differ in their objective functions. With functional maps and point-to-point maps from each approach, we assess the discrepancy between landmarks placed on bone by human experts and those algorithmically estimated by these shape matching procedures. Based on qualitative assessments, all four methods yield highly accurate vertex-to-vertex maps between pairs of hominoid cuboid meshes. However, BCICP and 'ZoomOut' have the most appeal, as they are fast and require little post-processing refinement relative to the learning-based approaches. Initial results from the BCICP experiments yield almost trivial distance discrepancies between twenty expert-placed cuboid landmarks on 25 meshes to those landmark placements derived algorithmically. Mean landmark discrepancies between hominoid species range from 0.96mm to 4.28mm. This work facilitates the rapid and accurate automated acquisition of morphological phenotypes and will have broad utility in comparative biology and forensic applications.

This work was supported in part by The National Science Foundation (1638756) to John D. Polk

Estimation of hominine femoral head diameter from incomplete femoral head remains via sphere-fitting methodology

INDYA J. THOMPSON¹, BECCA W. COOK², ZACHARY D. COFRAN³, MEGAN REYES³ and CHRISTOPHER S. WALKER¹

¹Department of Molecular Biomedical Sciences, North Carolina State University, ²Department of Evolutionary Anthropology, Duke University, ³Anthropology Department, Vassar College

Femoral head diameter (FHD) is an important variable for paleoanthropologists as it's highly correlated with body mass in humans and other extant primates. Although femora are relatively abundant in the fossil record, the head is often damaged, rendering many specimens' FHD unknown or uncertain. Previous work suggested that virtual sphere-fitting methods can be used to estimate FHD of incomplete femoral heads, but this research only examined a small portion of the subchondral surface. Likewise, researchers have established the utility of incomplete acetabular sections for estimating hip joint diameter, but

ABSTRACTS

the femoral head hasn't been similarly assessed. Accordingly, we examine how well spheres fit to different sections of the femoral head replicate its empirical diameter in a large sample of extant hominines and fossil hominins. We first present a streamlined and reproducible protocol for dividing the femur head into eight equal segments. To assess reproducibility, each author independently analyzed a subset of the femora. We then compared sphere diameters from different divisions of the FHD to empirically measured maximum supero-inferior FHD in the entire sample. Interobserver error is low, as each researcher obtained nearly identical results. In all groups, fitted-sphere mean PPE is lowest when most or all of the subchondral surface is used (ex. 7-8 segments), however, estimated FHD from spheres fitted to only a single segment are still reasonably accurate (mean PPE < 5%). These results suggest that hominin femoral head dimensions can be reliably estimated via sphere-fitting methods even when only small portions of subchondral bone are preserved.

Lemurs on the menu: new insights into the extent of and driving factors behind wildlife hunting in Western Madagascar

KATHARINE ETH. THOMPSON

The Interdepartmental Doctoral Program in Anthropological Sciences (IDPAS), Stony Brook University

In many regions across the globe, the illegal hunting and consumption of wildlife is depleting animal populations at an unprecedented rate. This is particularly true in developing nations such as Madagascar, which often face a dual challenge of gubernatorial and humanitarian crises that further complicate conservation agendas. Illegal hunting is particularly understudied in western Madagascar where we lack vital information on the intensity of wildlife exploitation as well as the socioeconomic, health-related and cultural factors that drive it. In order to address this gap and provide foundational data for both conservation and public health policy, I conducted semi-structured, questionnaire-based interviews; assessed dietary quality using recall journals and anthropometrics; and collected faunal bone data from local garbage deposits in one village (N = 425 individuals from 110 households) and across six months (September 2018 - March 2019). I quantified the extent of hunting and the species targeted, as well as investigated hunting practices. Annual interview results (N=397) suggest frequent hunting and consumption of protected primates (including *Lepilemur ruficaudus* and *Propithecus verreauxi*) as well as legal game species. Targeted hunting and consumption of the endangered *Pyxis planicauda* was also common. Results suggest that species considered "protected" by cultural prohibitions against consumption are still regularly killed and discarded. Community members identified

priorities and problems, which we then examined in relationship their influence on illegal hunting. Taken together, these data suggest that socioeconomic and health status may be important intervention points for future initiatives, benefiting human and wildlife populations alike.

Funding for this work was generously provided by the National Science Foundation, Stony Brook University, the American Philosophical Society, Global Wildlife Conservation (Award 5095.005-0175) and Primate Conservation Inc (Award 46).

Estimating ground reaction force position in the knuckle-walking chimpanzee hand

NATHAN E. THOMPSON¹ and SERGIO ALMÉCIGA^{2,3,4}

¹Department of Anatomy, New York Institute of Technology College of Osteopathic Medicine, ²Division of Anthropology, American Museum of Natural History, ³Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, ⁴New York Consortium in Evolutionary Primatology

Knuckle-walking (KW) is a unique form of terrestrial locomotion utilized only by chimpanzees and gorillas among primates. The bony correlates of KW, as well as the forces which shape morphology through ontogeny, continue to be heavily debated. Yet, few precise data on force generation and transmission during KW relative to the hand and wrist exist. Here we present detailed laboratory 3-D kinematic and kinetic (EMG) data on KW in two subadult chimpanzees (*Pan troglodytes*). We combined 3-D ground reaction forces (GRF) with digit-level metacarpophalangeal (MCP) motion and wrist motion in order to understand where the GRF lever arm falls relative to the phalanges, metacarpals, and carpals.

Initial data show that for most of KW stance phase, the GRF passes extremely close to the MCP joint. The GRF is typically just a few millimeters from the dorsal aspect of the proximal phalangeal bases and metacarpal heads, placing it just dorsal to the MCP joint axis. At the wrist, the path of the GRF is more variable. The GRF passes either dorsal or ventral to the bi-styloid axis (radial to ulnar styloid processes), implying either extension or flexion wrist moments, depending on wrist position. The GRF typically maintains a position within two centimeters from the bi-styloid axis. At both joints, the GRF lever arm changes little between 20% and 80% of stance. The short, and tightly-controlled lever arms suggest that KW is an efficient way to reduce hand and wrist joint moments, which may have been the selective advantage for KW.

This research is funded by the National Science Foundation Grants SMA 1719432, BCS 0935321, BCS 1316947, AEI/FEDER EU (CGL2017-82654-P), and the Generalitat de Catalunya (CERCA Programme).

Urinary markers of oxidative stress respond to infection and aging in wild chimpanzees

NICOLE A. THOMPSON¹, EMILY OTALI², ZARIN MACHANDA^{2,3}, MARTIN MULLER^{1,2}, RICHARD WRANGHAM^{2,4} and MELISSA EMERY THOMPSON^{1,2}

¹Anthropology, University of New Mexico, ²Kibale Chimpanzee Project, ³Anthropology, Tufts University, ⁴Human Evolutionary Biology, Harvard University

Oxidative stress (OS) plays a central role in aging and results from a variety of stressors, making it a powerful measure of health and a way to examine costs associated with life history investments within and across species. However, few urinary OS markers have been examined under field conditions, particularly in primates, and their utility to non-invasively monitor the costs of acute stressors versus the long-term damage associated with aging is poorly understood. We examined variation in 5 urinary markers of oxidative damage and protection under 5 validation paradigms in 37 wild, adult chimpanzees in the Kibale National Park, Uganda. We used 928 urine samples to conduct cross-sectional and within-individual analyses of responses to acute infectious challenge (respiratory illness or severe wounding) and variation with age. Within individuals, all markers of damage responded to at least one if not both types of acute infection. While OS is expected to increase with age, this was not generally true, though increases in OS were detected in older individuals as they approached their ages of death. Unlike in human and rodent tissues, 8-OHdG in chimpanzee urine decreased with age, both across and within individuals near death, suggesting a potential decline in DNA repair and/or metabolic rate during senescence. Our results suggest that OS can be measured using field-collected urine and integrates short- and long-term aspects of health. Our results confirm that using multiple markers and longitudinal sampling is optimal for determining the role of OS in health and lifespan in long-lived organisms.

Research was supported by the National Institute on Aging award R01AG049395

Prevalence of Condensed Tannins in the diet of Diademed sifakas (*Propithecus Diadema*) in Tsinjoarivo, Madagascar and its impacts on protein intake

EMMA THURAU^{1,2} and MITCHELL IRWIN³

¹Anthropology, Graduate Center, CUNY, ²Anthropology, New York Consortium of Evolutionary Primatology, ³Anthropology, Northern Illinois University

Condensed tannins (CT) function as digestion reducers due to their ability to bind to proteins and reduce their availability to herbivores. Although previous studies have investigated CTs in primate diet, few have done so using Sephadex column purification to determine tannin concentration or

ABSTRACTS

in vitro available nitrogen assays to determine the effectiveness of the CTs at binding to proteins. In this study, we observed diademed sifakas (*Propithecus diadema*) over a 2-month period (June–August 2018) at Tsinjoarivo, Madagascar, in order to quantify the impacts of CTs on protein intake in their diet within varying degrees of habitat disturbance. We found eleven of the fourteen top foods tested were positive for tannins, of these top foods, six were 100% effective in binding to proteins (e.g., no protein was available to the sifaka that consumed it), resulting in some top foods within their diet exhibiting little to no available protein. Overall our findings suggest sifakas are eating foods with virtually no protein, thereby relying on their foods for other macronutrients such as carbohydrates and/or fats, contradicting existing notions that large-bodied primates feed on leaves to obtain protein—that is if the sifakas do not already exhibit an adaptation to tannin-rich food items such as tannin-binding salivary proteins. This study is not only important for understanding the dietary constraints on sifaka populations and the evolution of their diet choice strategies but also adds to the growing evidence of plant defenses impacting primate diet.

Funding was received from the Primate Conservation Inc., Global Wildlife Conservation, Northern Illinois University Anthropology Department, and Graduate School.

High density of white-faced capuchins (*Cebus capucinus*) and habitat quality in the Taboga Forest of Costa Rica

ELIZABETH TINSLEY JOHNSON^{1,2}, MARCELA E. BENÁTEZ^{1,3}, ALEXANDER FUENTES¹, CELIA R. MCLEAN¹, ARIEK B. NORFORD^{1,4}, JUAN CARLOS ORDOÑEZ¹, JACINTA C. BEEHNER^{1,5,6} and THORE J. BERGMAN^{1,6,7}

¹Capuchins at Taboga Research Project, Taboga Forest Reserve, ²Integrative Biology, Michigan State University, ³Psychology, Georgia State University, ⁴Ecology and Evolution, Stony Brook University, ⁵Psychology, University of Michigan, ⁶Anthropology, University of Michigan, ⁷Ecology and Evolutionary Biology, University of Michigan

Across the globe, primates are threatened by human activities. This is especially true for species found in tropical dry forests, which remain largely unprotected. Our ability to predict primate abundance in the face of human activity depends on different species' sensitivities as well as on the characteristics of the forest itself. We studied plant and primate distribution and abundance in the Taboga Forest, a tropical dry forest surrounded by agricultural fields in Costa Rica. We found that the density of white-faced capuchins (*Cebus capucinus*) at Taboga is 2–6 times higher than reported at nearby sites. Using plant transects, we also found relatively high species richness, diversity, and equitability compared to other tropical dry forests. Edge transects (i.e., within 100 m from the forest boundary) differed from interior transects in two ways: (1) tree

species associated with dry forest succession were well-established in the edge; (2) canopy cover in the edge was maintained year-round, while the interior forest was deciduous. Sighting rates for capuchins were higher near water sources but did not vary between edge and interior forest. For comparison, we also found the same to be true for the only other primate in the Taboga Forest, mantled howler monkeys (*Alouatta palliata*). Year-round access to water might explain why some primate species can flourish even alongside anthropogenic disturbance. Some forest fragments, like Taboga, may support high densities of some species because they provide a mosaic of habitats and key resources that buffer adverse ecological conditions.

We would like to acknowledge the University of Michigan for their financial support.

Dietary modification of insulin receptor abundance in the growth plate

VICTORIA A. TOBOLSKY¹, JUDITH HOLLANDER², TERRENCE CAPELLINI¹, LI ZENG² and DANIEL E. LIEBERMAN¹

¹Human Evolutionary Biology, Harvard University, ²Department of Immunology, Tufts University School of Medicine

Insulin is the body's main mitogenic hormone, and children are known to go through a characteristic period of high insulin during the growth spurt. This and other evidence suggests that insulin may play a role in adolescent growth. However, the extent to which insulin acts as a regulator of linear skeletal growth has remained relatively obscure. Prior evidence demonstrates that insulin sensitivity in the growth plate can be experimentally induced with dietary changes (Tobolsky et al., 2018), but the mechanism by which this occurs is unknown. This study tests the hypothesis that such changes to insulin sensitivity in the growth plate are not merely a result of stochastic changes to insulin receptor abundance. We use a 2 x 2 design comparing *db/db* experimental mice with C57BL/6J controls under two different dietary conditions. Groups ($n = 5$ males) consumed either a high glycemic index diet or a low glycemic index diet from four to twelve weeks of age, typically considered the end of the growth period for mice. Immunohistochemistry experiments demonstrate that there are no differences in insulin receptor abundance between the four conditions, suggesting that changes to insulin receptor sensitivity in the growth plate are a result of other pathways. In total, these experiments suggest that the growth plate is responsive to environmental energetics through changes to insulin sensitivity. This may allow organisms to tailor energy allocation to somatic growth based on stimuli from their environment, with implications for disentangling the mechanisms by which diet regulates physical growth.

Primate hippocampal size and organisation are predicted by sociality but not diet

ORLIN S. TODOROV¹, VERA WEISBECKER¹, EMMANUEL GILLISSEN², KARL ZILLES³ and ALEXANDRA A. DE SOUSA⁴

¹School of Biological Sciences, The University of Queensland, ²Department of African Zoology, Royal Museum for Central Africa, ³Research Centre JuÄlich, Institute of Neuroscience and Medicine, ⁴Psychology, Culture and Environment, Bath Spa University

Brain size in primates has been shown to be influenced by both social and ecological pressures. Models of ecological intelligence usually emphasize how the brain evolves due to individual adaptations to the environment, whereas models of social intelligence emphasize changes related to social solutions. The hippocampus is a mosaic structure where different subregions process information related to different cognitive abilities: although best known for its role in memory and spatial cognition, more recently it has become clear that it has an important role in social cognition as well. For example the subregion CA1 has been shown to be related to episodic memory while the CA2 subregion is related to social, but not spatial cognition. Outside of primates, whole hippocampus size has been related to spatial ability both within species through sex differences, and between species. Here we investigate how the hippocampus and its substructures have evolved alongside social (group size) and ecological (home range and diet) factors in primates. We use a dataset comprising 43 species and utilise phylogenetic comparative methods to reveal that the hippocampus evolves mostly due to social pressures, but not diet; And only the volumes of CA1 and subiculum can be predicted by home range. We also show that body size sexual dimorphism is a good predictor of hippocampal size sexual dimorphism. This is in line with previous findings regarding sex differences in hippocampal volume in non-primates, related to social structure and sex differences in behaviour.

Health inequalities as seen through social status and regional trends during the Edo period in the Japanese archipelago

HIROTAKA TOMITA¹ and NORIKO SEGUCHI^{2,3}

¹Graduate School of Integrated Sciences for Global Society, Kyushu University, ²Faculty of Social and Cultural Studies, Kyushu University, ³Department of Anthropology, The University of Montana, Missoula

The Edo period (1603–1868) in Japan was marked by a feudal society with a rigid caste system (e.g. samurai, merchant, and farmer), and during this period the population density of urban areas increased significantly as compared to earlier periods. Economic inequality existed between

ABSTRACTS

social strata, with farmers periodically suffering from poverty, hunger, and poor health due to the rapid growth of the monetary economy during the Edo Period.

This study aims to identify how this social inequality might correlate with health status, using linear enamel hypoplasia (LEH) and cribra orbitalia (CO). This study examined 11 urban populations and nine rural populations in Japan, from northern Honshu through the southern island of Kyushu. First, we explore the relationship between health status during childhood and socio-economic status. Second, we analyze the prevalence of LEH and CO to distinguish health differences between genders.

Results suggest that the frequency of LEH in samurai (especially upper level samurai) was significantly higher than in other populations and the prevalence of CO in farmers in rural areas was slightly higher than in other populations. Logistic regression analysis showed that the prevalence of LEH was largely a factor of social rank, and the prevalence of CO was a factor in rural settlements. Also, regarding gender differences, the frequencies of LEH and CO were significantly higher among females in two urban merchant cities. Although no large gender differences were observed, this study revealed that socio-economic status significantly influenced health status during childhood during the Edo period.

This work was supported by JSPS KAKENHI Grant Number JP17J04347 for H.T. and JP19H05737 for N.S.

A Quantification of the Effect of Foraging Risk on the Prehistoric Foraging-Farming Transition in the Interior Eastern Woodlands of North America

MELISSA G. TORQUATO and ERIK R. OTÁROLA-CASTILLO

Anthropology, Purdue University

For over a century, subsistence strategy scholars have questioned why humans transitioned from foraging to farming. Early researchers proposed that climate change contributed to this transition by increasing foraging risk – the measured uncertainty of an expected return of food resources. Previous research examining the effects of climate change on the prehistoric foraging-farming transition in Midwestern North America (approximately 4,500–4,000 kya) suggested that climate change influenced subsistence behavior and led to an increase in the use of cultivated resources. The present study expands on these findings by quantifying the effect of foraging risk on observed dietary variation using a sample of archaeological components from Illinois ($n = 43$). This study quantifies expected risk by calculating the variance in the availability of prehistoric resources, estimated from species distribution models. The expected risk is compared to the observed risk, which is calculated from the archaeological data.

The use of these methods to quantify foraging risk is novel for studying the foraging-farming transition. A non-parametric MANOVA revealed a statistically significant effect of foraging risk ($F = 1.8107$; $p = 0.0102$) on diet changes through time. Principal coordinate analyses combined with vector fitting visualized the effects of dietary variables, dates, paleoenvironmental proxies, and foraging risk on diet. These results show that foraging risk within prehistoric Illinois increased throughout time, suggesting a decrease in availability and predictability of foraged resources during the foraging-farming transition. This finding may explain the previously observed increases in cultivated resources in the diet during this period.

Contributions by MGT were supported in part by the National Science Foundation Graduate Research Fellowship Program (Grant No. 106469).

Comparative anatomy and 3D geometric morphometrics of the SD-1663 hipbone from the El Sidrón Neandertal site (Asturias, Spain)

NICOLE TORRES-TAMAYO¹, MARKUS BASTIR¹, DANIEL GARCÍA-MARTÁNEZ¹, CAROLINE VANSICKLE², ANTONIO GARCÍA-TABERNERO¹ and ANTONIO ROSAS¹

¹Paleobiology Department, Museo Nacional de Ciencias Naturales (Madrid, Spain), ²Department of Anatomy, A.T. Still University

The adult pelvis morphology of the El Sidrón Neandertal site (49ka, Asturias, Spain) is represented by the right partial hipbone SD-1663. This specimen preserves the body of the ilium, the greater sciatic notch, the acetabulum with a crushed and eroded acetabular margin, the auricular surface, the arcuate line, the iliopubic eminence, a portion of the distal superior pubic ramus and part of the ischial tuberosity. Linear measurements were taken to compare SD-1663 with $N=50$ modern humans and with values reported for other fossils in the literature. 3D geometric morphometrics were conducted to assess the morphology of SD-1663 within a comparative evolutionary framework composed of $N=50$ modern humans and the fossil specimens A.L. 288-1 (*Australopithecus afarensis*), Sts 14 (*A. africanus*), KNM-ER 3228 (Early Pleistocene *Homo*), Pelvis 1 (Middle Pleistocene *Homo*) and the *H. neanderthalensis* specimens Kr. 207 and Kebara 2. Preliminary analyses showed that SD-1663 displays three main distinctive features compared to modern humans. (1) SD-1663 shows a supero-inferior flattening of the superior pubic ramus, which is thinner than that of modern humans. Principal component analysis shows that SD-1663 morphology falls outside the 95% confidence ellipse of modern humans, mainly due to the presence of a pronounced narrow J-shaped greater sciatic notch (2) and a slightly flaring ilium (3). These three features are shared with other *Homo* specimens (plesiomorphies), pointing to a

primitive Neandertal hipbone morphology within the genus *Homo*. Further analyses are necessary to fully characterize SD-1663 as a new addition to the fossil record of pelvic bones.

This research is funded by CGL-2015-63648-P and CGL2016-75109-P (Ministry of Economy, Industry and Competitiveness, Spain).

Musculoskeletal modeling: Human ACL rupture recognized as multifactorial using dog CCL rupture cases

SHARON A. TOTH, ALICIA R. GROSSO and MICHAEL I. SIEGEL

Anthropology, University of Pittsburgh

The anterior cruciate ligament (ACL) in humans and the cranial cruciate ligament (CCL) in dogs are homologous structures both susceptible to rupture and regularly result in secondary osteoarthritis. Human musculoskeletal problems are the third highest medical cost in the United States with \$170 billion spent annually. Women are more susceptible to rupture and it is uncertain why this occurs. Concurrently, different dog breeds exhibit unequal rupture rates, which make them appropriate anatomical models to better understand increased rupture risk factors. This study analyzed data collected from a veterinary hospital comparing CCL ruptured cases (16 females, 13 males) and non-ruptured cases (19 females, 9 males). It used a multicausal approach by looking at tibial plateau angle (TPA), patellar luxation (PL), breed, sex, and reproductively intact status. Among the ruptured cases only 4 of 29 were intact, while 21 of 28 non-ruptured cases were intact ($\chi^2 = 21.7$, $p < 0.01$). However, sex was not statistically significant ($\chi^2 = 0.97$, $p > 0.01$). Overall, these results show large breed, non-intact dogs with abnormal TPAs are more likely to rupture their CCL, suggesting hormonal removal is important in bone and ligament development in dogs. We propose hormonal stop signals in long bones are interrupted and change the bony angle, over-extending the ligament and increasing rupture susceptibility. This dog model supports human dimorphic ACL rupture rates as multifactorial and influenced by developmental hormonal variations.

The influence of diet, phylogeny and dental properties on tooth wear and fracture patterns

IAN TOWLE¹, CAROLINA LOCH¹ and JOEL D. IRISH^{2,3}

¹Sir John Walsh Research Institute, Faculty of Dentistry, University of Otago, ²Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University, ³Evolutionary Studies Institute and Centre for Excellence in PaleoSciences, University of the Witwatersrand

Tooth wear is the loss of dental hard tissue not caused by pathology or acute trauma. Crown chips also remove dental tissue, and patterns of both chipping and wear are often used for dietary

ABSTRACTS

and behavioral reconstruction in archaeological and paleoanthropological settings. It is debated whether dental properties and phylogeny should be incorporated into these studies. In this study, tooth chipping and overall occlusal wear were recorded in three species of extant primates (*Papio anubis*, *Gorilla gorilla gorilla* and *Pan troglodytes*) and five fossil hominin species (early *Homo*, *Australopithecus sediba*, *Homo naledi*, *Australopithecus africanus* and *Paranthropus robustus*). Dental chipping and wear patterns varied between species (e.g., angle/extent of wear, prevalence/position of fractures). Much of this variation likely relates to dietary and behavioral differences. However, dental characteristics also influence the interaction between different types of wear and fractures, with certain surfaces being more resilient to different forces and reflecting a functional adaptation. In all species, the molar surface (buccal/lingual) with less occlusal wear was also the one with more fractures. This pattern likely relates to a combination of the following: (1) masticatory cycle (e.g., differences in loads across the crown); (2) enamel properties (e.g., variation in enamel thickness, cusp morphology and enamel structure); (3) different types of stressors across the crown (e.g., tooth to tooth contact, grit, dietary items). In sum, broad dietary/behavioral conclusions can be made based on tooth wear/fracture patterns, but more refined differences among species appears to require that dental properties and phylogeny be incorporated into the analysis.

The behavioral ecology of climate-induced human migration

MARY C. TOWNER and ALANNAH TEMPLON
Integrative Biology, Oklahoma State University

In this talk, we present a framework for analyzing climate-induced migration. Humans are able to thrive in a multitude of ecological and social environments, including varied environments over an individual lifetime. Migration—leaving one place of residence for another—is a central feature of many people's life histories, and environmental change goes hand-in-hand with migration, both in terms of cause and consequence. Here, we focus on three overlapping dimensions relevant to understanding the impact of climate change on human migration. First, we consider the temporal and spatial nature of the climate change itself—for instance, more frequent extreme weather events (e.g., large hurricanes in the Caribbean) vs. more gradual environmental change (e.g., rising sea levels in Bangladesh). Second, we consider whether the contributions to migration are direct (e.g., displacement by fire in the Amazon) vs. indirect (e.g., loss of subsistence species in the Arctic). Third, we consider the magnitude of both ecological and social change required to adapt to the dispersal location (e.g., moving into a neighboring community vs. long-distance migration as refugees). For each of these dimensions, we

consider recent examples of people impacted by climate change, including extreme weather events. We identify insights that may be gained from a behavioral ecological perspective, keeping in mind that although human-induced climate change at the magnitude we are seeing now is a recent phenomenon, human migration in response to changing environmental conditions is not.

New Methods to Analyze Animal Vocalizations with Anthropological Applications

STEPHEN A. TOWNSEND¹, ANKE MEYER-BAESE^{1,2}, PETER BEERL¹ and DENNIS E. SLICE^{1,3}

¹Scientific Computing, Florida State University,

²Electrical and Computer Engineering, Florida State University and Florida A&M University,

³Anthropology, University of Vienna

Vocalizations are a very important source of information for the behaviors, social structures, cognitions and perceptions of both humans and animals. In humans, these vocalizations usually take the forms of complex patterns of intonation and phonetic articulation which we call language. In animals, the vocalizations are simpler in structure but hardly less informative. In this poster, we present several improvements of the Single Pulse Analysis method for analyzing geographic variations in animal vocalizations presented by the authors in a poster during the AAPA 2016 session. These improvements include advancements in pulse segmentation and characterization, advancements in acoustic signal alignment and the application of cutting-edge machine learning techniques including Random Forests and Voting Classifiers to the dataset. Our dataset consists of 186 mating calls of the Cope's Gray Treefrog, *Dryophytes chrysoscelis*, which were recorded by Dr. Carl H. Gerhardt between the 1960s and 1990s and donated to the MacAulay Library at the Cornell Lab of Ornithology. We also present comparisons between the improved methods and the previous method introduced in 2016 and show that our improvements provide a superior method for analyzing animal vocalizations.

This study is indebted to the Macaulay Library of the Cornell Lab of Ornithology for generously allowing us to download and use their frog calls for our research. This study is also indebted to the late Dr. Dennis E. Slice whose knowledge and expertise were beyond valuable to this research.

Telling different stories: Oxygen and strontium isotope variation in human tissues and baseline data from the northern coast of Peru

J. MARLA TOYNE¹, KELLY J. KNUDSON², CHRISTINE D. WHITE³ and FRED J. LONGSTAFFE⁴

¹Anthropology, University of Central Florida, ²Center for Bioarchaeological Research, Arizona State

University, ³Anthropology, Western Ontario, ⁴Earth Sciences, Western Ontario

Researchers may prefer strontium or oxygen isotopic tracers to test prehistoric mobility depending on existing baseline data or regional variation. Using a sample from northern Peru, we test three independent proxies for geographic origins and lifetime mobility in human enamel and bone tissues: oxygen isotope compositions in phosphate and structural carbonate portions, and strontium isotopic ratios. We analyzed paired samples from 77 individuals from different mortuary contexts (including local elites (n=30), urban tombs (n=23) and human sacrifices (n=24)) with the bioarchaeological question of identifying local and non-local individuals. We test the hypothesis that each isotopic indicator should predict the same non-local individuals or at least a similar range in variation around local baseline data. Bone samples average 16.03‰ (±1.68) for $\delta^{18}\text{O}_{\text{ph}}$, 23.65‰ (±1.48) for $\delta^{18}\text{O}_{\text{sc}}$, and 0.707000 (±0.00053) for $^{87}\text{Sr}/^{86}\text{Sr}$. Tooth enamel samples average 16.68‰ (±1.46) for $\delta^{18}\text{O}_{\text{ph}}$, 25.19‰ (±1.26) for $\delta^{18}\text{O}_{\text{sc}}$, and 0.707422 (±0.000991) for $^{87}\text{Sr}/^{86}\text{Sr}$. Bivariate graphs and statistical tests do not identify consistent correlations or individual outliers who exceed modeled local variation. When samples with poor collagen yields were removed, $\delta^{18}\text{O}_{\text{ph}}$ and $\delta^{18}\text{O}_{\text{sc}}$ correlate more consistently, but not significantly, suggesting additional preservation issues. These data show disparate variation in the number of local vs non-local individuals, which may relate to the complexities in oxygen isotope compositions due to climatological and cultural factors, or also the lack of variation in bioavailable Sr across the northern coast. We discuss further implications of these combined analyses for understanding isotopic variation and population mobility in the past.

Research sponsored by multiple Social Sciences and Humanities Research Council of Canada grants; Canada Research Chairs Program; Canada Foundation for Innovation; National Geographic Society; Fundación Backus; Universidad Nacional de Trujillo.

Temporal heterogeneity in quadrupedal locomotor rates in sympatric cercopithecids

JORDAN N. TRAFFI¹, TESSA H. CANNON², DAVID J. DAEGLING¹ and W SCOTT. MCGRAW²

¹Department of Anthropology, University of Florida,

²Department of Anthropology, The Ohio State University

Locomotor profiles report frequencies of behaviors but typically do not include information on rates of progression; furthermore, little attention has been paid to how such rates vary over the course of daily activities. Exploring temporal variation in step rates is important for understanding the daily stress stimuli applied to long bones. Higher step rates probably involve higher peak stresses and strain rates. Additionally,

ABSTRACTS

experimental evidence suggests shorter bouts of skeletal loading – separated by rest periods or intervals of inactivity – provide more potent osteogenic signals than uninterrupted activity. Here we focus on load frequency and continuity in two arboreal and one predominantly terrestrial cercopithecoid species.

One adult from each of three species (*Ptilocolobus badius*, *Cercopithecus diana*, *Cercocebus atys*) was followed all day for thirty days in Cote d'Ivoire's Tai Forest. We recorded time spent locomoting, resting, and the number of quadrupedal steps per minute every hour. We assessed whether hourly step counts and rates were uniform across hours.

C. diana and *Pi. badius* step rates were similar across hours of observation, but *C. atys* differed significantly in speed depending on time of day ($P < 0.005$). There was a slight negative correlation between speed and bout length for *C. diana* and *Pi. badius* ($P < 0.001$), suggesting short bursts with a higher step rate. Additionally, *Pi. badius* showed a preference for resting during specific periods (X^2 , $P < 0.01$). These results indicate that locomotor rate and spacing of rest periods are not consistent across taxa. These interspecific differences in loading patterns imply different osteogenic stimuli.

Supported by NSF BCS-1440278 and -1440532

Investment in innate immune defense in northern Kenya

TIN TRAN^{1,2,3} and MASAKO FUJITA^{3,4}

¹Anthropology, Grinnell College, ²Biological Chemistry, Grinnell College, ³Biomarker Laboratory for Anthropological Research, Michigan State University, ⁴Anthropology, Michigan State University

Life history theory has great potential to facilitate coherent explanation of variations in investment patterns between innate and acquired immunity. Due to the importance of resource allocation and conservation, tradeoffs between innate and acquired immunity may be influenced by internal and external conditions. Among infants who are too young to exhibit acquired immunity but protected by passive immunity from breast milk, febrile response may represent elevated investment in innate immunity. We tested the hypothesis that nutritional scarcity, low pathogen exposure, and high extrinsic mortality risk during development favors greater investments in innate immunity as indicated by higher odds of fever among breastfed infants. Archived data from Ariaal communities of northern Kenya ($n=79$) were utilized. Maternal energy, serum homocysteine (high levels indicate folate/vitamin B-12 deficiency), milk folate (FOLR1) and energy contents were indicators of nutritional abundance. Exclusive breastfeeding represented low pathogen exposure. Male sex and high parity represented high extrinsic mortality risk. Logistic regression models estimated the odds of fever

associated with these variables. Folate/vitamin B-12 scarcity (homocysteine) and FOLR1 were associated with higher odds of infant fever (OR 1.307, $p=0.020$; OR 1.14 $p=0.019$, respectively). Conversely, energy scarcity (maternal energy deficiency) and high parity were associated with lower odds of infant fever (OR 0.135, $p=0.016$; OR 0.080, $p=0.010$ respectively). Overall, the associations between energy scarcity, milk FOLR1, and high parity, contradict our initial hypothesis, suggesting that more complex relationships exist between innate and acquired immunity. Therefore, different nutritional resources may variably influence the level of investment in innate immunity among infants.

Support: Summer Research Opportunity Program and the Department of Anthropology, Michigan State University; National Science Foundation (BCS-0622358, BCS-1638167); Wenner-Gren Foundation for Anthropological Research (Gr. 7460, Gr. 9278).

Missionization and shifting mobility on the southeastern Maya Spanish frontier: Identifying immigration to the Maya site of Tipu, Belize through the use of strontium and oxygen isotopes

WILLA R. TRASK

Central Identification Laboratory, Defense POW/MIA Accounting Agency

The early Colonial Period *visita* mission cemetery Tipu represents an important opportunity to understand the role mobility played in indigenous Maya resistance on the southeastern Maya-Spanish frontier. Situated at a geographic and cultural frontier, Tipu experienced a dynamic history of fluctuating political alliances and was a pivotal player in frontier politics. This research seeks to identify the geographical origin of a subset ($N=195$) of the over 600 Postclassic and early Colonial period Maya buried at Tipu. To identify the impact of missionization on mobility of the Tipu population, strontium ($^{87}\text{Sr}/^{86}\text{Sr}$) and oxygen ($\delta^{18}\text{O}$) isotopes are used as geologic and climatic tracers to estimate potential childhood homelands.

The $^{87}\text{Sr}/^{86}\text{Sr}$ and $\delta^{18}\text{O}$ data obtained from Postclassic and early Colonial period individuals show a dramatic increase in the overall range and variability of isotope values between the two time periods. Nearly two-thirds (62.9%) of the Colonial Tipu population classify as non-local, suggesting that the community was primarily composed of recent, first-generation migrants; a highly mobile population is consistent with ethnohistoric records for Tipu. Sex-based differences in migration are also identified. These results suggest Spanish colonialism resulted in a significant and swift shift in mobility of the indigenous Maya, even in more peripheral frontier regions like Tipu, and underscores the importance of the Tipu community as a refuge for fleeing Maya. The presence

of migrants from both Spanish and Maya held territories provides evidence for the fluidity of the Maya-Spanish frontier and Tipu's importance as a gateway for trade between the two territories.

Human orbit size and latitude

SARAH TRAYNOR¹ and MICHAEL MASTERS²

¹Academic Affairs, University of Wisconsin School of Medicine and Public Health, ²Interdisciplinary Arts and Sciences, Montana Tech

The anatomic relationship among different aspects of the visual system and their correlation to latitudinal variation in modern and archaic humans has recently been the subject of a number of studies. Specifically, it has been proposed that light levels drive orbital development, and that bony orbital size shows a positive linear relationship with latitude, as a result of an incongruent quantity and intensity of light as distance from the equator increases. In this study, we evaluate this proposed hypothesis using orbital volume, and the three main components of orbit volume (orbital breadth, height, and depth measurements) collected on the dry skulls of modern human individuals ($n=191$) from populations that represent eight different latitudes in the northern and southern hemispheres (1° to 70° latitude). Results demonstrate that a quadratic regression represents the best fit to these variables, indicating that internal orbital size, as well as size of the orbital margins, does not increase linearly with increased latitude. However, a significant non-linear relationship between these orbital variables and latitude exists and warrants additional research, but does not suggest that variable light level is the selective pressure driving variation in orbital size.

First, Do No Harm: The Efficacy of a Late 19th and Early 20th Institution of Care

LORI A. TREMBLAY

Liberal Arts and Sciences, SUNY Delhi

Institutions of Care, which rose in popularity in the 19th century, were designed to protect society's most vulnerable from illness, injury, and death. While some, such as the Oneida State Custodial Asylum in upstate New York, were touted as state of the art medical facilities, their efficacy varied in protecting their charges in comparison to the poor who did not receive the relief and protections provided by Institutions of Care. This purpose of this study was to investigate whether being in an Institution of Care put its charges at a higher risk for physiological stress than those from a similar general population were. Human skeletal remains from the Oneida State Custodial Asylum in Rome, New York ($n=46$) and the Milwaukee County Institution Grounds Poor Farm Cemetery in Milwaukee, Wisconsin ($n=115$) and were examined for this study. Evidence of periosteal reactions, dental caries, antemortem tooth loss, and skeletal trauma was obtained via

ABSTRACTS

anthroposcopic analysis. The statistical analyses indicate that while inmates at the Oneida State Custodial Asylum experienced higher rates of general physiological stress that resulted in periosteal reactions in comparison to those from Milwaukee ($p=.024$), they suffered lower rates of dental disease ($p=.020$) and skeletal trauma ($p=.024$) than their Milwaukee counterparts. This indicates that although the Oneida Custodial Asylum in Rome, New York protected its inmates from a few certain and specific risks, it did not buffer them in general from suffering from a variety of physiological stressors when compared to their impoverished counterparts in Milwaukee, Wisconsin.

The Alumni Grant for Graduate Research and Scholarship and the Coca-Cola Critical Difference for Women Grant for Research on Women, Gender, and Gender Equity, both via The Ohio State University.

How small is small? Careful considerations for childhood stress using Vertebral Neural Canal (VNC) dimensions

TRENT M. TROMBLEY¹, PATRICK D. BEAUCHESNE² and SABRINA C. AGARWAL¹

¹Anthropology, University of California, Berkeley,
²Behavioral Sciences, University of Michigan, Dearborn

Metrics derived from vertebral neural canals (VNC) as a means of investigating early life stressors in bioarchaeological samples date to the 1980s, with the original studies of Clark and colleagues' (1985, 1986, 1988) outlining the morphogenesis model of vertebral neural canal growth. The use of VNC as an indicator of early stress and later mortality is an increasingly popular tool in bioarchaeological studies. However, a thorough review of clinical and primary literature suggests that the analysis of VNC contains both analytical and methodological discrepancies that need to be addressed prior to rigorous bioarchaeological implementation. For instance, clinicians have long distinguished between congenital and acquired narrowing of the canal (stenosis), yet bioarchaeologists have been slow to address whether canal measures are due to congenital or acquired (e.g. age, activity, ossification of the *ligamentum flavum*) means. Secondly, definitions of what constitutes a "small" vertebral canal varies significantly, suggesting a more rigorous reconsideration for what is biologically significant. Finally, methodological variation within both clinical and bioarchaeological studies has resulted in varying chronological ranges for the final achievement of adult canal size. We present here a synthesis of literature on VNC, in addition to results from the Late Medieval Italian (c. 1350-1500 AD) community of Villamagna ($n = 53$ individuals). Our results indicate that correcting for body size using vertebral body heights may

help to address sex-related differences in VNC, and that employing a distributional z-score approach to quantifying VNC dimensions may better characterize biological significance.

Genomic sequence assembly for the malaria-like parasite *Hepatocystis* using primate whole genome sequencing datasets

AMBER E. TRUJILLO^{1,2}, MORGAN E. CHANEY³ and CHRISTINA M. BERGEY⁴

¹Department of Anthropology, New York University,
²New York Consortium in Evolutionary Primatology,
³Department of Anthropology & School of Biomedical Sciences, Kent State University,
⁴Department of Genetics, Rutgers University

Malaria (*Plasmodium* spp.) and malaria-like (*Hepatocystis* spp.) parasites are important causes of parasitemia among humans and non-human primates. Though intensive measures have been undertaken to understand and eradicate *Plasmodium*, closely-related *Hepatocystis* is relatively understudied. This disparity is underscored by the surprising lack of genomic resources available for *Hepatocystis*, while nearly two dozen *Plasmodium* genomes exist in public databases. However, data from primate shotgun sequencing projects represent a potential opportunistic source of parasite genomic material because many of these animals come from free-ranging populations known to be hosts for various parasites. Capitalizing on the wealth of data from previously sequenced non-human primate blood samples, we isolate the first genome-scale data for *Hepatocystis*. We assembled portions of the *Hepatocystis* genome using sequencing reads that we characterized to be from the parasite through comparison to the human reference genome and that of a human-infective malaria (via BLAST and metagenomic classification). For instance, we isolate over 1 million basepairs of a malaria-like parasite from a sample of a Ugandan red colobus monkey (*Piliocolobus tephrosceles*), sequenced as part of efforts to generate a reference genome for this primate. Through phylogenetic comparison to sequences of malaria and malaria-like parasites, we conclude the sequences are from genus *Hepatocystis*. In addition to demonstrating a strategy for assembling parasite genome sequences without additional expense, our work provides the first genome-scale resource for this important primate parasite which will be useful in evolutionary studies of malaria and malaria-like parasites that impact humans and other primates.

Funding: Predoctoral Ford Fellowship Program

Mobility of people or cultural affinities? Strontium isotope research at Estark-Joshaqan, a multi-phase cemetery at the western border of Iranian Central Plateau

JOANNA TRĘBICKA¹, JAVAD HOSSEINZADEH² and ARKADIUSZ SOLTYSIAK³

¹Antiquity of Southeastern Europe Research Centre, University of Warsaw, ²Department of Archaeology, University of Kashan, ³Department of Bioarchaeology, Institute of Archaeology, University of Warsaw

Estark-Joshaqan is a cemetery located at the valley in the Karkas Mountains near Kashan. It was used from the Middle Bronze Age until the Early Iron Age (~1800-800 BCE). Four seasons of excavations, conducted since 2016, revealed that the majority of graves had shaft construction, an unusual feature for the Iranian Central Plateau. The nearest analogy in burial rite is observed at the territory of present-day southern Turkmenistan. Close similarities between Central Plateau and steppes of Central Asia may suggest either population movement or strong cultural affinities between these two regions.

In order to verify whether individuals inhabiting Estark were local or came from a more distant region, strontium isotope analysis (⁸⁷Sr/⁸⁶Sr) in human dental enamel was conducted. We studied 24 permanent first incisors and first molars of individuals from three different chronological phases: Middle Bronze Age, Late Bronze Age and Early Iron Age. Moreover, 6 individuals from nearby sites: Kashan (Parthian period) and Bidgol (Islamic period) were included for comparison. Isotopic signatures of all individuals suggest their local origin. Only two Late Bronze Age male individuals from Estark had slightly different strontium proportions that could have indicated immigration. However, their isotopic values fell into the local variability of the alluvial Kashan plain close to site, so most likely their movement consisted of only several kilometers within this region. Our preliminary results show that there is no evidence of long-distance migration of nomadic tribes from the steppes of Central Asia to the Iranian Central Plateau.

Project is financed by the Polish National Science Centre (decision no. DEC-2016/22/M/H3/00353, HARMONIA and DEC-2017/27/N/H3/01373, PRELUDIUM).

When populations are porous: admixture dynamics in a wild baboon hybrid zone

JENNY TUNG^{1,2,3,4}, TAURAS P. VILGALYS¹, ARIELLE S. FOGEL^{1,5} and SUSAN C. ALBERTS^{1,2,4}

¹Evolutionary Anthropology, Duke University,
²Biology, Duke University, ³Duke Population Research Institute, Duke University, ⁴Institute of Primate Research, National Museums of Kenya, ⁵University Program in Genetics & Genomics, Duke University

ABSTRACTS

Researchers working on wild primates often refer to their focal study systems in terms of “populations,” the basic unit of evolution. However, in most cases, our study subjects represent a small sample from a larger, geographically distributed set of interbreeding individuals that are connected via dispersal and migration. Contributions from this larger population can profoundly affect the evolutionary dynamics of the animals we directly observe, as is most clearly demonstrated in the case of admixture between species. Here, we draw on insights from a long-term study of naturally hybridizing baboons in Kenya to illustrate this point. First, we show that immigration of anubis baboons (*Papio anubis*) into our dominant yellow baboon (*P. cynocephalus*) study system has influenced variation in multiple fitness-related traits, including maturing timing, mating success, and social bond formation. Second, we combine functional genomic and population resequencing data to show that anubis-yellow hybridization also has a widespread effect at the molecular level, on gene expression and DNA methylation traits. Finally, we provide the first evidence that selection acts against introgression of anubis baboon ancestry into the yellow baboon genome. Specifically, anubis ancestry is depleted in regions of low recombination, consistent with models in which minor parent ancestry is reduced at loci where more potentially deleterious alleles are linked. Thus, our findings not only emphasize that our study system is porous, but highlight the importance of its links with the outside world—including members of a different baboon species—in understanding fitness-related phenotypic and genetic variation.

National Institutes of Health, National Science Foundation, Leakey Foundation, Sloan Foundation, and the North Carolina Biotechnology Center

Developmental plasticity and soft-tissue reconstruction: Using the Cayo Santiago macaques to predict somatic dimensions from skeletal material

CASSANDRA M. TURCOTTE^{1,2}, AUDREY CHOI^{1,2}, JEFFREY K. SPEAR^{1,2}, HANNAH G. TABOADA^{1,2}, MICHALA K. STOCK³, CATALINA I. VILLAMIL⁴, SAMUEL BAUMANN SURRAT⁵, JAMES P. HIGHAM^{1,2}, SCOTT A. WILLIAMS^{1,2} and SUSAN C. ANTÓN^{1,2}

¹Anthropology, New York University, ²New York Consortium in Evolutionary Primatology, ³Exercise Science, High Point University, ⁴Anatomy, Universidad Central del Caribe, ⁵Caribbean Primate Research Center, University of Puerto Rico

Interpreting the human and primate fossil record brings significant challenges, as only hard tissues are likely to fossilize. Although skeletal variation can be measured, it is unclear how well it matches and predicts the animal's somatic condition or life history as hard and soft tissue data often originate from different sets of animals in published datasets. The rhesus macaques of Cayo Santiago,

Puerto Rico provide an opportunity to evaluate the use of skeletal material to predict common soft tissue dimensions across ontogeny. In this study, we ground-truth the relationship between soft and hard tissues by comparing somatic and skeletal measures from the same >2-year-old individuals of a recent group (HH; n=84) from Cayo Santiago. Eighty antemortem somatic measurements, including limb lengths, were matched with post-maceration skeletal dimensions. Measures were modified from the set developed for bonesandbehavior.org. Here, we contrast length measures of the upper arm, forearm, thigh, and lower leg to corresponding skeletal lengths from the humerus, ulna, femur, tibia and fibula. Two-sample paired *t*-tests showed that although each skeletal measure significantly underestimated the corresponding somatic measure, they yielded similar patterns of variation (CV) and estimates of sexual dimorphism. These results suggest that it is feasible to aggregate such estimates across somatic and skeletal datasets. Additionally, all skeletal measures were able to predict the matched limb length ($p < 0.05$) with reasonable accuracy ($R^2 > 0.75$) using OLS regression models. These results demonstrate that it is possible to estimate living metrics using only skeletal remains if the appropriate correction factor is known.

NSF RAPID 1648676 NCE (to SCA, JPH, SAW). NSF BCS-1754024, Leakey Foundation (to JPH, SCA, SAW). National Center for Research Resources #8-P40-OD012217-25, NIH Office of Research Infrastructure Programs (to CPRC).

Endangered Anthropologists: Attrition Rates Among Ethnic Minorities in

EVONNE D. TURNER-BYFIELD
Anthropology, Ohio State University

Anthropology departments should strive to promote diversity and inclusion in researchers, students, and participants. However, despite university wide diversity initiatives in the last decade, Anthropology departments still struggle to attract, retain and train minority students. Of special importance is the attrition rate of minority students, which is not as often addressed as attraction initiatives at the institutional level. This study provides an initial empirical examination of enrollment and retention rates of ethnic minorities in graduate Anthropology programs in the United States. The data comes from a survey developed and circulated by the author querying racial/ethnic background, age, sex, enrollment, and withdrawal rates in programs that confer Masters and PhD degrees. The base of the results presented here represents data from 20 anthropology departments. Non-white students represent 31.49% of students in these programs, with self-reported Asian/Pacific Islander being the minority largest group (5.79%). There is a very high withdrawal rate (33.85%) withdrawal rate among ethnic minorities

from anthropology departments in the last decade. Minority students face several obstacles to their academic success and there are a number of explanations for this higher withdrawal rates, that probably relate to a disparity in academic training from undergraduate institutions leaving minority anthropologists struggling to keep up with graduate program demands. This preliminary data clearly demonstrates the need of improving and developing strategies that promote the retention of ethnic minority students in the field.

Sacral Traits as Age Indicators: A Validation Study

TAMARA L. TYNER
Anthropology, Texas State University

Wide prediction intervals in adult age estimation have fueled continuous research into potential age indicators and methods to narrow the predictive range. Several methods have been proposed and a new program—Transition Analysis 3 (TA3)—is currently being developed. TA3 uses indicators of several elements based on experienced observations (Ousley et al., 2019). The sacrum is a point of interest in TA3, as well as Passalacqua's (2009) method. To assess the use of the sacrum for adult age estimation, the seven traits from Passalacqua (S2/S3 fusion, S1/S2 fusion, microporosity, macroporosity, surface changes, apical changes, and S1 ring fusion) and the three dichotomized traits described in the proposed TA3 manual (S1 margin shape, S1/S2 fusion, sacral elbow) were scored preliminarily on 20 individuals from the Texas State Donated Skeletal Collection (TXSTDSC) ranging in age from 18-91 years. Results show that 85% of individuals scored using the Passalacqua coding system fall within the given ranges, 52% of those falling within the narrower 68% range. As TA3 does not have a given age range for each trait, the three features' scores were assessed using a Pearson correlation regression analysis. S1 Margin Shape shows a significant correlation to age at death ($r = 0.6887$, $p < 0.001$) as does S1/S2 Vertebral Fusion ($r = 0.6523$, $p < 0.01$). No individuals had the presence of a sacral elbow, indicating a lack of significance in the sample. These results indicate that scoring age-related sacral traits may be a useful addition to age estimation methods for a modern population.

MNI and sex estimation in two Umm an-Nar tombs from the UAE

JAIME ULLINGER¹, LESLEY GREGORICKA², CHÁYLEE ARELLANO³, QUENTIN BURKE⁴, VICTORIA CALVIN², CHARLES DOWNEY⁵, RACHEL HEIL⁶, ALYSSA MCGRATH⁷, SILVIO ERNESTO MIRABAL TORRES⁸ and JEREMY SIMMONS⁹

¹Sociology, Criminal Justice, and Anthropology, Quinnipiac University, ²Sociology, Anthropology, and Social Work, University of South Alabama, ³Geography and Anthropology, Louisiana State

ABSTRACTS

University, ⁴Biology, Quinnipiac University, ⁵Anthropology and Sociology, Albion College, ⁶Anthropology, California State University Fullerton, ⁷Anthropology, University of Notre Dame, ⁸Human Behavior, College of Southern Nevada, ⁹Anthropology, College of William and Mary

Commingle tombs are often overlooked in bioarchaeological studies because of the difficult nature of analysis, despite their prevalence across the ancient world. Tombs Unar 1 (U1) and Unar 2 (U2), located in the United Arab Emirates, date to the Umm an-Nar period (2700-2000 BCE), when people witnessed shifts in mortuary practices likely reflective of broader changes in subsistence and social organization. A collaborative project that trains undergraduates in anthropological research has examined tomb membership for U1 and U2 by estimating MNI and sex. Despite early descriptions of U1 and U2 holding similar numbers of individuals, this project found that MNI was greater in U2 when counting non-duplicating elements from the talus (U1: 88; U2: 228), mandible (U1: 101; U2: 290), and petrous portion of the temporal (U1: 190; U2: 403) whether using landmark or zonation methods. Metric analyses of the humerus found a relatively similar proportion of males and females in each tomb ($X^2=0.06$, $df=1$, $p=0.81$). While an assessment of the lateral angle of the internal auditory meatus and the mastoid process found greater numbers of women entombed in both tombs, there was no difference in sex distribution between the tombs (Fisher's exact: $p>0.05$ for both techniques). These results suggest that U2 was open to the interment of a larger number of individuals; however, while different sex estimation methods produced similar sex distributions between the tombs, the methods themselves varied considerably in estimating overall frequencies of males and females. Future research using additional sex estimation techniques is warranted.

This research was funded by the National Science Foundation - Research Experiences for Undergraduates grant (Award #1852426).

Why the long face? A study of cranial shape change in mice artificially selected for longer limbs

COLTON M. UNGER¹, JAY DEVINE² and CAMPBELL ROLIAN³

¹Biological Science, University of Calgary, ²Anatomy and Cell Biology, University of Calgary, ³Comparative Biology and Experimental Medicine, University of Calgary

Evolutionary developmental biology and quantitative genetic studies have provided important insights into the mechanistic basis of evolutionary change in primate skeletal traits. These studies, however, involve mostly retrospective assessment of morphological evolution under the assumption that skeletal changes occurred largely independently. In order to study

intra-species mammalian skeletal evolution in real time, we used selective breeding to produce the Longshanks mouse, which has 15% longer tibiae and unaltered mean body mass relative to random-bred controls. Previous studies have demonstrated systemic changes in the size, shape and material properties of the *Longshanks* post-cranial skeleton, suggesting a high degree of correlated responses to selection on tibia length. Here, we test the hypothesis that the *Longshanks* cranium has undergone indirect shape changes due to correlated changes in underlying bone development processes shared between the skull and limb. We investigated cranial shape changes using non-linear image registration-based automated landmarking of micro-CT cranium and tibia scans from over 300 adult *Longshanks* mice spanning several generations. Morphometric analyses of adult *Longshanks* cranium shape demonstrated longer crania with narrower and shorter cranial vaults after 20 generations of selection. Moreover, analysis of neonate crania and tibiae demonstrated that this pattern is structured early in ontogeny and becomes accentuated into adulthood. We show that indirect, and potentially non-adaptive, cranial and post-cranial skeletal changes can occur due to developmental overlap among anatomical parts. Thus, our work has implications for understanding processes involved in the shaping the evolution of the hominin hind limb and skull.

This work was funded by an NSERC Canada Graduate Scholarship (to CMU), NSERC Discovery grant 4181932 (to CR) and by the University of Calgary Faculty of Veterinary Medicine

Ancient Genetic Analysis of a North Alaskan Birnirk Inuit Population

SARAH L. UNKEL¹, LAUREN E.Y. NORMAN¹, JUSTIN TACKNEY¹, ANNE JENSEN², CLAIRE ALIX^{3,4}, OWEN MASON⁵ and DENNIS H. O'ROURKE¹

¹Department of Anthropology, University of Kansas, ²UIC Science LLC, Utqiagvik, Alaska, ³Department of Anthropology, University of Alaska Fairbanks, ⁴Archéologie des Amériques, Université de Paris 1 Panthéon Sorbonne, ⁵INSTAAR, University of Colorado

The complete set of "Beringian-specific" haplotypes A2a, A2b1 and D4b1a2a1a have yet to be reported in archaeologically identified Birnirk populations. These haplotypes are found in contemporary Inuit, coastal Siberian Indigenous groups of Chukotka, Thule Inuit from North America, and unaffiliated ancient Inuit individuals from Chukotka. However, Chukotkan Inuit sites are palimpsests, making it difficult to associate individuals with specific archaeological material culture. Only five individuals loosely associated with the Birnirk culture (650-1250 CE) have been sequenced. All five come from Paipelghak in

Siberia and exclusively have mitochondrial haplotype A2a. It is unclear if this low diversity is a result of sampling bias, incorrect cultural affiliation, or represents the true Birnirk maternal population.

We analyzed past individuals from Nunavak, Pigniq (Birnirk), Kugok, and Kugusugaruk, discrete Birnirk archaeological sites in Alaska. Segments from the first hypervariable region of the mitochondrial control region were sequenced from thirty-eight Birnirk individuals. Twenty-six individuals yielded full control region sequences and exhibited the expected mitochondrial lineages previously identified in the Inuit tradition: A2a, A2b1, and D4b1a2a1a. These results establish diverse maternal lineages within the Birnirk populations consistent with those found in the Inuit tradition. These conclusions, contextualized with archaeological knowledge, expand Inuit genetic ancestry to include individuals clearly associated with Birnirk material culture.

This research was supported by NSF grants 1523059 and 1523160 and the University of Kansas Ancient DNA Research Facility.

Childhood gut microbiome composition among the Amazonian Shuar: Testing links to changing diet, lifestyle, energy expenditure, and health

SAMUEL S. URLACHER¹, ANUKRITI SHARMA², JACK A. GILBERT², HERMAN PONTZER³, J. JOSH. SNODGRASS⁴, THERESA E. GILDNER⁵, FELICIA C. MADIMENOS⁶, MELISSA A. LIEBERT⁷, LAWRENCE S. SUGIYAMA⁴ and LARA R. DUGAS⁸

¹Department of Anthropology, Baylor University, ²Department of Pediatrics, University of California, San Diego, ³Department of Evolutionary Anthropology, Duke University, ⁴Department of Anthropology, University of Oregon, ⁵Department of Anthropology, Dartmouth College, ⁶Department of Anthropology, Queens College (CUNY), ⁷Department of Anthropology, Northern Arizona University, ⁸Department of Public Health Sciences, Loyola University Chicago

The gut microbiota is increasingly recognized as playing an important role in metabolism and the etiology of obesity in the developing world. However, the evolved pathways linking environmental/lifeway changes to altered gut microbial composition and energy regulation remain unclear. No research has directly investigated these topics among forager horticulturalist children characterized by growth stunting, heavy pathogen burdens, and physically active lifestyles. We characterized the stool microbiome of rural-living (N = 26, subsistence-dominant) and urban-living (N = 37, market-dominant) indigenous Shuar children (age 4-12 years) of Amazonian Ecuador using 16S rRNA gene sequencing. Significant urban-rural differences in gut microbial beta diversity were found for exact sequence variants (ESVs) belonging to *Coprococcus*, *Varibaculum*, *Dialister*, *Clostridium*, *Lachnospira*, *Oscillospira*,

ABSTRACTS

and *Desulfovibrio* ($p_{\text{PERMANOVA}} < 0.05$). We also identified significant enrichment of Firmicutes and Spirochaetes in urban-living children ($p\text{FDR} < 0.05$). More sensitive household-level analyses revealed significant effects of multiple dietary (e.g., market food items consumed), pathogen exposure (e.g., dirt floor home), and summary market integration (e.g., total income) measures on gut microbiome structure (mean AUC = 0.7, power = 0.5). Many of these specific bacterial signatures were also significantly related to child height-, weight-, and BMI-for-age (mean AUC = 0.7, power = 0.7), linking socio-environmental, gut microbiome, and nutritional status indices. To directly investigate the evolved metabolic pathways underlying these findings, we also present results describing relationships between gut microbiome composition and measures of child energy expenditure and dietary fat oxidation (obtained via doubly labeled water analysis, respirometry, and accelerometry) in the urban-living sample.

Support: NSF SPRF #SMA1606852; NSF DDIG #BCS1650674; Wenner-Gren Grant #9231

Double jeopardy: mental and physical health outcomes of exposure to genocidal rape versus genocide alone among Rwandan adults conceived during the 1994 genocide against Tutsi

GLORIEUSE UWIZEYE^{1,2}, CHANG PARK³, THOMAS W. MCDADE⁴ and JULIENNE N. RUTHERFORD¹

¹Department of Women, Children, and Family Health, University of Illinois at Chicago, Chicago, IL, USA, ²School of Nursing and Midwifery, University of Rwanda, ³Department of Health Systems Science, University of Illinois at Chicago, Chicago, Illinois, USA, ⁴Department of Anthropology, Institute for Policy Research Northwestern University Evanston, Illinois, USA

During the 1994 Rwandan genocide against Tutsi, ~350,000 women were raped by Hutu extremists. Health outcomes of the children, now adults, conceived during the genocide, especially the thousands conceived by genocidal rape, are underexplored. Predicating Developmental Origins of Health Disease and Allostatic Load perspectives, we hypothesized that early life exposure to genocide predicts worse adult health outcomes, and that individuals conceived by genocidal rape bear a double burden.

We recruited 91 24-year-old Rwandans: 30 conceived by genocidal rape (GRX), 31 born of genocide survivors not raped (GX), and 30 born of Rwandan women exposed to neither (UNX). Participants completed the Adverse Childhood Experiences International Questionnaire (ACE-IQ) and other instruments to measure adult health characteristics.

GRX had higher ACEs than both GX and UNX (bivariate linear regression $b = -1.486$, $p = 0.015$; $b = -3.448$, $p < 0.001$, respectively). Multiple linear

regression models controlled for sex, marital status, family structure, education, employment, and resilience: GRX fared worse than UNX in physical function ($b = 7.1$, $p = 0.001$), pain interfering with daily life ($b = -3.1$, $p = 0.018$), posttraumatic stress disorder ($b = -4.3$, $p = 0.035$), and depression ($b = -3.4$, $p = 0.001$). GRX fared worse than GX in physical function ($b = 4.1$, $p = 0.041$), pain interference ($b = -3.5$, $p = 0.008$), and depression ($b = -3.0$, $p = 0.004$). Relationships were moderated by ACEs; GRX with the highest ACEs had the worst outcomes.

The results support our hypothesis that early life exposure to genocide jeopardizes adult health, and that the periconceptual milieu and the specific lived experience of genocidal rape is a double burden. More research is needed to explore the biological pathways leading to these health disparities.

The pelvis relates to gut size differently in male and female humans

JEANELLE Q. UY^{1,2,3}, JOHN HAWKS³ and CAROLINE VANSICKLE⁴

¹Anthropology, Santa Monica College, ²Anthropology, California State University Long Beach, ³Anthropology, University of Wisconsin-Madison, ⁴Anatomy, AT Still University Kirksville College of Osteopathic Medicine

Obstetric demands have long been considered in the evolution of the pelvis but consideration of the interaction of pregnancy, the pelvis, and the gastrointestinal tract (gut) is lacking. Here, we explore sex differences in the relationship between gut volume and body size and pelvic dimensions. CT scans of living adult *Homo sapiens* (46 women and 42 men) were obtained to measure *in vivo* gut volume (GV) and to extract 3D models of the pelvis. We collected 19 3D landmarks from each pelvis model to acquire pelvic measurements. We used ordinary least squares regression to explore relationships between GV and body weight, height, and linear pelvic dimensions. The gut-pelvis relationship differs between men and women. Women do not exhibit any significant relationships between GV and any variable tested. GV correlates with body size and pelvic outlet size in men. GV in women scales with negative allometry possibly due to spatial constraints related to pregnancy. The lack of association between GV and body size in women, we suggest, may be due to limits imposed by the anticipation of accommodating a gravid uterus and/or the increased plasticity of the pelvis. The pattern of relationship between GV and the pelvic outlet suggests the role of the bony pelvis in supporting the abdomen in women is small relative to its role in childbirth. We conclude that gut size inference in fossil hominins from skeletal proxies is limited and confounded by sexual dimorphism.

This study was funded in part by the Vilas Fund of the University of Wisconsin-Madison.

Genomic and proteomic evidence for *Mycobacterium leprae* in human medieval dental calculus from Trondheim, Norway

ASHILD J. VAGENE¹, ANNA K. FOTAKIS¹, SEAN D. DENHAM², MIREN ORBEGOZO¹, MEAGHAN MACKIE^{1,3}, JESPER V. OLSEN³, ENRICO CAPPELLINI¹, AXEL CHRISTOPHERSEN⁴ and M.T.P. GILBERT¹

¹Section for Evolutionary Genomics, University of Copenhagen, Denmark, ²Museum of Archaeology, University of Stavanger, Norway, ³Novo Nordisk Foundation Centre for Protein Research, University of Copenhagen, Denmark, ⁴NTNU University Museum, Norwegian University of Science and Technology, Norway

Dental calculus is an excellent source of ancient microbial DNA associated with the oral microbiome, providing long-term information about microbial evolution and changes in the oral microbiome across time and populations. Opportunistic pathogens associated with the oral microbiome, which primarily cause disease in the oral cavity or respiratory tract, have previously been retrieved from dental calculus and characterized using genetic and proteomic methods. Here we present a *Mycobacterium leprae* genome, the causative agent of leprosy, recovered via shotgun sequencing of medieval human dental calculus from an individual from Trondheim, Norway. Moreover, through shotgun proteomics it was possible to retrieve ancient peptides that further validate the presence of this pathogen. Leprosy is characteristically known to manifest in the rhinomaxillary cavity and mucosal membranes, which likely contributed to *M. leprae* being deposited in this individual's dental calculus. This individual showed skeletal lesions associated with early stages of leprosy infection. To our knowledge, this is the first known example of multi-omic retrieval of *M. leprae* from archaeological dental calculus. Furthermore, this study offers new insights into dental calculus as an alternative sample source to bones or teeth for detecting and molecularly characterizing *M. leprae* in individuals from the archaeological record, especially in the absence of definitive osteological markers.

A functional comparison of primate blood microbiota and whole blood transcriptomes

NEGIN VALIZADEGAN^{1,2}, ELIZABETH K. MALLOTT^{3,4} and JESSICA F. BRINKWORTH^{1,2,5}

¹Department of Anthropology, University of Illinois Urbana-Champaign, ²Carl R. Woese Institute for Genomic Biology, University of Illinois Urbana-Champaign, ³Department of Anthropology, Northwestern University, ⁴Department of Anthropology, Dartmouth College, ⁵Department of Evolution, Ecology and Behavior, University of Illinois Urbana-Champaign

Primate immune systems have evolutionarily diverged such that management of microorganisms and responses to infectious pathogens differ

ABSTRACTS

between closely-related species. For example humans, rhesus macaques and common marmosets share ~89% genomic identity, yet strongly vary in response to bacterial pathogens/components that stimulate dysregulated inflammation in humans (e.g. *Neisseria gonorrhoeae*, *Mycobacterium tuberculosis*, bacterial endotoxin). Blood is an important immune compartment containing a high density of professional immune cells as well as a resident microbiome that may inform immune responses ahead of pathogenic infection. To assess how resident microbiota of blood may differ and correlate with immune function in primates, this study characterizes and compares the blood microbiome of three primate species representing major clades of the primate order to their whole blood transcriptomes. Blood from, humans, rhesus macaques and common marmosets was acquired from commercial sources (n=6 each), DNA isolated and sequenced for 16S rRNA genes (V3-4, Illumina Fluidigm Access Array, Miseq 2x250 V2), and bacteria cultured via enriched media, identified via mass spectrometry (MALDI-TOF MS). This data was compared to the species' whole blood transcriptomes (NHPRT). Primate blood microbiomes differed strongly in microbial species and diversity, with significant differences in Gram-negative bacterial species and load represented between primate species. Whole blood RNAseq comparisons show species differ in expression of microbial detection pathways, with canonical correlation analysis suggesting an association between bacterial membership and host immune gene expression. These results suggest that primates differ in their tolerance of particular types of blood-borne bacteria, which may affect responses to infection.

University of Illinois at Urbana-Champaign, Department of Anthropology; Franklin Mosher Baldwin Memorial Fellowships, Leakey Foundation (Award # 0888118, ID # 214236).

Demes in Disarray: Reconciling Evidence, Observation, and Population Structure in the Pleistocene

ADAM P. VAN ARSDALE¹ and MICHELLE M. GLANTZ²

¹Anthropology, Wellesley College, ²Anthropology and Geography, Colorado State University

Populations are the central unit used to measure evolutionary change. Researchers investigating the living world contend these are observable entities, often viewed as synonymous with biological species. Anthropologists, in contrast, loosely deploy the concept both in practice and theory. A survey of the 2018 American Journal of Physical Anthropology (AJPA) reveals 61 research papers that use "population" in their abstracts. The characteristics defining this analytical unit vary wildly, involving combinations of geography, language, sampling location, ethnic/

racial identity, archaeological context, occupation, class, indigeneity, and a host of other descriptors. Likewise, sample sizes for populations range from a single observation to thousands. This diversity of approaches to a term so central to the discipline implies that anthropological investigations of human evolutionary trajectories and demographic patterns are in crisis. What are the consequences of this lack of consistency? Using the published descriptions of populations taken from our flagship journal as a starting point, we explore the implications of divergent approaches to the term from two Pleistocene contexts, the lower Paleolithic site of Dmanisi and the Late Pleistocene paleoanthropological record of Central Asia. Consistent with the data from the AJPA survey, the way the term is operationalized in our two case studies mirrors the datasets explored, whether archaeological, genetic, or fossil. These differences critically undermine the ability to adequately test and represent the processes of evolution equivalently and uniformly across studies. It seems that the extent to which anthropological conceptions of 'populations' diverge from observable contemporary dynamics, the greater the interpretive peril.

Masticating in Maastricht: Quantifying the energetic cost of chewing in humans and its evolutionary significance

ADAM VAN CASTEREN¹, GUY PLASQUI², JONATHAN R. CODD³, WILLIAM I. SELLERS⁴, KORNELIUS KUPCZIK⁵ and AMANDA G. HENRY⁶

¹Department of Anthropology, Washington University in Saint Louis, ²Department of Nutrition and Movement Sciences, Maastricht University Medical Center (MUMC+), ³Faculty of Biology, Medicine and Health, University of Manchester, ⁴School of Earth and Environmental Sciences, University of Manchester, ⁵Max Planck Weizmann Center for Integrative Archaeology and Anthropology & Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, ⁶Faculty of Archaeology, Leiden University

Major evolutionary changes in hominin craniofacial morphology are often explained in terms of energetic optimization for the consumption of various foods. For example, the enlarged masticatory system of robust australopiths is thought to enable more efficient chewing of large volumes of hard or tough foods. Similarly, the adoption of tools and cooking are thought to provide energetic savings because processed food may provide more energy due to reduced chewing time. However, the actual energetic costs of chewing in hominoids have never been quantified. We collected data using mask respirometry to measure energetics and electromyography (EMG) to determine activity of the masseter of 25 human volunteers chewing flavourless gums of low and high stiffness. Chewing of both gums results in a significant increase in energy expenditure (kJ/min) relative to basal metabolic rate (mean±sd =

4.26±0.53), with stiffer gum (4.91±0.59) always requiring more energy than the compliant substrate (4.69±0.54) (paired sample t-tests all p<0.000). The compliant gum was chewed at a higher frequency, but with lower peak EMG value. Extrapolated over average daily chewing times, the cost of mastication is well below 1% of total energy expenditure (TEE). Apes chew longer, thus chewing may account for up to 4% of their TEE. This suggests that at least in modern humans, selection on chewing efficiency (change in particle size/chewing work) is likely biased towards traits facilitating food breakdown rather than energetic considerations. Strong selection to conserve chewing energetics are likely found only in primates that spend a large amount of time masticating.

Funding from the European Research Council (ERC) [grant number STG-677576 ("HARVEST")], and the Max Planck Society through the Max Planck Weizmann Center for Integrative Archaeology and Anthropology.

African Land Mammal Ages: Definition and inclusion of primate range data

JOHN VAN COUVERING^{1,2,3} and ERIC DELSON^{1,2,3,4,5}

¹Vertebrate Paleontology, American Museum of Natural History, ²NYCEP (New York Consortium in Evolutionary Primatology), ³PhD Program in Anthropology, CUNY Graduate Center, ⁴Anthropology, Lehman College/CUNY, ⁵Institut Català de Paleontologia Miquel Crusafont (ICP), Universitat Autònoma de Barcelona, Spain

We recognize and define 16 pan-continental African land mammal ages, or AFLMAs, spanning the Cenozoic Era and the Afro-arabian continent, the planet's second largest land mass. Almost 800 fossil genera from over 350 site units have been identified in coastal deposits, karst caves, and in the Neogene rift valleys. Given the well-developed geochronologic framework and continuing revision to the fossil record – both stimulated in large part by interest in the story of human evolution in Africa – and also to compensate for the variation of ecosystems across such great distances, the AFLMAs are biochronological units defined by basal reference localities, not biozones identified by selected genera. Africa is the highest of all continents, but almost every Paleogene locality was formed at sea level; the fossil record of its rainforest ecosystem remains virtually unknown, as does that of the great interior plateau; and the Paleogene fauna is highly endemic, whereas the Neogene begins with open exchange with Laurasia following the Tauride collision, with a simultaneous (and probably tectonically related) opening of the East African rift valleys in which the newly revolutionized fauna is abundantly preserved. Some transitions between AFLMAs are marked by major faunal turnovers, while others reveal little change. The primate record includes 100 genera, present in all 16 AFLMAs, including several recognized in

ABSTRACTS

2019. The AFLMAs document the continent-wide response to increased seasonality during the Neogene and the unusually rapid transformation of the hominin lineage under the novel conditions of the expanding open-country ecosystem.

Funded in part by National Geographic, Leakey Foundation, Wenner-Gren Foundation, National Science Foundation, Smithsonian Institution, University of Colorado, Goldfields Namibia, John Simon Guggenheim Memorial Foundation, PSC-CUNY and AMNH.

Subspecies in human evolution

LAURA A. VAN HOLSTEIN and ROBERT A. FOLEY
Department of Archaeology, University of Cambridge

The hominin lineage is exceptionally speciose. What remains unknown is whether the increased diversification this speciosity hints at also occurred *below* the species level, as Darwin predicted in his "Manufactory Hypothesis". That is, should we expect hominin species to have comprised more subspecies than other apes? And what evolutionary "role" might subspecies have played in the generation of hominin diversity?

We first establish the general trends in the relationship between subspecies richness and species richness in all mammals. Species range is the most significant predictor of subspecies richness in all clades ($p < 0.001$). Ecological substrate, further, mediates the strength of the correlation between generic speciosity and average subspecies per species: it is stronger in non-terrestrial mammals (Kendall's tau = 0.27, $p < 0.001$ in non-terrestrial groups and 0.11, $p < 0.001$ in terrestrial groups). Primates are an exception to this, with a tau of 0.24. We then simulate three models of diversification to predict, based on known species richness, how many subspecies per species a clade should comprise.

We then tested whether subspecies richness correlates with intrinsic traits (age at female maturity, body mass, and dietary diversity) regardless of extrinsic context in 386 species from four mammalian higher taxa (Primates, Carnivora, and Cetartiodactyla). In Primates, slower life histories are associated with higher subspecies richness.

Based on these results, we predict likely numbers of subspecies key hominin taxa will have comprised. We conclude by discussing whether or not hominin subspecies can be considered incipient species, and how we might detect them in the fossil record.

This work is funded by a St. John's College Benefactor's Scholarship and Cambridge University Vice-Chancellor's Scholarship.

Male hue, visibility and the evolution of pelage sexual dichromatism in primates

ANDREW VAN HORN¹, AMANDA N. SPRIGGS², BENJAMIN C. WILHELM³, JASON M. KAMILAR⁴, L. CHRISTIE ROCKWELL⁵ and BRENDA J. BRADLEY⁶

¹Department of Biology and Biochemistry, University of Houston, ²Department of Anthropology, State University of New York at Albany, ³Department of Natural Sciences and Mathematics, State University of New York at Cobleskill, ⁴Department of Anthropology, University of Massachusetts, Amherst, ⁵Department of Anthropology, Temple University, ⁶Center for the Advanced Study of Human Paleobiology, The George Washington University

It is generally assumed that pelage sexual dichromatism (PelSD) evolved in many primate species as a consequence of sexual selection on male pelage color. However, whether male coloration confers benefit through direct female choice or some other aspect of mate access is unclear. Further, it is unknown whether selection acts on hair hue (the relative concentration of melanins) or luminance (the absolute concentration of melanin) or both. We examined this using color-corrected high-resolution photographs of primate research skins (N = 85 species; 340 individuals) in museum collections. Measurements of luminance and hue were taken for the dorsal and ventral aspects of the trunk of each specimen. These measurements are proxies for the absolute and relative concentrations of melanin(s) in primate pelage. Highly dichromatic species were identified and the evolutionary patterns of luminance and hue in males and females of those species were analyzed using phylogenetic comparative methods. Species where male luminance or hue was under selection without concomitant selection on females were considered to be under sexual selection. There was little clear evidence of sexual selection on male luminance in highly dichromatic species. However, there was substantial evidence of sexual selection on male hue. Sexual selection on male hue and a trend toward yellower pelage in males of highly dichromatic species suggests a shift to phaeomelanin production in those males. Taken together, our results indicate that male hue has evolved to improve visibility to conspecifics, driving the independent evolution of PelSD in several primate lineages.

This work is funded by grants from the NSF (BSC-1546750) and The Wenner-Gren Foundation, and by The George Washington University.

An integrated (micro) finite element approach to analyze force distributions in the primate thumb during functional grasps

TIMO VAN LEEUWEN^{1,2}, MARCO TY. SCHNEIDER³, HARRY G. VAN LENTHE² and EVIE E. VEREECKE¹

¹Development and regeneration, KU Leuven, ²Department of mechanical engineering, KU Leuven, ³Auckland Bioengineering Institute, University of Auckland

The primate thumb, and specifically the trapeziometacarpal (TMC) joint, plays a significant role in manipulation as well as in locomotion. As bone is a dynamic tissue, we expect that the TMC joint will show adaptations to its dominant loading regime. We hypothesize that the force distribution in the TMC joint during a specific grip type will be different between primates with a distinct hand use: the suspensory hylobatids, the knuckle-walking bonobos and the palmigrade/digitigrade macaques.

The most suitable method to investigate differences in loading regime is using micro finite element (FE) modelling, however, to date it remains difficult to accurately implement force boundary conditions based on specific loading conditions. Therefore, we developed a new fully open source CT-based approach to simulate the force distribution within the TMC joint.

Primate cadaveric hands (7 hylobatids, 5 bonobos, 5 macaques) were CT scanned in five standardized functional grasps. After segmentation and 3D reconstruction, the bone models were fed into a pipeline to pseudo-automatically generate parametric models in a two-step approach. First, the force distribution on the articular surface is calculated using FE, and second, these subchondral forces are applied to micro CT based individual TMC bone models for the micro FE computation of the internal stress distribution in the trapezium and first metacarpal.

The pipeline we present allows for an efficient development of parametric FE models and advanced implementations of micro FE boundary conditions. Furthermore, the approach is suitable for use in other joint systems and taxa.

Morphological and functional adaptations in the hand of arboreal hylobatids and terrestrial macaques

MARIE J.M. VANHOOF, TIMO VAN LEEUWEN, MAARTEN VANNESTE and EVIE E. VEREECKE
Development and Regeneration, KU Leuven

Nonhuman primates have a diverse locomotor repertoire with an equally diverse hand use. Based on dominant hand use, we can distinguish between terrestrial and arboreal taxa. We expect the 'arboreal' hand to be adapted towards high mobility, whereas the 'terrestrial' hand will show morphological adaptations to loading.

ABSTRACTS

In our study, we quantify hand musculature and wrist morphology, as well as wrist mobility during radioulnar deviation, in arboreal hylobatids and terrestrial macaques. We collected data from 7 hylobatid (*Hylobatidae*) and 7 macaque (*Macaca mulatta*) specimens and compared the range of motion (ROM) with data from 18 human volunteers. We CT-scanned each specimen in neutral, and maximal radial and ulnar deviation using a rig to standardize wrist positions. We created 3D bone models of the carpal bones, third metacarpal, ulna and radius, which are used for kinematic and morphometric analyses (3DGM). Afterwards, we performed detailed dissections of arm and hand muscles.

For wrist mobility, ROM during radioulnar deviation is highest in hylobatids ($73.1 \pm 8.7^\circ$) and lowest in macaques ($42.2 \pm 5.2^\circ$), while humans ($62.7 \pm 9.1^\circ$) overlap with the hylobatid range. The large ROM in hylobatids appears to be linked to their ulnar and triquetral morphology. For muscle anatomy, macaques have relatively stronger radioulnar deviators, contributing to wrist stabilization, and hylobatids have flexors with relatively longer tendons, concomitant with their brachiating behavior. However, further research is needed to elucidate the precise contribution of muscle anatomy and 3D geometry of the carpal bones to overall wrist mobility in terrestrial and arboreal primates.

Exploring the effect of body mass on pelvic features that vary by sex

CAROLINE VANSICKLE^{1,2}, LOGAN JEPSEN³ and KAYCEE JOHNSON³

¹Department of Anatomy, Kirksville College of Osteopathic Medicine, A.T. Still University of Health Sciences, ²Evolutionary Studies Institute, University of the Witwatersrand, ³Kirksville College of Osteopathic Medicine, A.T. Still University of Health Sciences

Human bony pelvises have features that vary by sex and are used by anthropologists to estimate sex from skeletal remains. However, human pelvic shape does not fit a simple binary model where male pelvises look one way and female pelvises another. Instead, there is sometimes overlap between and variation within sexes for the morphology of these pelvic features.

Here, we examined the complexity of shape variation for two pelvic features that are used to estimate sex: the greater sciatic notch and the superior pubic ramus. Generally, the greater sciatic notch is narrow and J-shaped in males and wide and U-shaped in females, while the superior pubic ramus is short in males and longer in females. We hypothesized that differences in body mass would explain the range of morphologies found within each sex for these features.

We digitized landmarks and semilandmarks representing these features on 3D models of hip bones from the Bass Collection (M=20, F=23). We then analyzed the landmark data using 3D geometric morphometrics to determine if any pattern existed between body mass and the principle components explaining the shape variation of each sex. We found that while body mass does not fully explain the variation observed for each feature, it does contribute to that variation and have implications for future sex estimation methodologies.

Intra-population variation in non-metric cranial traits for ancestry determination. A case study with European populations

ALESSANDRA VECINO GAZABON

Department of Education, American Museum of Natural History

Most researchers default to a list of non-metric traits compiled by Rhine (1990) to assess ancestry based on inter-population contrasts. A close analysis of the study reveals critical issues with results that have become “standards” since: Broad ancestral groups (African, European, Asian) are distinguished though samples originate from narrow, often unidentified populations; extremely small sample sizes; and use of inconsistent categories and terminology. The current study seeks to test whether the widely used characterization for Europeans (square eyes, curved zygomatic sutures, bulging palatine sutures, parabolic dental arcades) was substantiated when intra-population variability was considered. 167 adult crania from three established regional divisions used by Krogman and Iscan (1986) were analyzed; Western (56), Eastern (67), and Southern (44). The non-metric traits—orbital shape, shape of zygomatic suture, shape of palatine suture and palate shape—were selected given their popularity in analyses of inter- and intra-population variability. Data were analyzed using frequency counts from trait-specific scoring systems, and chi-square test. Results confirm the general characterization of European crania. Though the contrasts were statistically significant, with one exception, each of the variants in all traits were found in all regions. No variant was present in frequencies greater than 60%, and for the second most common variant frequencies were as high as 25%. Results demonstrate more complex variability than considered in previous studies. These variants may not be a reliable “marker” for European ancestry. Future analyses should include non-European populations for comparison to gauge how increased variability affects the ability to classify individuals as European.

Eulemur Nasal Cavity Variation across Latitude and Forest Type

CIELA A. VEGA

Anthropology, Boston University

The genus *Eulemur* is prolific throughout Madagascar and shows variation across distinct habitat types. However, adaptations for habitat variation at the species and subspecies level are mostly studied in relation to behavior or diet. We acknowledge that the sense of smell has an influence on diet and it is also established that nasal morphology can differ based on climate and geographic locales. As a result, we hypothesize that *Eulemur* species living in different forest types and latitudes across Madagascar will display differences in their nasal cavity morphology. We used data from Morphosource of five *Eulemur collaris* known to live in sub-humid forests and eight *E. albifrons* known to live in lowland forests. To analyze shape variation, we placed 19 landmarks on six 2D coronal slices of the nasal cavity using ImageJ. In Morphologika we performed a Procrustes analysis then a Principle Components Analysis to determine if at various points throughout the nasal cavity we could see distinct clustering between the two species. Of the six slices we analyzed, *E. collaris* and *E. albifrons* displayed more distinct clustering in the more internal slices relative to the furthest rostral and caudal slices. This morphological variation could have implications for how these primates utilize their sense of smell in varying environments. Through further analysis and the inclusion of more *Eulemur* species we will be able to discern if the variation we see here can be related to their ecology.

We acknowledge the Undergraduate Research Opportunities Program (UROP) as a source of funding.

Detection of early postmortem changes in burnt bones through histotaphonomical analysis

EMESE I. VEGH¹, ANDREA CZERMAK¹, NICHOLAS MARQUEZ-GRANT² and RICK J. SCHULTING¹

¹Research Laboratory for Archaeology and the History of Art, School of Archaeology, University of Oxford, ²Cranfield Forensic Institute, Cranfield University, Defence Academy of the United Kingdom

Recent histotaphonomic studies have focused on the presence of features thought to be caused either by bacteria (microscopic focal destruction/MFDs and cyanobacterial tunnelling) or fungal (Wedl tunnelling types 1 and 2) attack on unburnt, mostly archaeological bones. Identifying these diagnostic characteristics on burnt bones could reflect some degree of decomposition before cremation, with important repercussions for both

ABSTRACTS

forensic and archaeological contexts. Thus, this study aims to establish the utility of diagenetic features as a proxy for the body's condition prior to incineration.

Fleshed pig (*Sus scrofa*, N=20) tibiae were left exposed on a field, then collected at 2 weeks, 1, 3, and 6 months intervals before being cremated in an outdoor fire (≤ 750 °C bone temperatures). Fresh (fleshed) legs (N=10) acted as unburnt and burnt controls. The fresh, decayed, and post-burnt bone thin sections (~50-70 μ m) were examined under transmitted light microscopy and backscatter scanning electron microscopy (BSEM). Diagenetic traits were quantitatively assessed by a data labelling application built in Python and Javascript programming languages. Statistical analysis showed no significant correlation between the time of decay and the presence of diagenetic features on either unburnt or burnt bones. Tunnelling is more pronounced in the cremated bones than in the pre-burnt ones in all postmortem intervals.

Histotaphonomic features survived cremation. However, their presence in freshly burnt bones and absence in the unburnt controls suggest that the presence of many, if not all of these features is, in fact, not due to bacterial bioerosion or fungal attack.

Meyerstein fund and Wolfson College (University of Oxford)

Development of the cranial sexual dimorphism during aging

JANA VELEMINSKA¹, NIKOL FLEISCHMANNOVA¹, BARBORA MUSILOVA¹, JAN DUPEJ^{1,2}, SARKA BEJDOVA¹ and JAROSLAV BRUZEK¹

¹Department of Anthropology and Human Genetics, Charles University, Faculty of Science, ²Department of Software and Computer Science Education, Charles University, Faculty of Mathematics and Physics

The most pronounced cranial differences between males and females are concentrated in regions with muscle attachment, which are highly influenced by physical constitution and by different hormonal distribution. Sexual dimorphic traits increased until adulthood but tended to change in both soft and skeletal tissues with the elderly age. Although ageing in both sexes shared common traits, the reduction of sexual dimorphism in senile age was supposed. The main goals of this multipopulation study were (1) to compare cranial aging in Czech and French contemporary samples of adult individuals; (2) to evaluate development of cranial sexual dimorphism during senescence.

The entire cranial surface was analyzed using coherent point drift-dense correspondence analysis. The study sample consisted of 245 CT scans of recent southern French (103) and Czech (142) populations. Virtual scans in age range from 18

to 92 years were analyzed using 3D software systems (Rapidform, Avizo, Morphome3cs) and innovative approaches in geometric morphometrics. Sexual dimorphism was very similar between the two populations, but the population specificity of cranial shape was high. The entire surface of the skull (cranial form) differed significantly between sexes at a significance level of $\alpha = 0.05$. After size normalization (cranial shape), females had more globular skulls, more convex foreheads with frontal eminence, and less prominent glabellar and nasal regions with lower and more vertically oriented premaxilla. Sexual dimorphism tended to diminish in the elderly age category (above 60 years). These most notable changes were observed in supraorbital, frontal and nuchal regions.

This research was funded by the Charles University Grant Agency, research grant GAUK No. 1590218.

Predicting human appearance from aDNA: first insights in an Imperial Rome sample

VIRGINIA VELTRE, FLAVIO DE ANGELIS and OLGA RICKARDS

Biology, University of Rome Tor Vergata

Forensic DNA Phenotyping (FDP) is an emerging molecular approach seeking to make probabilistic inferences about individual appearance traits through genetic markers typing. Despite the phenotypic identification being the ultimate goal of FDP, the bio-geographic inferential information is mandatory for individual profiling due to the close relationship between the environment and some phenotypic characteristics. The noticeable differences for genetic markers distribution in worldwide populations make them valid Ancestry Informative Markers. This work aims to identify genetic features of ancient Romans (1st-3rd sec. C.E.), by the dissection of their genomes in order to compile individual biological profiles. WGS (Whole Genome Sequencing) has been carried out on thirty-one ancient samples: specific pipelines were applied to list functional variants in order to constitute a panel of prioritized genes for skin tone identification. The preliminary results allow to identify heterogeneous landscape where pale skin could be proficiently identified in people sharing European ancestry. Remarkably, few people point out allelic frequencies suggesting their intermediate skin colour: their genomic make up is consistent with a North-African and middle eastern origin. The identification of foreigners might critical in the proper identification of demographical estimations about ancient Roman population. The identification of the homelands, therefore, could clarify the migration routes in Imperial Age, not only for humans, but also for the merchandise Rome imported from colonies. Finally, this project on the characterization

of putative immigrants to Imperial Rome will broaden the knowledge about the immigrant ratio of the population of the largest urban center in the preindustrial world.

Wood and meat as complementary sources of sodium for Kanyawara chimpanzees (*Pan troglodytes*)

EMILY M. VENABLE¹, ZARIN MACHANDA^{2,3}, LINDSEY HAGBERG², JORDAN LUCORE², EMILY OTALI², JESSICA M. ROTHMAN⁴, MOREEN UWIMBABAZ⁵ and RICHARD WRANGHAM^{1,2}

¹Human Evolutionary Biology, Harvard University, ²Kibale Chimpanzee Project, Fort Portal, Uganda, ³Department of Anthropology, Tufts University, ⁴Department of Anthropology, Hunter College, ⁵Faculty of Forestry and Nature Conservation, Makerere University

Sodium, a vital micronutrient, is often in scarce supply in tropical, inland environments; however, it is sometimes found at high concentration in decaying wood. Chimpanzees in the Kanyawara community of Kibale National Park, Uganda occasionally consume wood, primarily from decaying *Neoboutonia macrocalyx* (Euphorbiaceae) trees. Here, we test the hypotheses that wood-eating facilitates acquisition of sodium and that wood-eating occurs in response to low availability of sodium from other dietary sources. We studied the behavior of over 50 Kanyawara chimpanzees and quantified the sodium content of dietary items, including wood from tree species consumed or not consumed. To assess variation in sodium intake, we used data on seven years on feeding times on plant foods, 18 months on feeding rates by adult females, and 20 years on meat-eating. We found that wood consumed by chimpanzees had substantially higher sodium content than all other dietary items tested. Major dietary sources of sodium were wood, fruits and meat. Wood-eating was negatively correlated with fruit-eating ($F=5.905$, $p=0.015$). Females ate wood more often than males (Wald $X^2 = 4.589$, $p = 0.032$), while males had a greater probability of consuming meat at predation events ($F = 13.582$, $p < 0.001$). We propose that females ate wood more often than males because females had reduced access to meat, their preferred sodium source. Our findings suggest sodium acquisition motivates chimpanzees to consume both meat and wood and support the Meat-Scrap Hypothesis in that meat and wood are consumed in small quantities for their micronutrient content, particularly sodium.

Funding provided by the Harvard College Research Program, the Harvard University MCZ, Hunter College of CUNY, the NSF (grant #9807448, 0416125, 1355014, 1521528), and NIH-National Institute of Aging (grant 1R01AG049395).

ABSTRACTS

Osteology and Paleogenomics: Comparing Applications Using Commingled and Fragmented Pelvis Material from Midnight Terror Cave, Belize to Examine the Sex Dynamics of Human Sacrifice

CRISTINA VERDUGO¹, NASREEN BROOMAND¹, KIMBERLY ZHU² and LARS FEHREN-SCHMITZ¹

¹Anthropology, University of California, Santa Cruz, ²Anthropology, University of California, Los Angeles

This paper reports on the application of osteological and paleogenetic techniques to determine sex ratios of the sacrificial population in Midnight Terror Cave. Our analysis examined all pelvises (n=102) from the commingled and heavily fragmented skeletal assemblage. Anthroposcopic analysis identified 12 fragments as male and 23 fragments as female. After taking side, age, and sex into account, an MNI of 12 was determined, consisting of 5 women and 7 men. With paleogenetic techniques, we were able to establish sex for elements (n=5) that were either subadult material or too fragmentary for sex estimation via anthroposcopic analysis, including 4 females and 1 male. This data is particularly important at Midnight Terror Cave for assessing the link between sex and human sacrifice. Serious interest in human sacrifice developed in the 1990s at the same time that warfare was being proposed as a cause for the collapse of Maya civilization (Demerast 1990). As a result, models of human sacrifice tended to assume that victims were largely male war captives. However, few large skeletal assemblages related to sacrifice exist to provide hard data on the issue. Our study demonstrates the ability of paleogenetic data to augment osteological approaches by definitively determining sex of an inestimable skeletal element; adding to the overall demographic data used to answer hypotheses.

Comparative morphological study on the shape variance of the scapula in extant Cercopithecidae

MARIE VERGAMINI¹, LISA M. DAY², CHRISTINA MCGRATH^{2,3}, ERNESTO GAGARIN^{2,3} and AMY L. RECTOR³

¹Integrative Life Sciences, Virginia Commonwealth University, ²Department of Anthropology, Virginia Commonwealth University, ³Department of Biology, Virginia Commonwealth University

Morphological variation in forelimb bones has been tied to substrate use in Cercopithecidae. Studies of the distal humerus and proximal ulna (Rector et al., 2018) suggest that African and Asian monkeys' locomotor repertoires can be distinguished through analysis of variation of the elbow joint. Given that the scapula may be directly involved in weight-bearing during locomotion - similar to the elbow - the relationship between morphological variation and arboreality in the glenoid cavity, acromion, and coracoid process may be analogous.

Using a Microscribe, 25 landmarks were collected to capture the shape of the scapula from a sample of 50+ extant Cercopithecidae. Each species was placed in a locomotor category including ground quadrupedalism, branch quadrupedalism, arm-swinging, and branch quadrupedalism, and branch and ground quadrupedalism based on their primary locomotor strategy during traveling. Variation was analyzed using 3D geometric morphometric PCA, PGLs, and phylogenetic ANOVAs to determine if differential substrate use can be identified through analysis of shape variation in the scapulae of Cercopithecidae.

Results suggest that scapular morphology is more variable in branch quadrupedal cercopithecids than ground quadrupedal ones. However, variation in the scapula can be used to successfully differentiate ground quadrupeds and branch quadrupeds in modern Cercopithecidae. As a valuable factor in the ecology of these primates, this locomotor behavior contributes information on niche differentiation, resource competition, and community organization in living and fossil primates.

Funding from VCU's Rice Rivers Center.

A curious case of prehistoric patchwork: the manipulation of a Neolithic skeletal remains from Pommeroeul, Belgium

BARBARA VESELKA¹, DAVID REICH^{2,3,4}, GIACOMO CAPUZZO⁵, REBECCA BERNARDOS², LAURELINE CATTELLAIN⁶, KIMBERLY CALLAN^{2,3}, FATMA ZALZALA^{2,3}, CHARLOTTE SABAU⁷, MATHIEU BOUDIN⁸, HENRICA ANNAERT¹, SARAH DALLE⁷, MARTA HLAD¹, GUY DE MULDER⁷, IOANNIS KONTOPOULOS¹, KEVIN SALESSE⁵, AMANDA SENGELOV⁹, ELISAVET STAMATAKI¹, MARTINE VERCAUTEREN⁹, EUGENE WARMENBOL⁹, DRIES TYS¹ and CHRISTOPHE SNOECK^{1,10}

¹Department of Art, Sciences, and Archaeology, Vrije Universiteit Brussel, ²Department of Genetics, Harvard Medical School, ³Howard Hughes, Medical Institute, ⁴Broad Institute, of MIT and Harvard, ⁵Department of Anthropology and Human Genetics, and Biology of Organisms and Ecology, Université Libre de Bruxelles, ⁶Cedarc, Musée du Malgré-Tout, ⁷Department of Archaeology, University of Ghent, ⁸Royal Institute, for Cultural Heritage, ⁹Department of History, Arts, and Archaeology, Université Libre de Bruxelles, ¹⁰G-Time Laboratory, Université Libre de Bruxelles

The site of Pommeroeul, Belgium, was discovered in the 70's and was classified as a Gallo-Roman site, consisting of 117 cremations and only one inhumation. Since the preservation of the unburnt human skeletal remains was excellent, it was assumed that this inhumation also dated to the Roman period. Unexpectedly, radiocarbon analysis yielded a date around 3000 BC that dated the inhumation to the Late-Neolithic. The unburnt individual lay in a crouched position on its right side with one arm flexed under one of the femora and the other flexed next to the body. Macroscopic

analysis of the bones showed differences in metrics, morphology, and robusticity in many parts of the skeleton, such as the long bones, vertebrae, os coxae, and metatarsals. These differences suggested that the "single" individual actually was composed of body parts that belonged to multiple individuals, and afterwards being buried as "one" individual. Although it is not uncommon for a Late-Neolithic grave to contain a single individual with commingled parts of other individuals, the case of Pommeroeul is highly unusual. Ancient DNA analysis of two long bone and the cranium confirmed that the various bones belonged to multiple individuals, two males and a female, that were used to construct the inhumated individual. This study presents a unique way of burying the deceased in Late-Neolithic Belgium, thereby improving our understanding of funerary practices in prehistoric Western-Europe.

No funding.

Genetic affinities of pre-Columbian Mayas from Xcaret, Mexico

VIRIDIANA VILLA-ISLAS¹, MIRIAM BRAVO-LÓPEZ¹, ANGÉLICA GONZÁLEZ-OLIVER², ERNESTO GARFIAS-MORALES² and MARÍA C ÁVILA-ARCOS¹

¹International Laboratory for Human Genome Research, UNAM, ²Departamento de Biología Celular, Facultad de Ciencias, UNAM

The Maya civilization is one of the most well-known pre-Columbian civilizations of Mexico. They established mainly in the Southeastern Mexico, Guatemala, Belize and the western portions of Honduras and El Salvador. This civilization had a great development during the classic period followed by a political collapse in the Postclassic, which resulted in the abandonment of some of their cities and migrations of Maya people to other areas. During the colonization of Mexico by Europeans, Maya population, like most Native American populations, experienced a drastic population decline that potentially impacted their present-day genetic diversity. As a first step to contribute to the knowledge of the genetic composition of pre-Columbian Mayas, here we report the recovery of ancient DNA from four human pre-Columbian bones from the Postclassic period (1,100-1,500 CE), found in the archaeological site of Xcaret in Quintana Roo, Mexico. Shotgun low-depth sequencing data were generated for all samples. We observed a high frequency of damage patterns and low endogenous content, as expected for remains found in tropical environments. As anticipated, Principal Components and ADMIXTURE analyses of genome-wide data from the best-preserved sample, showed a greater genetic affinity of the pre-Columbian individual with present-day Maya population from the Yucatan Peninsula. Interestingly, f3-outgroup tests showed that the ancient Maya also shares a considerable level of genetic drift with present-day Central-East

ABSTRACTS

Mexican populations, in agreement with previous findings of IBD sharing between present-day Mayas and present-day indigenous groups from Central-East Mexico, like the Totonacs.

Integration of the hominoid spine, part I: Shoulder function and integration of the cervical and thoracic vertebrae

CATALINA I. VILLAMIL¹ and EMILY R. MIDDLETON²

¹School of Chiropractic, Universidad Central del Caribe, ²Dept. of Anthropology, University of Wisconsin-Milwaukee

Shoulder anatomy has evolved substantially in hominins relative to other hominoids, and these anatomical changes have been linked to the loss of locomotor function in the shoulder and to the increase in manipulative activities in hominins. Importantly, the evolution of modern human-like shoulder morphology likely enabled high speed, high accuracy throwing, which is used for hunting. Many of the muscles involved in shoulder function attach to the vertebral column, and shifts in shoulder anatomy and function would have inevitably impacted relationships between muscles and vertebrae, as well as the potential evolutionary trajectories of the cervical and thoracic vertebrae. This study aims to clarify how shoulder evolution may be linked to the evolution of the cervicothoracic regions by investigating integration of these regions in *Homo* (N=151), *Pan* (N=92), and *Hylobates* (N=77). Four variables were calculated for vertebrae C3 through T12 and their paired relationships: VE, mean integration, mean evolvability, and mean conditional evolvability. Results show that *Homo* tends to display the highest evolvability and conditional evolvability, while *Pan* is intermediate, and *Hylobates* is the lowest. *Hylobates* has greater integration between the lower cervicals and thoracics than the other taxa, and *Pan* is intermediate in overall integration between *Hylobates* and *Homo*. These results are consistent with the hypothesis that the locomotor function of the hominoid shoulder significantly constrains the evolution of the cervicothoracic region and suggest that shoulder morphologies associated with swinging and climbing may result in significantly more constraints in non-human hominoids and a *Pan*-like hominin ancestor than in *Homo*.

Funding provided by the Wenner-Gren Foundation, Leakey Foundation, New York University, and an American Association for Anatomy postdoctoral fellowship.

ABO blood type variation in archaic humans: haplotype structure in Neanderthals and Denisovans

FERNANDO A. VILLANEVA¹, KEOLU FOX² and EMILIA HUERTA-SÁNCHEZ¹

¹Center for Computational Molecular Biology, Brown University, ²Department of Anthropology, UC San Diego

Genetic variation of the ABO gene is well characterized in modern humans, corresponding to phenotype variation observed globally in ABO blood types. However, little attention has been paid to ABO blood type variants in our archaic relatives: neanderthals and denisovans. Here, we analyze coding variation at the ABO locus from next-generation sequencing in ~2,500 individuals from 28 populations, including two neanderthal and one denisovan individuals. Our analysis validates previous estimates of ABO blood type frequencies in living populations. We then use the modern human haplotypes to impute ABO genotypes for the three archaic human genomes. We found that the Altai neanderthal is homozygous for a derived neanderthal variant of the O allele, while the Vindija neanderthal is an AO heterozygote, the A allele is a derived neanderthal variant, and the O allele is an ancestral variant shared with modern human populations. The denisovan individual is homozygous for an ancestral variant of the O allele, also shared widely with modern humans. Perhaps more surprisingly, the O allele variant found in the Altai neanderthal is also found at very low frequencies in modern European and Southeast Asian individuals, and our genetic distance analysis suggests this allele was introgressed through neanderthal-human gene flow. Our study explores the genetic variation of the ABO gene in two extinct archaic human populations, and highlights how neanderthal-specific ABO variants were inherited by modern humans, which are still retained in observable frequencies today.

New Pliocene hominin specimens from East Turkana are associated with extensive C₄ resources

AMELIA VILLASEÑOR¹, DAVID R. BRAUN², KEVIN UNO³, ELDERT ADVOKAAT⁴, MARION BAMFORD⁵, ANNA K. BEHRENSMEYER⁶, BOBE RENÉ⁷, CARVALHO SUSANA⁸, HAMMOND S. ASHLEY⁹, KINYANJUI RAHAB¹⁰, DAN V. PALCU¹¹, MARK SIER¹² and CAROL V. WARD¹³

¹Department of Anthropology, University of Arkansas, ²Center for the Advanced Study of Human Paleobiology, The George Washington University, ³Lamont-Doherty Earth Observatory, Columbia University, ⁴Department of Physical Geography, Utrecht University, ⁵Evolutionary Studies Institute, University of the Witwatersrand, ⁶Department of Paleobiology, National Museum of Natural History, ⁷Gorongosa, Gorongosa National Park, ⁸Institute for Cognitive and Evolutionary Anthropology, Oxford University, ⁹Division of Anthropology, American Museum of Natural History, ¹⁰Department of Earth Sciences, National Museums of Kenya, ¹¹Department of Physical Oceanography and Geochemistry, University of Sao Paulo, ¹²Department of Earth Sciences, University of Oxford, ¹³Department of Pathology and Anatomical Sciences, University of Missouri

The mid-Pliocene corresponds to a peak in hominin diversity. Two species, *Australopithecus afarensis* and *Kenyanthropus platyops*, are known from the Turkana Basin region after 3.44 million years ago (Ma). Here, we describe four hominin specimens, the first occurrences from East Turkana between 3.9 and 3.44 Ma, and the paleoecological evidence from the associated faunal community and paleovegetation proxies. Existing geochronology and paleomagnetic analysis of sediments constrain the age of these specimens from 3.55-3.44 Ma. Stable carbon isotopes from pedogenic carbonates (n=50) indicate that East Turkana was less wooded than concurrent habitats in the Nachukui and Hadar Formations, though there is no difference in mean $\delta^{13}\text{C}$ values. When converted to percent C₄ values, pedogenic carbonates suggest that C₄ abundance was less than 50% (median 28%). In contrast, stable carbon isotopes from leaf wax biomarkers (n=14) show C₄ abundance up to 97% (median 51%). Mammal abundance associated with the hominin fossils includes primarily alcelaphin bovids, as well as a greater proportion of small cercopithecine primates compared to the whole East Turkana region. Stable carbon isotopes from mammal enamel (n=45) show that many large herbivores had a mixed C₃/C₄ diet dominated by C₄ resources (median 60%). These data suggest that mid-Pliocene hominins in East Turkana were associated with environments that supported extensive C₄ resources and a diverse primate community. Our findings suggest that multiple paleoecological proxies are necessary to demonstrate a cohesive picture of the paleoecosystem at fossil sites.

This research was funded by the Leakey Foundation, National Science Foundation (BCS-1624398 and DGE-1246908) and the Ford Foundation.

Testing repeatability in dental morphology: Interobserver error in a worldwide collection

TATIANA VLEMINCQ-MENDIETA¹, LAURA E. CIRILLO¹ and DOROTHY DECHANT²

¹Anthropology, University of Nevada, Reno, ²Center for Dental History and Craniofacial Study, AA Dugoni School of Dentistry, University of the Pacific

Despite the standardization of dental morphology (Turner et al., 1991; Edgar, 2017; Scott and Irish, 2017) and its broad use in biological anthropology, very few publications have evaluated the levels of interobserver error inherent in these data. This study identifies levels of error across several traits. Using the Arizona State University Dental Anthropology System definitions (Scott and Irish, 2017), three observers scored 17 traits on 20 skulls found in the Atkinson Collection housed at the University of the Pacific AA Dugoni School of

ABSTRACTS

Dentistry. The two experienced observers scored an additional 32 skulls to expand sample variation. A weighted Cohen's kappa (k) was used to evaluate rater agreement.

Traits with the highest k between all three observers included UI2 shoveling (0.64-0.86), UM2 hypocone (0.74-0.84), UM1 Carabelli's cusp (0.79-0.92), and LM1 cusp number (0.74-0.84). Lowest agreement came from upper canine distal accessory ridge (DAR) (0.03-0.21), UI2 *tuberculum dentale* (TD) (0.10-0.53), and LM2 deflecting wrinkle (0.11-0.15). Seven traits showed improved rater agreement in relation to experience level: UI1 TD, UM1 hypocone, UM3 Carabelli's cusp, enamel extension (all molars), lower canine DAR, LM3 anterior fovea, and LM2 and LM3 protostylid. Conversely, one trait showed declined agreement with greater observer experience: LM1 deflecting wrinkle. When limited to experienced observers, only 65% of tooth-specific traits resulted in $k > 0.6$, and 20% in $k > 0.8$, suggesting increased training does not necessarily resolve issues of rater disagreement. This research highlights several problematic traits that may need revised definitions to enhance observer agreement.

Modelling the disease impacts of migration and trade in prehistoric East and Southeast Asia

MELANDRI VLOK¹, MARC F. OXENHAM², KATE DOMETT³, ERDENE MYAGMAR³, HIROFUMI MATSUMURA⁴, NGUYEN T. MAI HUONG⁵, TRAN T. MINH⁵, DANIEL TEMPLE⁶, NGHIA T. HUU⁵, HIEP H. TRINH⁵, HIKARI ISHIJIMA⁷ and HALLIE R. BUCKLEY¹

¹Department of Anatomy, University of Otago, ²School of Archaeology and Anthropology, Australian National University, ³College of Medicine and Dentistry, James Cook University, ⁴School of Health Sciences, Sapporo Medical University, ⁵Department of Prehistoric Archaeology, Vietnam Institute of Archaeology, ⁶Department of Sociology and Anthropology, George Mason University, ⁷Department of Anthropology, National Museum of Nature and Science, Japan, ⁸Department of Archaeology and Anthropology, National University of Mongolia

Migration and trade are processes which facilitate the spread of infectious diseases globally through human mobility and interaction. However, bioarchaeological research has not attempted to directly address how these human mobility processes influenced the spread and prevalence of infectious disease in the past. This research analyses a total of 450 individuals in skeletal assemblages from prehistoric Asia (Japan (3000-300BC), Vietnam (4900-1500BC) and Mongolia (2500BC-200AD)), which represent before and during/after population interaction events to test whether increasing trade and/or migration results in increasing morbidity and diversity of infectious diseases (e.g. tuberculosis). A three-stage statistical approach was employed following

diagnosis of specific infectious disease and non-specific subperiosteal reactions as indicators of systemic non-specific infection. The first two analytical stages involved site and regional level evaluation of changes to the prevalence and diversity of infectious diseases. The third stage employed generalised linear modelling to assess the "universal" impact of human interaction across the assemblages. There were no significant differences between overall prevalence of adult combined non-specific and specific infection across the interaction events, and no clear increase in number of specific diseases. However, human specific infectious diseases were only identified in the assemblages where a large inter-population interaction event had occurred such as one case of possible treponematosi in Iron Age Mongolia, and 7 possible and probable cases in Neolithic Vietnam. Furthermore, considerable diachronic changes to the overall epidemiology of infectious diseases were present. This research demonstrates that mobility resulting in population interactions influencing disease dynamics can be visible in the archaeological record.

Funded by University of Otago Doctoral Scholarship, National Geographic Early Career Grant (EC-54332R-18), Royal Society of New Zealand Skinner Fund Grant, and Australasian Society for Human Biology Studentship.

Disentangling the effects of population history on modern human cranial variation

NOREEN VON CRAMON-TAUBADEL¹ and MARK HUBBE²

¹Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, ²Department of Anthropology, The Ohio State University

The effects of neutral diversification on contemporary patterns of human skeletal variation have been assessed by comparing the congruence of matrices quantifying geographic distance and matrices representing genetic or morphological dissimilarity. Numerous studies have demonstrated a strong correlation between craniometric variation and global geography, as would be expected if cranial form diversified largely under neutral expectation (i.e., due to gene flow and genetic drift). However, matrix correlation methods make it difficult to identify the specific instances where non-neutral factors (such as climate) play a role, as these tend to be limited to specific morphologies in particular populations. Moreover, implementing tree-based methods in modern humans is difficult due to gene flow among lineages causing extensive reticulation among tree branches. As an alternative, we explore the potential of matrix rotation techniques, whereby 2D Multidimensional Scaling projections of craniometric dissimilarity matrices were compared against 2D projections of geographic and climatic distances. We used a rigid rotation whereby geographic distance was

held constant and all other matrices were rotated to minimize the least squares distances among population centroids. Analyses of the resultant residuals reveal some consistent trends: sub-Saharan African and Australian populations appear craniometrically convergent, Native Americans appear more similar to Asians, and Inuit populations were more divergent than expected based on a (neutral) geographic model. Therefore, this methodology is powerful in identifying which populations diverge most from neutral expectation, making it possible to then consider specific underlying causative factors, such as departures from mutation-drift equilibrium or the effects of diversifying natural selection.

Investigating population genomic continuity between the fifth and sixth century

DEVEN N. VYAS¹, ALESSANDRA MODI², STEFANIA VAI², ISTVÁN KONCZ³, WALTER POHL⁴, LUISELLA P. BARICCO⁵, ELENA BEDINI⁵, CATERINA GIOSTRA⁵, TIVADAR VIDA^{3,6}, BALÁZS G. MENDE⁶, DAVID CARAMELLI², JOHANNES KRAUSE^{7,8}, PATRICK J. GEARY⁹ and KRISHNA R. VEERAMAH¹

¹Department of Ecology and Evolution, Stony Brook University, ²Dipartimento di Biologia, Università degli Studi di Firenze, ³Institute of Archaeological Sciences, ELTE - Eötvös Loránd University, ⁴Institut für Mittelalterforschung, Österreichische Akademie der Wissenschaften, ⁵Dipartimento di Storia, Archeologia e Storia dell'Arte, Università cattolica del Sacro Cuore, ⁶Institute of Archaeology, Research Centre for the Humanities, ⁷Department of Archaeogenetics, Max Planck Institute for the Science of Human History, ⁸Institute for Archaeological Sciences Archaeo- and Palaeogenetics, University of Tübingen, ⁹School of Historical Studies, Institute for Advanced Study

The fourth through sixth centuries CE in Europe are commonly known as the Migration Period. Historical texts document that a group known as the Lombards, had settled in Pannonia (present-day western Hungary and surrounding regions) in the early sixth century, abandoned Pannonia in 568 CE and invaded Italy, ruling much of Italy for the next two centuries. We analyzed paleogenomic data from cemeteries associated with their migration and the communities that preceded them to test if and to what extent the population of Pannonia in the sixth century showed a change (possibly due to the arrival of the Lombards) and whether the migration/invasion into Italy may have occurred.

We generated genomic data from 40 individuals from fifth century (pre-Lombard era) cemeteries from Hungary (Balatonszemes and Hács) and Italy (Bardonecchia and Lavazza). We analyzed these data alongside previously generated data from nearby sixth/seventh century (Lombard-era) cemeteries from Szólád (Hungary) and Collegno (Italy). We found that individuals from Bardonecchia and Lavazza predominantly had ancestry associated with contemporary southern

ABSTRACTS

Europeans, consistent with their geography. However, many of the individuals from Collegno possessed almost exclusively ancestry associated with contemporary northern Europeans, supporting the proposed Lombard migration into Italy during the sixth century. In contrast, we found that individuals from Balatonszemes and Hács possessed both northern and southern ancestry, as previously observed for Szólád. We analyzed the sharing of rare variants using medium (5-14x) coverage whole genomes to test whether this was representative of population continuity or migration between the fifth and sixth centuries.

This project was funded by a grant from the Institute for Advanced Study

Aggression from resident females delays first birth in dispersing female chimpanzees

KARA K. WALKER¹, CLAUDIA WRAMPMEIER² and ANNE E. PUSEY²

¹Clinical Sciences, North Carolina State University, ²Evolutionary Anthropology, Duke University

Unlike many primates, chimpanzees are characterized by complete male philopatry with female dispersal. Across sites, dispersing females are met with hostility from resident females in their new community and give birth for the first time 2.5 years later than non-dispersing females. Nevertheless, there is great variation in the interval from immigration to first birth, ranging from 1 – 8 years. Some females seem to escape the costs associated with dispersal while others suffer for years. Because female chimpanzees primarily increase their reproductive success by lengthening their reproductive career, an early start should be advantageous and selection should favor strategies to reduce this interval. Here we investigate the effect of grooming and aggression among immigrant and resident females on interval to first birth in two communities of chimpanzees in Gombe National Park, Tanzania. Survival analysis ($n = 24$) finds that females who receive less aggression from other females give birth significantly earlier than those who receive more aggression but there is no difference in time to first birth between immigrants who frequently initiate aggression against residents and those who do not. Preliminary data ($n = 8$) show that immigrants who groom more with other females take longer to give birth and were likely to receive more aggression than those who groomed less. These results support the idea that reducing aggression from females is key in reducing time to first birth but that grooming with females may not be sufficient to prevent aggressive acts and might instead serve as a coping mechanism.

Beyond sex and gender: Human pelvic morphology from an integrative context

CARA M. WALL-SCHEFFLER^{1,2} and HELEN K. KURKI³

¹Biology, Seattle Pacific University, ²Anthropology, University of Washington, ³Anthropology, University of Victoria

One of the greatest detriments to our understanding of how evolution has worked throughout human history is the packaging of structural variation into two discrete groups (e.g. male versus female or non-obstetric versus obstetric) as a broad sweeping statement across all human populations. With the increased resolution of datasets, particularly of a complex structure such as the pelvis, it has become abundantly clear that there is no single picture of pelvic variation that stands for all human populations, and that human populations show dramatic variation in solutions to the locomotor, thermoregulatory and potentially obstetric selection pressures acting on the pelvis, as well as to the actions of drift on small populations. Part of the earlier consensus relegating the pelvis into a few simple categories stemmed from a presupposition that the pelvis is generally geometrically similar as it changes size: given that bigger humans do have larger pelvises generally, a subtle consensus exists that a larger single measure (e.g. iliac flare necessitates similarly larger measures in the rest of the pelvis (e.g. acetabula cross sectional area). Obviously when looking at large enough samples, this is clearly not the case, because the shape of the pelvis is flexible within its constituent bones. Here we will use data on human pelvic morphology from a wide range of geographic areas to show that a combination of selection and drift has created a multiplicity of pelvic shape options for effective locomotion, thermoregulation, and obstetrics.

Knee osteoarthritis susceptibility among non-industrial societies undergoing rapid lifestyle changes

IAN J. WALLACE^{1,2}, DAVID T. FELSON³, STEVEN WORTHINGTON⁴, JEFFREY DURYEY⁵, MARGARET CLANCY⁶, PIRAN ALIABADI⁵, GEETA N. EICK⁶, JOSH SNODGRASS⁶, AARON L. BAGGISH⁷ and DANIEL E. LIEBERMAN¹

¹Department of Human Evolutionary Biology, Harvard University, ²Department of Anthropology, University of New Mexico, ³Rheumatology Section, Boston University School of Medicine, ⁴Institute for Quantitative Social Science, Harvard University, ⁵Department of Radiology, Brigham and Women's Hospital, ⁶Department of Anthropology, University of Oregon, ⁷Cardiovascular Performance Program, Massachusetts General Hospital

Because obesity is a primary risk factor for knee osteoarthritis (OA), non-industrial societies with low obesity levels are expected to have low levels of knee OA. However, individuals born under conditions of limited energy availability have been

shown to be predisposed to accumulate excess abdominal (visceral) adipose tissue if they subsequently encounter lifestyle changes that promote positive energy balance. We therefore hypothesized that individuals in non-industrial societies undergoing an energy balance transition may have larger abdomens relative to body weight and hence a heightened risk of knee OA for a given body mass index (BMI). We tested this hypothesis by comparing knee radiographs and anthropometry among males aged ≥ 40 years from two populations: Tarahumara subsistence farmers in Mexico undergoing an energy balance transition ($n=157$) and urban Americans from Framingham, Massachusetts ($n=565$). We found that average BMI among Tarahumara and Framingham individuals was 24 and 29 kg/m² and the probability of obesity was 6% and 41%, respectively. However, controlling for body weight, average abdomen circumference among Tarahumara and Framingham individuals was 109 and 99 cm, respectively. Due to their relatively low-BMI, large-abdomen phenotype, the Tarahumara had 13% higher probability of knee OA for a given age and BMI than Framingham individuals. Moreover, knee OA probability increased more markedly with greater abdomen size among Tarahumara than Framingham individuals. These findings indicate that knee OA risk among non-industrial societies experiencing an energy balance transition is potentially much greater than presumed, which is alarming since such populations constitute much of the global population.

The association of parturition scars with pelvic shape and obstructed labor

LUKAS WALTEBERGER^{1,3}, DORIS PANY-KUCERA^{1,2}, KATHARINA REBAY-SALISBURY¹ and PHILIPP MITTEROECKER³

¹Institute for Oriental and European Archaeology, Austrian Academy of Sciences, ²Department of Anthropology, Natural History Museum Vienna, ³Department of Theoretical Biology, University of Vienna

Although pelvic scars (preauricular sulcus, dorsal pubic pitting, interosseous groove, sacral preauricular extension, extended pubic tubercle) are well known in the anthropological literature, their interpretation remains controversial because the factors and mechanisms of their formation are still insufficiently understood. We placed 335 landmarks and semilandmarks on 3D surface models of articulated pelvises of a Bronze Age skeletal collection ($n=19$) and a 19th century collection ($n=58$) from Austria with background information about the deceased. We analyzed the Procrustes shape coordinates using multivariate statistical methods (PCA, PLS, multivariate regression) to detect diachronic changes in pelvic shape as well as shape features associated with the expression of pelvic scars. The two populations mainly

ABSTRACTS

differed in inlet shape, sacral length and width. Expression of pelvic scars differed between sexes and populations but was only weakly associated with pelvic shape.

Furthermore, we present first results of a new interdisciplinary collaboration on this topic with gynecologists and radiologists. We use clinical CT data to study the association of pelvic shape with pregnancy and birth variables, pathological conditions (pelvic pain, back pain, pelvic floor disorders) and biometric variables of mothers and newborns. These results will help to detect causes of pelvic scars, risk factors of obstructed labor and pelvic floor disorders, and may offer new strategies for personalized medicine.

This project has received funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation program (grant agreement No 676828).

The reproductive and social context of whinny vocalizations in female Geoffroy's spider monkeys (*Ateles geoffroyi*)

JESSICA T. WALZ¹ and MICHELLE A. RODRIGUES²

¹Department of Sociology, Criminology, and Anthropology, University of Wisconsin - Whitewater, ²Beckman Institute for Advanced Science and Technology, University of Illinois, Urbana-Champaign

Spider monkey whinny vocalizations and chimpanzee pant hoots are often compared because of the role these calls seem to serve in maintaining group cohesion in similarly structured primate societies. Despite the overall similarities in these primates' social organization, there are important sex differences between the species in the expression of these calls; in chimpanzees males produce pant hoots at higher rates, while in spider monkeys females produce whinnies at higher rates. Researchers interested in these comparisons suggest that while whinnies may serve a general contact function, they may serve important sexual functions specific to females. We explored this further, focusing on female spider monkey whinny expression. Behavioral data (mean=14.72 hours/individual) and fecal hormone data (mean=11.27 samples/individual) were collected over 15 months at El Zota Biological Field Station, Costa Rica. The best predictor of female calling is party composition; females express higher calling rates in the context of all female parties (GLMM: $F_{5,116}=4.097$; $p<0.01$). The interaction of party composition and female reproductive state (cycling and newly pregnant) also predicted calling rates in the best fit model (GLMM: $F_{13,116}= 1.694$; $p=0.07$). These results suggest that both social and reproductive information may be conveyed in spider monkey whinnies, and ours is the first study to demonstrate that whinny vocalizations in spider monkeys may serve both social and reproductive functions for females. We discuss the implications of this

work for revealing interspecific differences in vocalizations as well as the importance of considering important sex differences and sex-specific functions for vocalizations more broadly.

Research was funded by the Wenner-Gren Foundation, American Philosophical Society Lewis and Clark Fund, The Ohio State Chapter Sigma Xi, and The Ohio State University Alumni Grant.

Reactive vs. proactive strategies for milk immunity

KATHERINE WANDER¹, MEGAN GAUCK¹, MARGARET DURIS¹, TESSA HOPT¹, IREEN KIWELU², FRIDA MOWO² and BLANDINA MMBAGA²

¹Anthropology, Binghamton University (SUNY), ²Kilimanjaro Clinical Research Institute, Kilimanjaro Clinical Research Institute

Immune factors in human milk are numerous, and together constitute the immune system of milk. The immune system of milk represents a substantial maternal investment, which is important to infant survival. We have observed that stronger pro-inflammatory responses in milk (*in vitro* interleukin-6, IL-6, production during incubation with *Salmonella*) decrease infants' risk for infectious disease (ID). We further predict that ID in a breastfeeding infant will lead mothers to bolster milk pro-inflammatory responses. We evaluated this hypothesis among mother-infant dyads in Kilimanjaro, Tanzania. Milk IL-6 responses to *Salmonella* were characterized at baseline and during infant ID among 55 mother-infant dyads. The median change in IL-6 response (sick - baseline) was 0 (range: -55, 162), and it was inversely associated with the strength of the baseline visit IL-6 response (B: -7.7; $p: 0.001$); those with the lowest initial IL-6 responses exhibited the most positive change in IL-6 response for children undergoing an ID. This may reflect a constraint on milk immunity: the higher the initial IL-6 response, the less it could be further increased. This may also reflect a divergence in strategies: a "proactive" strategy of high milk pro-inflammatory responses to decrease infants' risk for ID vs. a "reactive" strategy of increasing milk pro-inflammatory responses for a sick infant. Additional independent predictors of the change in IL-6 response to *Salmonella* were maternal anemia (B: 13.22; $p: 0.064$) and prior pregnancy loss (B: 15.69; $p: 0.034$); these may be indicators of poor maternal condition, which could push mothers toward a "reactive" strategy.

Funding for this project was provided by the Wenner-Gren Foundation, the Leakey Foundation, The American Philosophical Society, and Binghamton University (SUNY)

Stressing over a childhood stress indicator: Assessing the etiology and scoring of cribra orbitalia through the age distribution of porosity activity and degree

XIAOJIA WANG¹ and MATTHEW C. VELASCO²

¹Division of Nutritional Sciences, Cornell University, ²Department of Anthropology, Cornell University

Traditionally interpreted as anemia-induced marrow hypertrophy, cribra orbitalia (CO) has long been considered a childhood stress indicator useful for investigating the health status of ancient communities. Recent debates regarding whether orbital roof porosities could be manifestations of other metabolic diseases such as scurvy and osteoporosis bring to question the reliability of current scoring protocols for assessing the presence of diploic expansion. This study explores the distributions of porosity activity and degree scores across different age categories in a prehispanic population from highland Peru ($n=184$) to determine if data collected using the Buikstra and Ubelaker (1994) scoring protocol conform to the expected distribution of age-conditioned marrow hypertrophy. The prevalence of active porosities in the left orbit is significantly higher among juveniles compared to adults ($p < 0.05$), with the most marked shift occurring from 26.1% in children to 8.7% in the adolescent/young adult group, consistent with the epidemiological model of anemia. However, pinpoint porosity is relatively evenly distributed across age categories, ranging from 37.0% in the adolescent/young adult group to 47.6% among infants and neonates. Combined with 38.9% of the pinpoint porosity cases ($n=74$) being noted in association with orbital vascularization, these data suggest that orbital porosities collectively coded as CO could be reflecting multiple conditions as well as normal developmental variants. In light of recent etiological debates and findings of inter-observer error in the scoring of orbital lesions, the results of this study further suggest that standard scoring methods have low construct validity for measuring the intended pathology.

This research was supported by a Cornell University Institute for the Social Sciences Small Grant to Velasco and the Melissa and Robert Lewin Award for Undergraduate Archaeological Fieldwork at Cornell University.

Bony Labyrinth Fluctuating Asymmetry does not Reflect Gestational Malnutrition in Rats

DEVIN L. WARD¹, EMMA POMEROY², LAUREN SCHROEDER³, JOCELYN E. ROY¹, LAURA T. BUCK^{2,4}, JAY T. STOCK^{5,6}, MARY T. SILCOX⁷ and T. BENICE VIOLA^{1,8}

¹Department of Anthropology, University of Toronto, ²Department of Archaeology, University of Cambridge, ³Department of Anthropology, University of Toronto Mississauga, ⁴Department of Anthropology, University of California Davis,

ABSTRACTS

⁵Department of Anthropology, Western University,
⁶Department of Archaeology, Max Planck Institute
for the Science of Human History, ⁷Department of
Anthropology, University of Toronto Scarborough,
⁸Institute for Archaeology and Ethnography,
Russian Academy of Sciences, Siberian Branch

The bony labyrinth encloses the sensory structures of the inner ear, which process motion and sound during life. It reaches adult shape and size before birth and exhibits restricted subsequent remodelling. As a result, labyrinthine morphological variation may partly reflect instability in the maternal gestational environment. We hypothesized that fluctuating asymmetry, a common measure of developmental instability, would be higher in individuals with a poor gestational environment.

To test this, we collected cranial μ CT data from offspring of two groups of laboratory raised rats, one fed a protein-restricted diet during gestation and lactation, and the other a control sample fed a normal diet. Resulting offspring were sampled at 22 days (weaning), 3 months (sexual maturity), and 15 months (old age) to track longitudinal change. Labyrinthine volumes were segmented and sliding landmarks were collected on the skeletonized semicircular canals and common crus. After generalized Procrustes analysis, we performed a Procrustes ANOVA to assess the impact of fluctuating asymmetry on overall shape variation.

Results show no significant differences in asymmetry between protein-restricted and control dietary groups, nor amongst the different age categories. Fluctuating asymmetry accounted for approximately 20% of shape variation ($p < 0.01$) across all groups (n.s. variables: directional asymmetry ~%6, replication error ~%2, individual variation ~70%). This result suggests that the bony labyrinth's morphology and development are conserved to protect function. Stability in labyrinthine shape supports its use as an indicator of locomotor style and of phylogeny, but the effect of other environmental variables on fluctuating asymmetry should be explored.

UoF Research Grant to DLW; NSERC Discovery Grant to MTS; SSHRC Insight & Connaught Grants to BV; Sidgwick Research Fellowship (Newnham College, Cambridge) to EP; ERC grant 617627 to JTS.

The efficacy of human evolution education in South Africa

KERRYN A. WARREN^{1,2}, ROBYN A. HUMPHREYS^{1,2}
and REBECCA R. ACKERMANN^{1,2}

¹Archaeology, University of Cape Town, ²Human
Evolution Research Institute, University of Cape
Town

In South Africa, the Life Sciences curriculum in the final year of High School is assessed at a national level. Within this curriculum, a large proportion of the final exam is on evolution, and human

evolution more specifically. There are considerable evolutionary/cultural heritage resources within South Africa, and therefore having a population with a grounded understanding and acceptance of evolution is important for social, economic and political reasons, and benefits the discipline more broadly. However, our understanding of the efficacy of human evolution education in South Africa is poor. Existing indices and evaluations around this are largely developed for a North American audience, with religious dogma identified as the primary barrier for acceptance of evolution. Here we report on evolution education/training workshops held in several schools in South Africa. These workshops were designed to identify barriers to understanding and accepting human evolution among learners, and to determine whether a curriculum focused on more relevant examples (e.g. skin colour) shifts attitudes around, and acceptance of, evolution. Our data suggest that the recent racialised history of South Africa has resulted in inadequate adjustment of the terminology used to communicate evolutionary concepts and examples used by researchers, museums and curriculum advisors. Current content may be interpreted as racialized in some contexts, contributing to a breakdown in trust between researchers and the public. Furthermore, narrative approaches of fossil hominin discovery that focus on predominantly wealthy, white, foreign experts, do not spark interest in the subject of human evolution in the majority of learners.

This research is sponsored by the Centre of Excellence in Palaeosciences (CoE-Pal), and the National Research Foundation (NRF) in South Africa.

Adaptation, evolutionary factors and the "obstetrical dilemma"

ANNA G. WARRENER

Anthropology, University of Colorado Denver

In 1960, Sherwood Washburn coined the term "obstetrical dilemma" to describe the competing demands that a bipedally adapted pelvis and large brained human infant placed on childbirth. Since that time, research on human pelvic shape has focused on an adaptive trade-off scenario delineating difficult modern childbirth, locomotor compromise in females and other functional tasks of the pelvis. I argue research on the obstetrical dilemma has often followed the "adaptationist programme" outlined by Gould and Lewontin (1979), excluding thorough consideration of other evolutionary factors shaping the human pelvis. First, I outline the atomization of the pelvis into traits and discuss recent research that undermines the strict functional arguments relating pelvic shape to locomotion and parturition. Locomotor cost is not negatively impacted by greater pelvic width in females, and childbirth difficulty in industrialized societies is a poor proxy for evolutionarily relevant complications.

Second, I examine current research into other evolutionary factors acting on the pelvis mainly, genetic drift, phyletic inertia and genetic linkage. Interpopulation variation in pelvic shape demonstrates drift, while the fossil record indicates a mediolaterally wide pelvis likely defined much of the hominin lineage. Genetic and developmental mechanisms underlying variation in pelvic shape are in the early stages of investigation. Finally, I assess new epigenetic hypotheses regarding nutrition on the development of female pelvic shape and fetal size and propose lines of research necessary to fully accept this new model of childbirth complication in modern humans.

Population dynamics at Chavín de Huántar and contemporary Canchas Uckro: A molecular examination of human skeletal remains dating from 1100-500 cal BCE

EDEN WASHBURN¹, JASON NESBITT², VICKY M. OELZE¹, RICHARD BURGER³ and LARS FEHREN-SCHMITZ¹

¹Anthropology Department, University of California Santa Cruz, ²Anthropology Department, Tulane University, ³Anthropology Department, Yale University

The archaeological site of Chavín de Huántar (950-400 cal BCE) is recognized as one of the most important ceremonial centers of the Peruvian northern highlands. The bulk of archaeological research conducted at Chavín focuses on the site's monumental ceremonial complex and its role as a pan-regional center. However, little is known about the origins of the founders of the site and their connections with nearby (~25km) populations like Canchas Uckro (c. 1100-800 cal BCE). This study combines paleogenomic and strontium isotope (⁸⁷Sr/⁸⁶Sr) analysis to identify local and non-local individuals and to investigate the genetic relationships between locals from Chavín and the surrounding valleys. Here we analyzed three individuals buried at Chavín (CHN 2,4: ~900 cal BCE; CHN 7: ~750 cal BCE) and compare them to those found at Canchas Uckro (n=7). We determined bioavailable ⁸⁷Sr/⁸⁶Sr ranges for both sites using a collection of modern snail shells and plants. Of the three Chavín individuals, one is considered "local" to Chavín, while two are considered non-local. Individuals from Canchas Uckro exhibit ⁸⁷Sr/⁸⁶Sr values consistent with the established range for the valley. We then compared the ~1x coverage genomes we obtained for three Canchas Uckro individuals and the "local" Chavín individual with genomic data from other Andean individuals. Genomic analyses suggest that the Chavín individual closely resembles the genetic diversity of other Northern Peruvian highland

ABSTRACTS

populations. This study reports the first genetic data for individuals buried at Chavin and illustrates the benefits of combining molecular data to address questions of locality.

Research was funded by the National Science Foundation (NSF - 1842447)

The fig and the bean: How primates' two most consumed plant families interact with their endocrine system

MICHAEL D. WASSERMAN¹, SABRINA KRIEF², JESSICA M. ROTHMAN³, COLIN A. CHAPMAN⁴, JORIN VEEN⁵, W. DANIEL KISLING⁵ and EMILY CHESTER¹

¹Anthropology & Human Biology, Indiana University, ²Ecoanthropology and Ethnobiology, Muséum National d'Histoire Naturelle, Paris, France, ³Anthropology, Hunter College - CUNY, ⁴Anthropology, George Washington University, ⁵Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam

Most primates rely heavily on plants to meet their nutritional needs, especially from the Moraceae and Fabaceae plant families. Previous research has shown that many Moraceae species are consumed due to being asynchronous in phenology, thus having resources available year-round, while Fabaceae species are consumed due to their high protein content. We have also documented that both plant families contain species that produce phytoestrogens, thus showing estrogenic activity in mammalian cells. By screening plant foods of multiple primate species of western Uganda, including red colobus monkeys, black-and-white colobus monkeys, chimpanzees, and mountain gorillas, using transfection assays that identify plant compounds that bind to estrogen receptors and upregulate the transcription and translation of estrogen dependent genes, we have identified estrogenic activity in 45.5% of Moraceae species, all within the genus *Ficus*, and 33.3% of Fabaceae species, all within the Papilionoideae subfamily. Further, *F. sansibarica*, *F. capensis*, *F. natalensis*, *Milletia dura*, and *Erythrina abyssinica* had the greatest estradiol equivalency. Given the unique characteristics of these two plant families, we also evaluated their relative contribution to primate diets globally using an analysis of published dietary lists. We found that Moraceae made up 12% and Fabaceae 10% of the average primate diet, making them the two most consumed plant families globally. Although not all species in these two families have estrogenic activity, given their presence in 55.5% of *Ficus*, most primates are likely consuming plants with estrogenic activity, with implications for endocrine functioning and possible effects on reproduction, stress physiology, and the microbiome.

Financial support was provided by Indiana University, University of Amsterdam, McGill University, St. Edward's University, and the National Science Foundation.

The 'Man-Wearing' Myth? A Colonial Period Human Tooth Belt from Brazil

ANDREA L. WATERS-RIST^{1,2}, LEANDRO MATTHEWS CASCON² and MARIANA FRANÇOZO²

¹Anthropology, University of Western Ontario, ²Archaeology, Leiden University

Depictions of Indigenous Brazilians by early European colonists reveal conceptual frameworks meant to emphasize exoticism and primitiveness. Especially common were accounts and objects showing behaviours purportedly related to anthropophagy (cannibalism). The Pigorini Museum, Italy, contains items from the 'curiosity cabinet' of German Jesuit A. Kircher supposedly collected in Northeastern Brazil prior to 1650. One item is a woven belt to which human teeth are affixed by strings. The belt retains 81 strings on which 65 teeth remain, including all types of deciduous (n=12) and permanent (n=53) teeth. Using tooth formation standards for age estimation, the belt has the teeth of a minimum number of nine individuals, including six nonadults (<18 years) as young as 1.0 year \pm 3.0 months and three adults (\geq 18 years). None of the teeth appear to have been naturally exfoliated or extracted during life; around one-third have post-mortem damage. Wear ranges from absent to moderate. Of the teeth with observable surfaces, seven have caries, seven have linear enamel hypoplasia, and nine have slight calculus. Rare morphological variants include a Tome's root and a paramolar on a deciduous lower M2. These data suggest the belt's creator possessed or had access to the skeletonized remains of many individuals. Thus far, no ethnographic accounts have been found that mention such an object, leading to speculation that it may have been commissioned by Kircher or others as a means to spread ethnocentric portrayals of Indigenous Brazilians that were used to justify colonization and oppression.

ERC Project BRASILIAE. Indigenous Knowledge in the Making of Science.

Demographic change and male reproductive competition drive permanent fission of a chimpanzee (*Pan troglodytes*) community at Ngogo

DAVID P. WATTS¹, JOHN C. MITANI² and KEVIN E. LANGERGRABER^{3,4}

¹Anthropology, Yale University, ²Anthropology, University of Michigan, ³School of Human Evolution and Social Change, Arizona State University, ⁴Institute of Human Origins, Arizona State University

New chimpanzee communities form by rare permanent fissions of existing ones. These are unusual in comparative context because they involve replacement of male-male bonds by mutual antagonism, including lethal coalitionary aggression. Between 2014 and 2018, one occurred at Ngogo in an unusually large, socially

and spatially sub-structured community as a large western subgroup split off. We hypothesized that changes in the number and age structure of females and in the primary sex ratio, combined with pre-existing sub-structuring, led to dissolution of male social networks and reproductive monopolization of western females by western males.

We constructed annual male grooming and association networks for 1998 through 2018 using observational data and recorded all demographic events. We applied likelihood-based parentage analysis to DNA extracted from fecal samples to make paternity determinations.

The number of reproductively mature females increased 40% overall and disproportionately in the western subgroup (140%; rest of community 10%). The age structure of the western female cohort shifted to greater representation of young and prime aged females. The primary sex ratio increased overall (from 1.72 to 2.13), disproportionately so in the western subgroup (3.00 vs. 1.83). Male social network cohesion decreased as the number of western females increased. The last infant of a western females known to be sired by a non-western male was born in 2013. Since 2013, mean per capita paternity success has been greater for western males (0.35) than for others (0.17). These results support the hypothesis that male reproductive competition helped drive the fission.

NSF; L.S.B. Leakey Foundation; National Geographic Society; Max Planck Institute for Evolutionary Anthropology; Nacey-Maggioncalda Foundation, Primate Conservation Inc.; Yale University; University of Michigan; Boston University; Arizona State University.

Which evolutionary processes produced cranial differences between Neandertals and Upper Paleolithic or more recent humans?

TIMOTHY D. WEAVER^{1,2}, PHILIPP GUNZ² and SARAH E. FREIDLIN²

¹Department of Anthropology, University of California, Davis, ²Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

A long-standing question in paleoanthropology is which evolutionary processes produced cranial differences between Neandertals and Upper Paleolithic or more recent humans? In a series of studies, Weaver, Roseman, and Stringer (Weaver et al. 2007; Weaver et al. 2008; Weaver and Stringer, 2015) used approaches based in evolutionary quantitative genetics to argue that neutral evolutionary processes (genetic drift and mutation) played an important role in producing cranial differences between Neandertals and recent humans. These conclusions were based on traditional linear measurements rather than the 3D landmarks used in many modern morphometric analyses. It is therefore possible that

ABSTRACTS

deviations from neutral expectations were not detected because morphological differences were not characterized to the level of detail that can be achieved with landmarks and particularly semilandmarks.

Here we address this issue by using the new methods introduced by Weaver and Gunz (2018) to analyze cranial variation in two datasets: 815 3D landmarks and semilandmarks recorded on 247 Neandertals, Upper Paleolithic humans, and recent humans; and 347 landmarks and semilandmarks recorded on 260 great apes and recent humans. We show that deviations from neutral expectations are rarely observed in the first dataset, while they are often seen in the second dataset. The results on both datasets, considered together, appear to indicate that cranial divergence among Neandertals, Upper Paleolithic humans, and recent humans has been more neutral than among great apes and humans.

The Max Planck Society supported this research.

How to make a bipedal primate: 1 part phylogeny, 2 parts selection and a pinch of body size

NICOLE M. WEBB^{1,2}, WILLIAM E.H. HARCOURT-SMITH^{3,4,5,6}, HERMAN PONTZER⁷, MARTIN HAEUSLER¹ and MARK GRABOWSKI⁸

¹Institute of Evolutionary Medicine, University of Zurich, ²Department of Paleoanthropology, Senckenberg Research Institute and Natural History Museum Frankfurt, ³Department of Anthropology, The Graduate Center of the City University of New York, CUNY, ⁴The New York Consortium in Evolutionary Primatology, NYCEP, ⁵Department of Anthropology, Lehman College, CUNY, ⁶Division of Paleontology, The American Museum of Natural History, ⁷Department of Evolutionary Anthropology, Duke University, ⁸Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

Reconstructing the morphology of the *Pan-Homo* last common ancestor (LCA) has become increasingly difficult in light of the unexpected combination of postcranial features in recently described hominin taxa and evidence of homoplasy within the Miocene apes. In addition, despite bipedalism's critical role in human evolution, uncertainty persists as to how and why this transition occurred. Here we use phylogenetic comparative methods and data from a broad comparative sample of extant ($n=429$; 55 species) and extinct primates (*Sivapithecus*, *Pieralopithecus*, *Rudapithecus*, *Ekembo*), including several fossil hominin reconstructions (*Ardipithecus ramidus*, *Australopithecus afarensis*, *A. africanus* and *A. sediba*), to test hypotheses about the relationship between pelvic morphology, locomotion, phylogeny and body size. Our

comprehensive sample permits assessment of the influence of phylogeny and selection on pelvic trait evolution while simultaneously measuring the efficacy of existing locomotor classification schemes. Our results show that locomotor categories that included postural preferences, i.e. orthograde vs. pronograde, and body size were the strongest predictor variables. This finding suggests that the relationship between biomechanically relevant pelvic measures and body size may be a useful tool for fossil locomotor assessment ($R^2=86\%$). Further, the best models included those that indicated a pronograde trunk orientation coupled with above-branch quadrupedalism for the LCA. This finding adds to the mounting evidence that arboreal, pronograde locomotion persisted in Miocene ape locomotor repertoires for longer than previously thought, implying that orthograde postural adaptations may have played a less significant role in the acquisition of hominin bipedalism.

This research was funded by the National Science Foundation IGERT (0966166) and the Swiss National Science Foundation (31003A_176319).

Do behavioral and gut microbiome shifts associate with changing reproductive states in wild primates?

SHASTA E. WEBB¹, JOSEPH D. ORKIN², RACHEL E. WILLIAMSON¹ and AMANDA D. MELIN^{1,3,4}

¹Anthropology & Archaeology, University of Calgary, ²Institut de Biologia Evolutiva, Universitat Pompeu Fabra-CSIC, ³Medical Genetics, Cumming School of Medicine, ⁴Alberta Children's Hospital Research Institute, University of Calgary

Primates address the increased energy demands of pregnancy and lactation by selectively eating energy-dense foods, decreasing physical activity, and/or undergoing physiological changes. Additionally, the gastrointestinal microbiome, which influences host metabolic processes, host immunity, and energy acquisition, is influenced by reproductive state and may increase energy harvest from foods during pregnancy or lactation. However, this hypothesis remains relatively unexplored, especially in wild animal populations in which individuals are monitored over multiple pregnancies. We analysed activity budgets ($n=13,750$ scans) and collected fecal samples ($n=359$) from 33 wild, female white-faced capuchin monkeys in Sector Santa Rosa, Costa Rica, tracked across reproductive cycles during 22 months during 2014-2018. To analyse gut bacteria, we sequenced the V4 region of the 16S rRNA gene from fecal DNA. Gross activity budget did not differ significantly with reproductive state, suggesting that capuchins face ecological or social constraints that preclude them from adjusting behavior at this scale. Shannon alpha diversity of gut bacteria was not associated with reproductive state, nor did gut microbiome composition reflect typical indicators

of increased energy harvest capacity. However, several bacterial genera typically associated with gastrointestinal inflammation in humans were over-represented in lactating capuchins. Time-series analysis investigating compositional changes per individual incorporating host diet and ecological factors through multiple pregnancies may reveal more subtle microbiome adjustments to host reproductive states. Investigating reproductive microbial ecology in wild primates directly contributes to a deeper understanding of the poorly known roles microbes play in the reproductive cycle and in potential links to maternal health and fitness.

Head pitch during load carrying and running: Possible semicircular canal adaptation to non-agile behaviors

JAMES T. WEBBER¹ and DAVID A. RAICHLLEN²

¹School of Anthropology, University of Arizona, ²Department of Biological Science, University of Southern California

Excessive head pitch rates due to running impact forces may have posed a significant challenge to early hominins. Researchers have suggested that enlarged semicircular canal diameters were an adaptation to these perturbations. Yet, running head pitch rates are reduced by many kinematic mechanisms, including arm swing, and may not be the only locomotor mode which causes excessive head motion. Specifically, walking while carrying a load was likely common in early hominins and presents challenges which could increase head pitch rates including added effective body mass and removal of arm swing. Here, we test the hypothesis that load carrying could increase maximal head pitch rates similar to those experienced during running by having 18 subjects walk and run with a rate gyro affixed to their foreheads. Subjects carried 0, 8, or 19kg in their arms while walking at four speeds. Subjects also ran unloaded at two speeds. Supporting our hypothesis, a comparison of linear mixed effect models found including the independent variable, load carrying, significantly improved estimates of the dependent variable, maximal head pitch ($p < 0.0001$). In the model, carrying increased head pitch $24.7 \pm 6.1^\circ$ per ms^{-1} during walking ($p < 0.0001$), whereas running increased head pitch by $18.2 \pm 5.6^\circ$ in women only ($p = 0.001$). Additionally, post-hoc multiple comparisons analysis found no significant difference between fast loaded walking and jogging or running (jog- $p = 0.47$, run- $p = 1.00$). Thus, non-agile activities such as carrying may have played a role in the development of derived inner ear morphology.

This study was funded by the University of Arizona Social and Behavioral Sciences Research Institute dissertation grant 18DRF0885.

ABSTRACTS

New analyses of the 55,000-year-old modern human partial cranium from Manot Cave, Israel

GERHARD W. WEBER^{1,2}, ISRAEL HERSHOKOVITZ^{3,4}, PHILIPP GUNZ⁵, SIMON NEUBAUER⁵, AVNER AYALON⁶, BRUCE LATIMER⁷, MIRYAM BAR-MATTHEWS⁸, GAL YASUR⁸, OMRY BARZILAI⁸ and HILA MAY^{3,4}

¹Department of Evolutionary Anthropology, University of Vienna, ²Core Facility for Micro-Computed Tomography, University of Vienna, ³Department of Anatomy and Anthropology, Sackler Faculty of Medicine, Tel Aviv University, ⁴Dan David Center for Human Evolution & Biohistory Research, Shmunis Family Anthropology Institute, Sackler Fac. of Med., Tel Aviv University, ⁵Department of Human Evolution, Max-Planck-Institute for Evolutionary Anthropology, ⁶Department of Geology, Geological Survey of Israel, ⁷Departments of Anatomy and Orthodontics, Case Western Reserve University, ⁸Department, Israel Antiquities Authority

A partial cranium dated to >55ka (thousand years ago) by uranium–thorium dating was recently discovered at Manot Cave (Israel) and identified as modern human. Other recent findings from Misliya (Israel) indicated an early dispersal of modern humans out-of-Africa between 194–177ka, and a quite long existence of *Homo sapiens* in Africa at Jebel Irhoud (~300ka). While the faces of the latter appear quite modern, the shape of the braincase seems to lack behind, reaching nearly modern state only around 35ka. Here we apply new data (micro-CT scans) and approaches to the Manot 1 calvaria. Using ecto- and endocranial shape analyses based on landmark-semilandmark data, and including multiple virtual reconstructions, we can confirm that Manot 1 is unequivocally modern human. However, its endocranial shape is different to some extent from the earliest known *Homo sapiens* but close to the Levantine Qafzeh/Skulh assemblage (120–90ka) and to modern humans, nevertheless showing differences to the latter which might indicate that the Manot population had not yet fully reached the brainshape of modern humans evident after 35ka. A continuous occupation or local evolution of modern humans in the Levant is not directly supported due to the absence of other *Homo sapiens* fossils during the long period between Qafzeh/Skulh and Manot populations. Manot 1 might rather represent a population migrating out-of-Africa and reaching the Levantine corridor during warmer and wetter climatic conditions. Manot 1 definitely shows that Neanderthals (e.g. Kebara, Amud) and modern humans both contemporaneously inhabited the Levant during the Middle to Upper Paleolithic interface.

Dan David Foundation, Israel Antiquities Authority, Case Western Reserve University, Shafiran Family Foundation, Leakey Foundation, Irene Levi Sala CARE Archaeological Foundation, Keren Kayemet L'Israel, Binational Science Foundation, Israel Science Foundation.

Mosaic X Chromosome Inactivation in Rhesus Macaques (*Macaca mulatta*)

TIMOTHY H. WEBSTER¹, TANYA N. PHUNG^{2,3}, MICHAEL J. MONTAGUE⁴, OLGA GONZALEZ⁵, SAMUEL BAUMAN⁶, MICHALA STOCK⁷, CATALINA VILLAMIL⁸, MELWEEN MARTINEZ⁶, JAMES P. HIGHAM⁹, NOAH SNYDER-MACKLER^{10,11,12}, MICHAEL L. PLATT⁴ and MELISSA A. WILSON^{2,3}

¹Department of Anthropology, University of Utah, ²School of Life Sciences, Arizona State University, ³Center for Evolution and Medicine, Arizona State University, ⁴Department of Neuroscience, University of Pennsylvania, ⁵Southwest National Primate Research Center, ⁶Caribbean Primate Research Center, University of Puerto Rico, ⁷High Point University, ⁸School of Chiropractic, Universidad Central del Caribe, ⁹Department of Anthropology, New York University, ¹⁰Department of Psychology, University of Washington, ¹¹Center for Studies in Demography and Ecology, University of Washington, ¹²Nathan Shock Center of Excellence in the Basic Biology of Aging, University of Washington

Across mammals, genetic males and females differ in number of X chromosomes, with females (XX) possessing two and males (XY) possessing one. Because the X chromosome contains genes important to both sexes, males and females require the same amount of gene expression. This is accomplished via X chromosome inactivation (XCI), during which one of the X chromosomes is silenced in each female cell. Because XCI is female-specific, a better understanding of variation in XCI among individuals and across tissues has the potential to lead to a deeper insight into female phenotypic variation, health, and disease. In this study, we ask (1) whether there are tissue-specific patterns of XCI and (2) whether aspects of XCI are heritable. We generated data from 14 Cayo Santiago rhesus macaques (*Macaca mulatta*) from five pedigreed matrilineal lines. For each individual, we sequenced and assembled an exome from blood DNA as well as a transcriptome for six different tissues derived from three germ layers. Analyzing allele specific expression in expressed RNA for more than 13,000 filtered heterozygous X chromosome sites (2,929–3,817 per individual), we found that, while there was variation in the balance of allele expression among tissues and individuals, alleles were generally balanced overall (allele balance between 0.2 and 0.8), a pattern consistent with completely random, or mosaic, XCI from cell to cell. We discuss the implications of mosaic XCI for female phenotypic variation and highlight considerations for future work on XCI in primates.

The Leakey Foundation; ASU School of Life Sciences and The Biodesign Institutes; NIH MIRA R35GM124827; NCR/ORIP #8-P40-OD012217-25; NIH R01 MH096875; NIA R00 AG051764; NIMH R01 MH108627

Oral Pathological Conditions and Age Structure in Early Postcontact Gule, St. Catherines Island, Georgia

KENDRA S. WEINRICH¹, FABIAN CRESPO², KATHRYN E. MARKLEIN² and CLARK S. LARSEN¹

¹Anthropology, The Ohio State University, ²Anthropology, University of Louisville

Oral pathological conditions (carious lesions, periodontal disease, antemortem tooth loss, and abscesses) reflect the outcome of multifaceted etiological circumstances, including nutrition, physiological stress, age, sex, and general health status. In particular, carious lesions involve enamel demineralization of the tooth by bacterial acid byproducts, thereby increasing susceptibility of the pulp chamber to infection, abscess formation, and antemortem tooth loss (AMTL). Periodontal disease (PD) results from the permeation of gingival inflammation into surrounding alveolar bone. Documentation of oral conditions in individuals from the pre-Spanish mission, early 16th century Fallen Tree site, St. Catherines Island, Georgia, provides a record of oral health within the larger context of initial European contact and, consequently, the oral conditions influencing general health. We test the hypothesis that age-at-death correlates directly with presence of dental caries, PD, AMTL, and abscesses in adult individuals (n=56) from Fallen Tree. Results from binomial logistic regressions revealed a significant relationship between increased age and carious lesion presence by tooth (p≤0.05), although age and sex did not affect presence of PD, AMTL, or abscess by tooth/alveolus. These findings demonstrate the important role age-at-death factors into understanding oral health, especially in relation to dental caries presence in the Fallen Tree community. Regarding the lack of correlation with PD, we argue that the differential presence of periodontal disease reflects heterogeneous immune competence within the Fallen Tree population that is influenced by other factors than biological sex and age.

Funding support by the St. Catherines Island Foundation and the National Science Foundation.

A case of auditory exostosis during the Late Fort Ancient period: Evidence for a seasonal adaptation to a riverine ecosystem in the Ohio River Valley

KAREN J. WEINSTEIN

Anthropology and Archaeology, Dickinson College

This study reports a case of auditory exostosis, a pathological condition in the temporal bones, in an adult male from Neale's Landing, a mid-16th century Fort Ancient site in Blennerhassett Island, West Virginia. The differential diagnosis of this condition allows for testing of the hypothesis that fishing was an important part of the Fort Ancient seasonal subsistence cycle. Subsistence practices of Fort Ancient groups from the Ohio

ABSTRACTS

River Valley are generally modeled as farming and hunting supplemented with only limited riverine-based fishing and shellfish collecting. Faunal remains and settlement patterns, however, indicate that Fort Ancient groups practiced diverse subsistence activities across marked seasonal cycles that included fishing. Reports of auditory exostosis in the medical and archaeological records show that it commonly develops in individuals who regularly immerse in cold water over a 5-10-year period. The presence of auditory exostosis in an adult male from Neale's Landing, coupled with associated fish and shellfish remains, indicates that riverine-based fishing was an important part of the seasonal subsistence cycle at this Fort Ancient site. Bioarchaeological evidence for riverine resource extraction adds further evidence that Fort Ancient groups engaged in diverse subsistence activities across marked seasonal cycles.

A geometric morphometric approach to quantify the longitudinal curvature of primate proximal phalanges from 3D surface data

SOPHIE E. WENNEMANN¹, KRISTI L. LEWTON^{2,3}, CALEY M. ORR^{4,5}, SERGIO ALMÉCJA^{6,7,8} and BIREN A. PATEL^{2,3}

¹Biological Sciences, University of Southern California, ²Integrative Anatomical Sciences, University of Southern California, ³Human and Evolutionary Biology, University of Southern California, ⁴Cell and Developmental Biology, University of Colorado School of Medicine, ⁵Anthropology, University of Colorado Denver, ⁶Anthropology, American Museum of Natural History, ⁷Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, ⁸NYCEP, New York Consortium in Evolutionary Primatology

Paleoanthropologists use measures of phalangeal curvature to infer if fossil hominins and other extinct primates engaged in arboreal behaviors. Current approaches to quantify curvature assume that the phalanx's longitudinal axis approximates either a portion of a circle (i.e., included angle method) or a parabola (i.e., quadratic polynomial method). Here we used an innovative geometric morphometric (GM) analytic approach to quantify a proximal phalanx's longitudinal curvature "shape" and then compared curvature shape with other curvature metrics across hominoids. AMIRA and ImageJ software were used to extract 100 landmarks of the proximal phalanx's central longitudinal axis from 3D surfaces of >300 individuals representing eight hominoid species. Landmarks were subjected to GM methods, including generalized Procrustes Analyses. Principal components (PC) analyses were performed and PC scores were compared across taxa. PC1 (>80% of variation) represented the shape of the bone's longitudinal axis and separated taxa consistently and in accord with known behavioral preferences.

Suspensory hylobatids and *Pongo* specimens were more curved and had significantly lower PC1 scores while bipedal *Homo* specimens were flatter and had significantly higher PC1 scores; African ape specimens were intermediate and were not significantly different from each other. PC1 scores were significantly correlated with both included angle and quadratic polynomial but had higher correlations with the former. This new virtual approach for quantifying phalangeal curvature is replicable and does not assume a circle or parabola model. Moreover, it successfully separates hominoid phalanges based on "curvature shape" along known behavioral lines, and thus should prove useful for future paleoanthropological research.

National Science Foundation (BCS-1317047; BCS-1317029; BCS-1539741; 1316947); The Leakey Foundation; The Wenner-Gren Foundation; AEI/FEDER EU (CGL2017-82654-P); Generalitat de Catalunya (CERCA Programme); The University of Southern California's URAP Program.

Human-specific gene duplications underlying heterochronic change in human neural development

ELIZABETH A. WERREN^{1,2} and STEPHANIE L. BIELAS¹

¹Human Genetics, University of Michigan Medical School, ²Anthropology, University of Michigan

Humans have an exceptionally large prefrontal cortex for a primate, suggestive of evolved heterochronic shifts during neural development. Fixed human-specific genetic variants are good candidates for proximate molecular mechanisms of heterochrony. A common driver of molecular evolution is gene copy number expansion. The neuroblastoma breakpoint gene family (*NBPF*) represents the greatest copy number expansion of any protein coding sequence in the human genome, yet *NBPF* function remains unknown. The ancestral single-copy *NBPF* gene first arose in the genomes of placental mammals. Its copy number expansion is specific to primate genomes, with extreme amplification in humans. Recent studies show that human-specific *NBPF* genes are highly expressed in neural progenitor cells of the developing brain. Alteration of the rate and/or timing of neural progenitor cell cycle dynamics is a well-described mechanism to increase neuron number. Other human-specific gene duplications, such as *ARGAP11B* and *NOTCH2NLA-C*, are known to influence neural progenitor cell proliferation and differentiation, yielding a greater number of cortical neurons. To test the hypothesis that human-specific *NBPF* dosage functions during neural development to alter cell cycle dynamics

resulting in increased neuronal output, we perform CRISPR/Cas9 gene editing of human *in vitro* brain organoid models and over-express human-specific *NBPF* in chimpanzee brain organoids.

This work has been funded by the NSF DDRIG (BCS-1919671), Leakey Foundation Research Grant, NIH (NINDS & NICHD), Simon's Foundation Director's Award, and University of Michigan Rackham Candidate Research Grant.

Ethno-geographic origins and genomic diversity of Afro-descendants in colonial Mexico City

JULIE K. WESP¹, MARCELA SANDOVAL-VELASCO² and MARÁA ÁVILA-ARCOS³

¹Sociology and Anthropology, North Carolina State University, ²The GLOBE Institute, University of Copenhagen, ³International Laboratory for Human Genome Research, National Autonomous University of Mexico

The transatlantic slave trade is one of the largest forced migrations of people in recorded history with immense impacts on the population history of all the three continents that it connected. Approximately 250,000 enslaved Africans were brought to the viceroyalty of New Spain from the sixteenth to the eighteenth centuries, yet few studies have focused on this biocultural change in demographics. This project is a genomic study of skeletal remains associated with the *Hospital Real San José de los Naturales*, the first royally-financed hospital for the indigenous population established in Mexico City in 1553. Historical documents and bioarchaeological analyzes show that the hospital served a more representative sample of the actual demographic diversity of the colonial city, including people of African descent. We generated genome-wide data from ancient DNA libraries for 21 individuals to examine their ethno-geographic origins within the African continent. Through comparison with available reference panels of modern genomic variation around the world, we identified 16 individuals with African ancestry, including the areas of Senegambia (n=5), West-Central Africa (n=9), and 2 individuals with similarities to East African populations. The additional samples identified individuals with Native American ancestry (n=3), European ancestry (n=1), and admixed ancestry (n=1). These data highlight the biological diversity of the colonial society and the heterogeneity of the people forcibly brought to the Americas. This research provides a new source of evidence to complement historical documents and enables us to better understand the impact of these colonial changes for the inhabitants of Mexico City.

Financial support from the Wellcome Trust; North Carolina State University; National Autonomous University of Mexico; and the CAS Mellon Faculty Development Fund at American University

ABSTRACTS

Seasonal variation in diet and ranging patterns in Kinda baboons (*Papio kindae*)

ANNA H. WEYHER¹, AMANDA J. FUCHS¹ and JASON M. KAMILAR^{1,2}

¹Anthropology, University of Massachusetts, ²Organismic and Evolutionary Biology Graduate Program, University of Massachusetts

Baboons are a large bodied, predominantly terrestrial primate taxon, that inhabit a variety of ecozones throughout Africa. Most well studied populations inhabit habitats with homogenous vegetation structures. Conversely, Kinda baboons (*Papio kindae*) of Kasanka National Park (KNP) live in the Miombo ecoregion of northeastern Zambia. This field site exhibits a complex set of habitat types, including Miombo and Dwarf Miombo woodlands, evergreen forests, bushland and grassland. Here, we examine how a habituated troop of Kinda baboons ranging patterns respond to seasonal variation in climate and food availability. We collected behavioral data 20 days per month from 2011-2013. We used the Home Range Extension package in ArcView 3.1 to calculate the troop's home range and foraging range. We calculated percentage of foods eaten using data from 30-minute scans. The troop's home range is 1,050 ha and its foraging range is 733 ha. Additionally, the troop utilizes different habitat types and food sources seasonally. For example, the troop largely concentrates on eating fruits and underground storage organs in the rainy season, and seeds/legumes during the cold/dry season. This study is the first to report on habitat, ranging, and diet in Kinda baboons. It also serves as an interesting comparison to other well studied baboon species, particularly because Kinda baboons' range throughout a heterogenous environment compared to other baboons that are largely found in drier, more open savanna habitats. Furthermore, it has important conservation implications for primate ranging patterns considering the onset of climate change and human disturbance on non-human primate habitats.

Sex estimation using the calcaneus in a modern American skeletal population

LEIGHANN WHARTON

Anthropology, California University of Pennsylvania

One of the most important aspects of the analysis and identification of human skeletal remains is determination of the biological profile, which consists of the age, sex, ancestry, and stature of an individual. Typically, anthropologists analyze the pubic bone in adult human skeletal remains, which is highly sexually dimorphic due to a female's capacity for childbirth. However, when these fragile bones are broken, damaged, or altogether missing, it is necessary to look to other areas of the skeleton for sex information. DiMichele and Spradley (2012) developed a method of sex estimation using four measurements of the

calcaneus. For this project, this method was tested using the left calcanei of modern American skeletal remains from the Texas State University Donated Skeletal Collection (TXSTDSC). This skeletal sample consists of 264 individuals (151 males, 113 females) with an average age-at-death of 65.2 years, 91.3% of whom are classified as white. Data analysis shows that the discriminant function equation developed by DiMichele and Spradley (2012) was able to correctly classify sex for 84.4% of individuals in the current study. The sectioning points for individual measurements were able to accurately estimate sex for 76.7–80.9% of this skeletal sample. The results of this study further validate that the calcaneus is sexually dimorphic and can be used to estimate sex in a modern American skeletal sample.

Spatial Demography, Population Size, and Genetic Drift: A Model-Based Approach

ANDREW A. WHITE

South Carolina Institute of Archaeology and Anthropology, University of South Carolina

Minimum viable population (MVP) size is defined as the minimum size at which a population is immune to extinction through normal stochastic perturbations in mortality, fertility, and sex ratio. Human MVP size is of particular interest to anthropologists studying how the low-density, hunter-gatherer societies of the Pleistocene adapted to different environments and colonized empty landscapes. Recent work with a non-spatial computational model suggests that a stable population size of about 150 persons is demographically viable over long periods of time under a wide range of conditions, and that many populations of lower size could have had a good probability of long-term survival depending on the specifics of mortality, fertility, and the cultural rules governing marriage behaviors. This paper extends that work by using a spatially-situated model to systematically explore how simple parameters of spatially-structured interaction affect: (1) MVP size; and (2) the patterns of genetic diversity that emerge as drift processes play out over time and across space. Relationships between population size, the spatial configuration of population, and patterns of genetic diversity are investigated and used for building basic theory that can be applied to the interpretation of archaeological and biological data relevant to the demography and dynamics of past populations.

Dopamine receptor methylation is correlated with aspects of chimpanzee personality

CASSANDRA M. WHITE¹, NICKY STAES^{1,2,3}, ELAINE E. GUEVARA^{1,4}, STEVEN J. SCHAPIRO⁵, WILLIAM D.

HOPKINS^{5,6}, CHET C. SHERWOOD¹ and BRENDA J. BRADLEY¹

¹Department of Anthropology and Center for the Advanced Study of Human Paleobiology, The George Washington University, Washington DC 20052, ²Behavioral Ecology and Ecophysiology Group, Department of Biology, University of Antwerp, Wilrijk, Belgium, ³Centre for Research and Conservation, Royal Zoological Society of Antwerp, Antwerp, Belgium, ⁴Department of Evolutionary Anthropology, Duke University, Durham, NC 27708, ⁵Michale E. Keeling Center for Comparative Medicine and Research, The University of Texas MD Anderson Cancer Center, Bastrop, TX 78602, ⁶Division of Developmental and Cognitive Neuroscience, Yerkes National Primate Research Center, Atlanta, GA 30322

Personality (i.e. behavioral tendencies or styles) is generally considered a stable trait in primates. Individual variation in the dimensions that make up personality exists in humans and their close relatives, chimpanzees. Recent research has found that patterns of DNA methylation are sometimes associated with these personality dimensions, suggesting that they may be influenced by environmental factors, such as rearing. The purpose of this study was to examine whether epigenetic modifications might be associated with personality dimensions in chimpanzees. Personality was measured and validated along the dimensions *Reactivity*, *Extraversion*, *Dominance*, *Openness*, and *Agreeableness* for 99 chimpanzees at Keeling Center for Comparative Medicine and Research, UT MD Anderson Cancer Center, Bastrop, TX. Peripheral whole blood samples were extracted from 53 of these chimpanzees and used to measure genome-wide methylation levels from microarrays. We examined the amount of CpG methylation at sites associated with eight behavior-related candidate genes: *OXTR*, *AVPR1a*, *HTR1A*, *SLC6A4*, *DRD2*, *DRD4*, *NR3C1*, and *BDNF*. The results suggest a strong association between methylation of the *DRD2* gene, which codes for a key dopamine receptor, and the personality dimension of *Extraversion* (p corrected=0.021), as well as a lesser association with the dimension of *Openness* (p corrected=0.059). Variants in *DRD2* have been associated with exploratory and sensation-seeking behavioral tendencies in humans, which are consistent with the chimpanzee personality dimensions of *Extraversion* and *Openness*.

Funded by the Leakey Foundation, Yale MacMillan Center for International Studies, National Science Foundation, Center for the Advanced Study of Human Paleobiology, Yale Institute for Biospheric Studies, and Yale Anthropology.

Developmental Origins of Tuberculosis in a Documented Skeletal Collection

JACOB WHITE^{1,2} and FABIAN CRESPO³

¹Anthropology, University of Nevada, Las Vegas, ²Archaeology, Durham University, ³Anthropology, University of Louisville

ABSTRACTS

Stress in early life is often attributable to health and disease outcomes in adulthood. The same physiological stress responses that cause growth disruptions during critical developmental stages can lead to a decreased immune response to infections like tuberculosis. Tuberculosis has been causing disease in humans since prehistory. Its long co-evolution and adaptability have allowed it to persist and remain a global health problem today. The key to the pathogen's success is the spectrum of latent to active infection it causes. The pathogen's virulence varies depending on host immunocompetence, even potentially offering mutualistic benefits to some hosts through training the immune system to be more robust. This study analyzed individuals from a documented modern skeletal collection in Lisbon, Portugal to explore if disruptions in long bones and vertebral neural canals correlated to a higher likelihood of having tuberculosis listed as the individual's cause of death. The results found that growth disruptions and dying of tuberculosis are inversely correlated. Potential explanations for these results could be (1) growth disruptions in this collection are due to tuberculosis infections in early childhood, and these individuals developed a resistance to the disease later in life or (2) that an immunological trade-off occurred to promote the less energetically costly immune reactions during a time of physiological adversity. Also, this paper discusses the pertinence of applying the Developmental Origins of Health and Disease framework to pre-vaccine era bioarchaeological adult populations when infant and childhood mortality would be extremely high.

Ill at Home vs Hospital: Survival and Physiological Stress Comparison of Medieval England

SINA D. WHITE

School of Anthropology and Conservation,
University of Kent

During the 11th to 16th centuries, catastrophic events and adverse environmental conditions caused people in England to become ill. Lower status individuals who became ill were cared for by family or sought out a hospital. This study compared age-at-death, biological sex, and linear enamel hypoplasia between individuals associated with a hospital and almshouse from Chichester and lay cemeteries from Gloucester and Pontefract, England. Linear enamel hypoplasia was analyzed to identify the relationship between childhood stress and age-at-death of individuals from St. James and St. Mary Magdalene Hospital (n=34) and Almshouse (n=56), Box Lane (n=34), and Blackfriars (n=56) cemeteries. The results show no significant differences were found between the age distributions of individuals from the hospital and lay cemeteries ($P > 0.05$) and age distributions and linear enamel hypoplasia ($P > 0.05$). Also, the survival curves display that the

individuals from the hospital were more likely to survive before the age of 30, whereas, lay males with linear enamel hypoplasia were more likely to survive compared to lay and hospital females and hospital males. This study provides preliminary insight on demographic comparison of individuals being ill under the care of family and hospitals during the medieval period in England.

Analyzing the Impact of DISH on Enteseal Changes in a Modern Documented Population

EMILIE L. WIEDENMEYER¹ and LAUREN E. RATLIFF²

¹Anthropology, Texas State University, ²,
Tennessee Valley Archaeological Research

Musculoskeletal markers, or enteseal changes (EC), have frequently been used to predict and analyze activity patterns in bioarchaeological populations. Several EC studies, including the Coimbra Method (2013), interpret various pathologies as confounding variables. The Coimbra Method is a standardized method for analyzing EC that exempts individuals with diffuse idiopathic skeletal hyperostosis (DISH), which primarily results in irregular ossification along the vertebral column. However, there has been little research on the extent of the correlation between DISH and EC. Thus, this study focuses on two issues: 1) are EC scores of an individual with DISH higher than those of an individual without DISH? and 2) should individuals with DISH be definitively removed from EC studies? Seven enteseal sites of recently deceased individuals were examined from the Texas State Donated Skeletal Collection (n=60, age=<75, DISH=30, non-DISH=30) using the Coimbra Method. All individuals were pair-matched by documented sex, age, and occupational type to focus on differences dependent on DISH. Preliminary results suggest that EC are not significantly correlated with the presence of DISH. Logistic regression shows no statistically significant correlation between DISH and EC scores, but results do show a positive trend, suggesting that the number of vertebrae affected by DISH alters EC expression. Although these initial results do not conclusively support removing all individuals with DISH from EC studies, they support removing individuals with more severe manifestations of DISH. This research could potentially improve the Coimbra method by better understanding its assumptions, which in turn would improve its application for bioarchaeological samples.

Cranial fluctuating asymmetry from high and low status ossuaries in Colonial Mexico City

CATHY WILLERMET^{1,2}, EMILY MOES³, KATELYN RUSK³, HEATHER J.H. EDGAR^{3,4}, COREY S. RAGSDALE⁵ and PAIGE LYNCH⁵

¹Department of Sociology, Anthropology, and Social Work, Central Michigan University,

²Maxwell Museum of Anthropology, University of New Mexico, ³Department of Anthropology, University of New Mexico, ⁴Office of the Medical Investigator, State of New Mexico, ⁵Department of Anthropology, Southern Illinois University, Edwardsville

The Colonial Period in Mexico (1521-1696) was characterized by turbulent socioeconomic, political, and biological changes. Interactions between indigenous peoples, colonizing Europeans, and free and enslaved Africans exacerbated inequality. We used two colonial-era ossuaries in Mexico City to examine social stratification: the *Catedral Metropolitano* and *Iglesia de la Soledad*. Historically, Catedral, in the city center, served individuals from higher socioeconomic status (SES), whereas Soledad, located more peripherally, served lower SES individuals. Lower SES is often linked to more fluctuating asymmetry (FA). FA refers to small, unilateral divergences from bilateral symmetry due to environmental forces during development. Higher levels of FA should reflect more developmental stress. This study aims to assess whether the two ossuaries differ in levels of FA; we hypothesize FA will be higher among those buried at Soledad.

We photographed 88 individuals from six angles, averaging 250 photographs per individual, to create three-dimensional photogrammetric models. Samples come from Catedral (n= 25) and Soledad (n=63); males and females were roughly equally represented. We placed 60 paired and unpaired cranial landmarks for geometric morphometric examination. Procrustes analysis using MorphoJ software revealed significant differences between the FA scores by site but not by sex; average FA scores for Catedral (M: 0.027, F: 0.025) are more than twice those for Soledad (M: 0.013, F: 0.010; $p=0.0057$). Surprisingly, the historically wealthier Catedral individuals presented higher FA levels. This study demonstrates the utility of using FA to test assumptions about health and stress among burial samples representing different SES districts.

CMU FRCE Research Grant #48945; American Association of Physical Anthropology Professional Development Grant; SIUE Seed Grant for Transitional and Exploratory Projects (STEP) Grant; UNM Research Allocations Committee.

ABSTRACTS

Male dispersal of the introduced green monkey (*Chlorocebus sabaues*) population in Dania Beach, Florida

DEBORAH (MISSY) WILLIAMS and KATE M. DETWILER

Anthropology, Florida Atlantic University

This study recorded male dispersal of the green monkey (*Chlorocebus sabaues*) population in Dania Beach, Florida from 2014-2018. It is known that male vervet monkeys disperse out of their natal group at sexual maturity and then transfer to a new social group every 2-3 years. However, the dispersal of vervets in urban areas is poorly documented. Here, we collected dispersal data using a novel approach of a citizen science web application, alongside community reports from social media, law enforcement reports, and direct observation. We confirmed the identity of each male using our ongoing photo database collection. The time, date, and GPS location were recorded for each sighting, and plotted on a map. Our results included ten dispersal events, of which four males left the Dania Beach area and successfully returned to join to a new social group. Four dispersal events included males who were not reported or documented again after leaving their social groups. Notably, two adult unknown males immigrated into the study population from an unknown origin. In one of the successful dispersal events, the returning male located the one lone female in the study population and established a new social group. Our study highlights the adaptability of the Dania Beach green monkeys and raises fascinating questions about the cognitive abilities of male *Chlorocebus* monkeys to map out successful dispersal routes in a highly urbanized environment.

Inferring the diet of Kůlna 1 and Svědův stůl 1 from the Moravian karst of the Czech Republic using dental microwear texture analysis

FRANK L. WILLIAMS¹, CHRISTOPHER W. SCHMIDT², JESSICA L. DROKE³, JOHN C. WILLMAN⁴, PETR NERUDA⁵, GAËL BECAM⁶ and MARIE-ANTOINETTE DE LUMLEY⁷

¹Anthropology, Georgia State University,

²Anthropology, University of Indianapolis,

³Anthropology, University of Wyoming,

⁴Paleoanthropology and Èrea de Prehistòria,

Institut Català de Paleoeologia Humana i

Evolució Social (IPHES) and Universitat Rovira i

Virgili, ⁵Anthropology, Ústav Anthropos, Historické

múzeum, Moravské zemské museum, ⁶Department

of History of Art and Archaeology, Université de

Perpignan and CERP de Tautavel, ⁷Anthropologie,

Institut de Paléontologie Humaine

Two Neandertals of the Moravian karst of the Czech Republic preserve *in situ* permanent molars, Kůlna 1, a partial juvenile maxilla associated with the final appearance of the Micoquian Mousterian tradition of Marine Isotope Stage (MIS) 3, and

Svědův stůl (Ochoz) 1, an older-aged adult mandibular fragment from an uncertain context. Previous studies indicate that Neandertals were heavily reliant on meat resources. Whether such dietary proclivities characterize Kůlna 1 and Svědův stůl 1 is addressed using dental microwear texture analysis. Comparative materials including Hortus (n = 5), La Quina 5, Malarnaud, Spy I, Krapina (n = 19), Vindija (n = 5) and Holocene foragers, pastoralists and agriculturalists (n = 173) are utilized to formulate predictions about anisotropy, which may be patterned according to life stage, as well as complexity, which is contingent on the degree of plant food consumption in recent humans. Dental casts were scanned using a white-light confocal microscope. The point clouds were visualized to check for postmortem defects and subsequently processed using scale-sensitive fractal analysis software. As expected both Kůlna 1 and Svědův stůl 1 have low values for anisotropy, suggesting a division of diet by age existed in Neandertals whereby only young adults have extreme values while juvenile and older-aged individuals have lower anisotropy. Svědův stůl 1 likely had a meat-rich diet reflected in a relatively low complexity value, whereas Kůlna 1 probably consumed more plant foods perhaps available from an interval of slightly warmer temperatures during an interstadial period of MIS 3.

Funding was received from Fulbright-Belgium, Marie Skłodowska-Curie Actions (H2020-MSCA-IF-2016 No. 749188), AGAUR (Ref. 2017SGR1040), URV (Ref. 2017PFR-URV-B2-91) Projects, MICINN/FEDER (PGC2018-093925-B-C32), the Leakey Foundation and the National Science Foundation (BCS 0922930).

Activity patterns in an early medieval German community: the association of degenerative joint disease and traumatic injury

LESLIE LEA. WILLIAMS¹ and KENDRA S. WEINRICH²

¹Anthropology, Beloit College, ²Anthropology, The Ohio State University

Bioarchaeologists have numerous tools at their disposal to interpret activity in past communities. Accidental trauma has been used as evidence for labor patterns in past societies, as have rates of degenerative joint disease (DJD). To understand labor and activity in early medieval central Europe, 116 individuals from the early medieval (7th-9th c. AD) site of Altenerding-Petersberg were examined for evidence of traumatic injury and DJD. Trauma was quantified in terms of body region: cranial, long bones, ribs, and other. DJD was scored according to Global History of Health Project standards for the major limb joints and the vertebral column.

Eighty-eight individuals were examined for both traumatic injury and DJD of the major limb joints. The odds of having traumatic injury were 4.8 times higher for individuals with moderate-severe DJD than for those without (Odds Ratio: 4.84;

X²: p=0.004). For the vertebrae, the presence of traumatic injury is significantly associated with DJD in the cervical (X², p=0.02, n=56), thoracic (X², p=0.017, n=72), and lumbar (X², p=0.005, n=75) regions. These associations are seen especially in middle and older adults, but are not statistically significant within age groups.

For individuals with trauma, DJD is not confined to the joints closest to the injury but is often distributed across the skeleton. This indicates that overall activity patterns and/or age rather than trauma-specific biomechanical disruptions are contributing to joint degeneration. The association of trauma and DJD (and the relatively high frequencies of both in this population) suggests intensive labor practices in early medieval Altenerding.

This research was funded by the Deutscher Akademischer Austauschdienst, the City of Erding, The Ohio State University Alumni Grant for Graduate Research, and Sigma Xi.

Kinetics of stone tool production in novice and expert toolmakers

ERIN MARIE WILLIAMS-HATALA^{1,2}, KEVIN G. HATALA^{1,2}, ALASTAIR KEY³, CHRISTOPHER J. DUNMORE³ and TRACY KIVELL^{3,4}

¹Biology, Chatham University, ²Center for the Advanced Study of Human Paleobiology, The George Washington University, ³Animal Postcranial Evolution Lab, Skeletal Biology Research Center, School of Anthropology and Conservation, University of Kent, ⁴Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

A wealth of studies have focused on the relationship between skill level and knapping outcomes, revealing important similarities and differences between groups of novice and expert knappers. Less is known, however, about the relationship between skill level and knapping kinetics.

Here we investigate this relationship by recording dynamic manual pressures experienced by the thumb and fingers of the dominant hand during Oldowan flake production in 23 novice and 9 experienced knappers. We used Novel Pliance textile pressure sensors to dynamically record peak pressures (kPa) and the pressure-time integral (kPa*sec) across all five digits cumulatively and on each digit individually.

At the cumulative level, the variables driving differences between peak pressures and the pressure-time integral were distinct: only skill level had a significant effect on peak pressures, whereas skill level and hammerstone mass significantly affected the pressure-time integral.

Considerable differences were present regarding the ways novices and experts use individual digits. For both peak pressures and the pressure-time integral, experts emphasized the 1st and 2nd digits to a similar extent, in contrast to lower pressures

ABSTRACTS

acting on the ulnar digits. Novices, in contrast, tended to hold the hammerstone such that pressures were similar across the 2nd-5th digits. Skill level was the primary determinant of these differences, rather than confounding factors that we also evaluated, including hammerstone mass and hand size.

Coupled with kinematic studies, these data provide a robust framework for experimental design and hypothesis testing in experimental archaeology.

Supported by the European Research Council Starting Grant #336301, British Academy Postdoctoral Fellowship, Wenner-Gren Foundation #7995, the George Washington University's Selective Excellence Fund, Chatham University and the University of Kent.

From Households to Bathing Rituals: Biocultural Aspects of Life in Late Prehistoric North Georgia

MATTHEW A. WILLIAMSON¹ and MARK C. GRIFFIN²

¹Health Sciences and Kinesiology, Georgia Southern University, ²Anthropology, San Francisco State University

During the late prehistoric to early historic period (AD 1550-1650) in north Georgia, native peoples lived in villages consisting of primary domestic structures arranged around a central plaza or earth mound. Since the 1950s, archaeologists have discovered several villages of this kind including the King, Little Egypt, Sixtoe, Bell Field and Pott's Tract sites. According to Hally (2008) village inhabitants lived in a stratified society that was organized into regional political units called "polities" and that all polities were all included within a paramount "Coosa" chiefdom; the center of which was the Little Egypt site. At these sites, human burials were distributed within and outside of primary domestic structures, rectangular seasonal use structures, public structures, and public open spaces. Hally believes that at the King site, individuals buried in and around a primary domestic structure represent a single, conjugal family. For this study, we examined human remains from a total of 386 burials in order to uncover patterns in lesion frequency or intentional cranial modification that might be connected to households, status, or village membership. Results show that neither caries nor periosteal lesion frequency varied significantly between households or between public spaces and households at the King site. However, there was a higher number of modified crania consisting of the frontal and fronto-occipital types at the King site compared to all the others and a significantly greater frequency of auditory exostoses at the King site. All the individuals with auditory exostoses were male and were probably caused by ritual bathing.

Pre-Natufian Epipaleolithic evidence for dental ablation in southwest Asia? Revisiting Ohalo II H2

JOHN C. WILLMAN^{1,2} and SARAH A. LACY³

¹Paleoanthropology, IPHES, Institut Català de Paleocologia Humana i Evolució Social, ²Èrea de Prehistòria, Universitat Rovira i Virgili (URV), ³Department of Anthropology, California State University-Dominguez Hills

The well-preserved burial of Ohalo II H2 (Oh2, Late Upper Paleolithic/Early Epipaleolithic) is pivotal to our understanding of biocultural dis/continuity during the Epipaleolithic in southwest Asia. We contribute to this discussion with an assessment of overall oral health and dental wear of Oh2.

Results show that the alveolar bone exhibits minor to moderate alveolar resorption in the anterior portion. The left M³ is missing antemortem but cannot be definitively attributed to pathological AMTL or agenesis. The right M³ exhibits minor caries. The AMTL of the left I¹ is characterized by well-healed resorption of the alveolus. The right I¹ exhibits minor supereruption and angled occlusal wear corresponding to the missing I¹. Contrary to previous assessments, incisor wear (relative to first molar wear in the same jaw) is low compared to Natufian and Iberomaurusian individuals.

In the context of Late Pleistocene circum-Mediterranean foragers, Oh2 oral health and dental wear is not exceptional. However, differential diagnosis of the I¹ AMTL is suggestive of intentional ablation, trauma, or pathological loss via caries. Minor non-penetrant caries and modest anterior wear provide little support for pathological AMTL. Oh2 exhibits a major thoracic injury that could correspond to AMTL via trauma. Albeit, AMTL through ablation – the culturally-mediated, intentional removal of teeth – cannot be ruled out either. The latter cause would make Oh2 among the earliest examples of ablation in Western Eurasia and provide biocultural evidence of possible long-term behavioral trends throughout the Epipaleolithic of southwest Asia.

Leakey Foundation, Marie Skłodowska-Curie Actions (H2020-MSCA-IF-2016 No. 749188), AGAUR (Ref. 2017SGR1040) and URV (Ref. 2017PFR-URV-B2-91) Projects, MICINN/FEDER: PGC2018-093925-B-C32.

Fertility Magic and Childbirth During a Malaria Epidemic: An examination of sixty burials from a Roman infant cemetery

JORDAN A. WILSON¹, SIERRA W. MALIS¹ and DAVID G. PICKEL²

¹Anthropology, The University of Arizona, ²Classics, Stanford University

While studies of childhood stress and infant mortality are prevalent in bioarchaeology, there are far fewer analyses of the corresponding experiences of pregnancy, childbirth, and child loss by ancient women. This poster presents an examination of sixty burials from the Roman *Necropoli*

dei Bambini of fetuses and infants, aged six gestational months to three years old, who perished during an epidemic of *Plasmodium falciparum* malaria ca. 450 A.D. Results of this analysis not only show bony pathology consistent with malarial infection, but also birth-related trauma such as clavicle fracture resulting from shoulder dystocia and cervical injury from possible breech presentation. The localization of the trauma, along with the state of healing of the injuries, strongly suggest these were midwife-assisted deliveries, and that mother and infant received a degree of postnatal care. Previous research on faunal and botanical remains from the burials indicated attempts at magico-medical cures for the malarial infection. These new findings specifically suggest the presence of women with knowledge of medicine and midwifery in this rural community and contain added significance in the context of an epidemic that would have disproportionately affected pregnant women, babies, and young children. This has also offered new interpretations of ritual artifacts recovered from the burials as forms of fertility magic. Our analysis contradicts male-centric historical accounts of childbirth and mortality in the Roman world and suggests a high degree of female agency during a public health crisis that changed the course of history.

Day of menstrual cycle does not have a significant effect on urinary cortisol levels in a sample of Polish American women

MEREDITH A. WILSON¹, KATHARINE NM. LEE¹, MARY P. ROGERS¹ and KATHRYN BH. CLANCY^{1,2}

¹Department of Anthropology, University of Illinois, Urbana-Champaign, ²Beckman Institute, University of Illinois, Urbana-Champaign

With the National Institute of Health recognizing the need for more inclusion of female and menstruating subjects in animal and clinical research, understanding how and if the menstrual cycle effects biological outcomes is particularly important. In this study, we examined whether day of cycle had an effect on urinary cortisol levels. We collected daily urine samples for one full cycle from 24 healthy, Polish-American women (age=18-45), living in urban regions of the United States. Participants were instructed to collect a urine sample daily, starting the first day of menstruation until the start of their next period, resulting in n=555 samples (some days of cycle missing). Mid cycle estradiol drop was used to estimate timing of ovulation, which was coded as day 0. We performed a generalized linear model to test the effect of day of cycle on cortisol levels and found a near significant effect (p=.067). However, to account for individual variation, we tested a second model including individual. There were no significant effects (day of cycle, p=.336). Our results suggest that controlling for cycle day or phase may not be necessary when collecting urinary cortisol from a group of healthy,

ABSTRACTS

homogenous adults. Additionally, omitting cycling participants from research because of concerns of increased variation or fears of the menstrual cycle impacting results may be unjustified and should be further explored.

Research supported by the NSF (BCS-1317140, DDRIG BCS-1732117, DDRIG BCS-1650839, GRFP DGE-1144245), Wenner-Gren Dissertation Fieldwork Grants, APS Lewis and Clark Fund, Beckman Institute CS/ AI Award, Sigma Xi & more.

Bigger on the inside: Using agent-based models in the classroom to explore big questions in evolutionary anthropology

MICHAEL L. WILSON^{1,2}, KRISTIN N. CROUSE¹ and CARRIE M. MILLER¹

¹Anthropology, University of Minnesota, ²Ecology, Evolution and Behavior, University of Minnesota

Students face several obstacles to understanding concepts in evolutionary anthropology, including: the timescale is long; evolution happens at the population- rather than individual-level; and diverse evolutionary outcomes can emerge from similar initial conditions. To overcome these obstacles, we have developed agent-based models in the NetLogo modeling environment. We discuss three of these here. First, "Population Genetics" explores alleles, genes, genotypes, phenotypes, and the mechanisms of evolution. It connects students at different computer terminals; each terminal a different population within a larger ecosystem. Simulations demonstrate how the mechanisms of evolution shape variation in allele frequencies within and between populations. Second, "Prisoner's Tournament" explores game theory, prisoner's dilemmas, cooperation and defection. This model replicates classic game theory tournaments, in which students design strategies for a class-wide competition. Finally, "B3GET" teaches students how behavioral adaptations emerge from a given environmental context. Agents possess chromosomes that code for their behavioral strategies and are subject to recombination and mutation. We designed B3GET to conduct research, but also find it is useful in the classroom, as it allows students to perform experiments and observations in an artificial petri dish. Overall, we have found that these models help students learn. In a survey of 78 students, a median 55.5% reported that they liked the agent-based model assignments (range: 36–64%), whereas only 11.5% disliked these assignments (range: 4–44%; $n = 8$ assignments). This compares favorably with the 4 assignments that used other methods, which a median 32.5% liked (range: 23–73%) and 23.5% disliked (range: 5–68%).

Increasing diversity in biological anthropology: Lessons from a laboratory-based undergraduate mentorship program

TERESA V. WILSON

Department of Geography and Anthropology, Louisiana State University

Based on an assessment of the state of race and diversity in biological anthropology, the largest discrepancy we face for retaining underrepresented minority scholars is the transition from the undergraduate degree to graduate school. The key to this dilemma may be a lack of mentorship and support at the undergraduate level for those who feel excluded from academia. By providing a space where students can gain experience and confidence, mentorship programs can support those who may feel like a career in biological anthropology is unattainable. The Louisiana State University Forensic Anthropology and Computer Enhancement Services (LSU FACES) Laboratory developed an undergraduate volunteer program in human skeletal biology and forensic anthropology in 2016 with the mission to provide support and guidance for a diverse group of students interested in human osteology. This program places undergraduates inside a working forensic anthropology laboratory and offers the opportunity for self-guided osteological learning. Students have self-paced milestones they must meet while in the program. Each milestone culminates in the passing of a proficiency exam (i.e., basic osteology, advanced and fragmentary osteology, and biological profile techniques) and leads to greater laboratory privileges. Of the 15 students who have completed the program, 10 of our volunteers are from underrepresented groups and four of these 10 have enrolled in a graduate or dental school. Although the program is small, the past three years of the program have shown that a structured mentorship program can create an environment that will promote advancement in the field and support diversity.

Whole mitochondrial sequences reveal substantial heterogeneity within African descendants in the Caribbean

TAIYE WINFUL, MA¹, LIJUAN CHEN, MA¹ and JADA BENN TORRES, PHD^{1,2}

¹Anthropology, Vanderbilt University, ²Vanderbilt Genetics Institute, Vanderbilt University

The Caribbean took in an estimated 3 million enslaved African peoples during the Transatlantic Slave Trade (TAST). Puerto Rico specifically received about 16,000 of these individuals. Despite the relatively small number of enslaved people that were brought to Puerto Rico, there are gaps in knowledge about the impacts of the TAST on all aspects of island life. To this end, we consider mitochondrial diversity of Afro-Puerto Ricans (AfPRs) in order to comment on the demographic histories of AfPRs and other African descendants

in the Americas. Building from our previous work, we expanded our sample size from 31 to 53 whole mitochondrial DNA sequences and compared them to data from various African and American populations. While 32% of the sample belonged to Indigenous American or Eurasian haplogroups, most individuals, 68%, belonged to a sub-Saharan African L type haplogroup. Of the L-types, 6% belonged to L0, 33% to L1, and 28% to L2 and 33% to L3. We used Fisher Freeman analysis to compare haplogroup distributions between Afro-Puerto Ricans and comparative populations with African descent. We found significant differences between AfPRs and comparative groups from US Americans (NHB), Kenya (LWK), Nigeria (YRI), and Haiti ($p < 0.05$); while the remaining comparisons were not significantly different. Summary statistics indicated increased levels of nucleotide (> 0.003) and gene diversity (> 0.991), with the additional AfPR samples. Analysis of whole mitochondrial sequences from Afro-Puerto Ricans illustrates genetic diversity that is characteristic of African-descended populations, yet highlights heterogeneity among populations within the African Diaspora.

Development of sex differences in play in wild white-faced capuchins

SASHA L. WINKLER^{1,2} and SUSAN E. PERRY^{1,2}

¹Department of Anthropology, University of California-Los Angeles, ²Behavior, Evolution and Culture Program, University of California-Los Angeles

Cross-sectional research demonstrates higher rates of social play among males than females in many mammal species. Yet, the animal literature largely lacks longitudinal data on developmental patterns of play over the lifespan. We analyzed sex-specific patterning of play and grooming using an 18-year dataset on a cohort of wild white-faced capuchin monkeys. We measured the proportion of point samples taken during focal follows in which each individual was engaging in social play, solo play, and grooming. To determine sex differences for each behavior, we ran Poisson generalized linear mixed models with a random effect for each individual. Results for social play showed significant fixed effects for sex ($\beta = 0.322$, $P = 0.002$), age ($\beta = -0.215$, $P < 0.001$), and the interaction between sex and age ($\beta = 0.103$, $P < 0.001$). The interaction was partially driven by males, but not females, increasing rates of social play over time in the early juvenile period. Results for solo play did not have a significant fixed effect for sex ($\beta = -0.104$, $P = 0.633$); however, females reduced rates of solo play over time more quickly than males ($\beta_{\text{year}} = -0.487$, $P < 0.001$, $\beta_{\text{sex} \times \text{year}} = 0.086$, $P = 0.018$). Females had higher rates of grooming than males and greater increases in grooming over time ($\beta_{\text{sex}} = 0.103$, $P = 0.0479$; $\beta_{\text{year}} = 0.073$, $P < 0.001$; $\beta_{\text{sex} \times \text{year}} = -0.139$, $P < 0.001$). Our results

ABSTRACTS

suggest that males allocate more time toward social play than females throughout the juvenile period, and females may compensate for lower play rates through increases in grooming. This longitudinal perspective demonstrates that play behavior may be critical for the development of sex-specific life history strategies.

MPI-EVAN, UCLA and grants to S. Perry: NSF (1638428, 0613226, 848360), National Geographic Society (7968-06, 8671-09, 20113909, 9795-15, 45176R-18), Templeton World Charity Foundation (0208), and 5 Leakey Foundation grants.

Mortality and resilience: questioning the immutability of non-specific stress indicators in paleopathology

AMANDA WISSLER

School of Human Evolution and Social Change,
Arizona State University

Numerous scholars have highlighted the problems inherent in using nonspecific indicators of skeletal stress to infer past health, particularly our reliance on untested assumptions about their etiology and uncertainty on how to best interpret these markers. Despite widespread acknowledgement of these issues, data on nonspecific indicators of skeletal stress are ubiquitously collected in bioarchaeology and paleopathology. This study explores an untested assumption of nonspecific indicators of stress: does the impact of these skeletal indicators on mortality change over time? Or are these skeletal lesions immutable signals of physiological stress? To answer this question, data on age-at-death and skeletal indicators of stress – femoral length, linear enamel hypoplasia, periodontal disease, periostosis, and vertebral neural canal diameter – were collected from a sample of individuals (N=193) from the Hamann-Todd documented skeletal collection in five-year intervals from between 1910-1929. The force of mortality for each of these skeletal indicators was assessed using Usher's (2000) multi-state model of mortality and compared across each time interval. Results demonstrate that not only does the magnitude of the force of mortality for each indicator change over time, but they can change from being markers of increased mortality to markers of increased survival. While additional study is needed to support these findings, the results of this project have significant implications for how future studies should collect and interpret nonspecific indicators of skeletal stress. These results also suggest that past studies that rely on these skeletal indicators may need to be revisited.

Center for Bioarchaeological Research Pilot Grant, 2018.

Characterizing Archaic Hominin Variation in Human Populations

KELSEY E. WITT and EMILIA HUERTA-SANCHEZ
Center for Computational and Molecular Biology,
Brown University

Modern human genetic variation has been shaped by thousands of years of population movements and interactions. Non-African populations have acquired a number of novel variants since leaving Africa, due both to random mutation and admixture with Neanderthals and Denisovans. After these initial admixture events, archaic alleles were further shaped by local selective and demographic events. Here we quantify how much "archaic" variants contributed to new genetic variation in non-African populations by examining uniquely shared mutations between archaic humans and non-Africans that are rare in Africa ($f < 0.01$), and likely arose after humans left Africa. We further identified these alleles as derived or ancestral relative to the chimp-human ancestor, and compared the "archaic" variants to novel variants that likely arose in non-African populations as new mutations. 5.5-7% of derived and 65% of ancestral novel alleles are shared with archaic hominins, and were likely introduced through introgression. The patterns of "archaic" genetic variation in non-African populations largely match what is expected given the successive bottlenecks that occurred as humans migrated across Eurasia and into the Americas. However, some populations have excess common ($f > 0.2$) or rare variants ($f < 0.2$) than expected, reflecting that selective pressures have acted differently in different regions of the world. Despite low archaic levels of archaic ancestry, we find that archaic alleles contain sufficient information to classify individuals by geographical region, suggesting that surviving archaic alleles in modern-day individuals are often unique to a single population or are shaped by distinct evolutionary processes.

Vertebral neural canal dimensions as indicators of socio-economic status and population-level differences in contemporary subadult samples

CHRISTOPHER A. WOLFE, LOUISE K. CORRON,
ELAINE Y. CHU and KYRA E. STULL

Anthropology, University of Nevada, Reno

Antero-posterior and transverse diameters of the vertebral neural canal (VNC) are often used in anthropological studies as indicators of environmental and genetic components influencing growth. This study aims to evaluate the relationship between VNC measurements, socio-economic status (SES), and population affiliation in five contemporary subadult samples. Lumbar and thoracic antero-posterior and transverse VNC diameters of vertebrae L5 to T10 were measured on dry skeletal remains or CT scans from individuals aged between 0 and 19 years from Colombia (n=57), France (n=200), the Netherlands (n=24), Taiwan (n=31) and the United States (n=838). The Gini coefficient, measuring inequality (0 = high equality; 1 = high inequality),

and Human Development Index (HDI), measuring life expectancy, education, and standard of living (0 = worst HDI, 1 = best HDI) were used to capture SES. Principal component analyses (PCA) and factor analysis of mixed data (FAMD) were employed to explain the contributions of quantitative (measurements) and qualitative (HDI, Gini, population) variables to overall variance. Vertebral size is consistently smaller for Colombian individuals compared to other populations in both transverse and antero-posterior dimensions, while vertebral shape remains comparable among all groups. PCA and FAMD analyses suggest that individuals in low HDI and high Gini categories present with discordant dimensions compared to all other combinations of variables. Additionally, a high Gini explains a larger portion of variance than any other qualitative variable. These results seem to confirm that, in contemporary populations, environmental factors may have a stronger influence on VNC growth than genetic background.

This research was funded by two federal grants (NIJ 2015-DN-BX-K409 and NIJ 2017-DN-BX-K144).

Conundrum: *Homo erectus* in Middle and Late Pleistocene maritime Southeast Asia and Australia

MILFORD H. WOLPOFF and VINCENT M. BATTISTA
Anthropology, University of Michigan

Homo erectus is unquestionably present in the Early Pleistocene, but what about later, and what about Australia? The larger Middle/earlier Late Pleistocene maritime sites are from Java: Sambungmachan and Ngandong. The crania are similar to the earlier Sangiran crania, and often classified with them, but there are also striking similarities of Ngandong to certain later nearby Australian fossils, especially WLH 50. Anatomical and limited genetic comparisons suggest that some ancestors of Australians are from populations such as Ngandong.

The Middle Pleistocene dentognathic sample from Mata Menge, Flores island, mostly does not preserve parts comparable to those from Sambungmachan or Ngandong, but they are clearly a smaller and more gracile sample. Pleistocene Australian fossils show (albeit more limited) evidence of mixture from these ancestors as well; Australians, like virtually all recent populations, have multiple ancestors. Every modern scientist familiar with the Australian fossil record agrees that by virtue of their anatomy, and the time, place, and cultural associations where they are found, Australian fossil hominids are unquestionably *H. sapiens*.

If similarities indicate a population like Ngandong is among the ancestors of Australians, the evolutionary pathway in maritime southeast Asia cannot be portrayed as "a somewhat different path from the lineage that led to *Homo sapiens*" (as it has been) because this path *did*

ABSTRACTS

demonstrably lead to *H. sapiens*. If this lineage, based on similarities, began as *H. erectus* and ended as *H. sapiens*, and we reject anagenesis as an explanatory mechanism, there can only be one name for it: *Homo sapiens*.

This research was supported by grants from NSF, NAS, and the University of Michigan

Investigating dental health of the owners and sacrificial victims in burials at the Imdang site, South Korea (A.D. 3rd -7th centuries)

EUN JIN WOO¹, HYUNWOO JUNG², YANGSEUNG JEONG³ and DAE WOOK KIM⁴

¹History, Sejong Univ, ²Anthropology, University at Buffalo, SUNY, ³Biology, Middle Tennessee State University, ⁴Archaeology, Yeungnam University Museum

The purpose of this research is to explore the correlation between the dental health condition and social hierarchy in the past Korean population by analyzing the prevalence of dental pathologies of the owners and sacrificial victims of the ancient Korean burials.

A total of 515 teeth from 35 individuals from the Imdang site, which is dated between A.D. 3rd and 7th centuries, were macroscopically examined to compare the prevalence of caries, chipping trait, and attrition score between the individuals of different social status. The Chi-square test and Wilcoxon's test were conducted for each tooth type with the age-at-death controlled for. Sexes were pooled to maximize the sample size.

Statistically significant differences were not found in the prevalence of the caries and attrition score between the two groups despite the overall higher attrition score in the sacrificial victim group. In the upper M1 and lower M2, the owner group had more chipping traits than the sacrificial victims, of which difference is significant. These findings suggest not only the possibility that the prevalence of dental pathologies are related to social hierarchy in ancient Korea but also the necessity to take the cultural and archaeological context into account in investigating more detailed etiologies of dental pathologies in the past populations. Further research with a larger sample size and additional pathologic markers will be necessary for deeper understanding of the multi-faceted nature of dental pathologies of ancient populations.

This work was supported by the Korea Government (MSIT) (National Research Foundation of Korea, 2018R1A5A7023490).

An expanded character set for evaluating the phylogenetic position of *Homo floresiensis*

TODD WOOD

Biology, Core Academy of Science

Homo floresiensis represents the best attested of three potential hominin species exhibiting insular dwarfism in southeast Asia, yet the phylogenetic affinities of the taxon remain uncertain. Argue et al.'s (2017) phylogenetic analysis of 133 characters and eleven taxa imply a close affinity between *H. floresiensis* and *H. habilis*, but Dembo et al.'s (2016) phylogenetic analysis of 391 characters and 24 taxa placed the branching of *H. floresiensis* at the base of the *Homo* clade. Here the character states of *Homo floresiensis* have been expanded by adding 29 states from Argue et al.'s characters to the supermatrix of Dembo et al. A further 55 *H. floresiensis* character states were newly scored based on published photographs and anatomical descriptions. The known character states of *H. floresiensis* have now been tripled from 42 in the published version of Dembo et al.'s supermatrix to 126 in the current version. The supermatrix was also updated with 48 character states for *Ardipithecus ramidus* from Mongle et al. (2019), 50 character states for *Australopithecus anamensis* from Haile-Selassie et al. (2019), and one character state for *Homo antecessor* from Trafi et al. (2018). A preliminary, undated Bayesian phylogenetic analysis was conducted using the updated supermatrix in MrBayes. Using the same procedure as Dembo et al.'s previous undated Bayesian analysis, the maximum clade credibility tree matched Dembo et al.'s almost exactly. The positions of *H. floresiensis*, *Au. anamensis*, and *Ar. ramidus* are unchanged. *H. floresiensis* appears to be a recently-surviving member of an early branch of the *Homo* clade.

Intraspecific variation within the forearms of non-human primates

NIKOLE WORDEN¹, SIDNEY R. SWINDELL¹, MARISSA L. BOETTCHER^{1,2}, EDWIN DICKINSON¹ and ADAM HARTSTONE-ROSE¹

¹Biological Sciences, North Carolina State University, ²College of Medicine, Medical University of South Carolina

Many studies have sought to describe variation in musculoskeletal anatomy within the primate forelimb interspecifically. However, little has been done to explore the variation that exists within individual species. Developing an understanding of intraspecific variation is necessary to better understand interspecific variation; otherwise, it is impossible to confirm that descriptions reflect true differences in the anatomical profiles of taxa. In this study, we analyze nine intraspecific samples across three families: callitrichidae, cebidae, and lemuridae. We report both qualitative and quantitative data on variation within the antibrachial musculature of each species. The most common variant within each taxon reflected the extent of fusion between *M. flexor digitorum superficialis* and *profundus*: within each family, one species demonstrated no variation, while all other taxa varied intraspecifically.

Within two families, variation was also observed within the digital extensors: three callitrichid and one cebid species possess accessory extensor muscles. None were observed within any lemurid. Interestingly, only two species (*Saguinus bicolor* and *Sapajus apella*) demonstrated no intraspecific variation in muscle presence/absence or fusion. From an architectural perspective, fiber length displayed the greatest variation, while muscle mass was most conservative within species. Among the species we analyzed, *Callithrix pygmaea* displayed the greatest variation in architectural properties while *Saguinus bicolor* and *Sapajus apella* displayed the least. Future interspecific studies may wish to account for such variation when reporting myological trends between taxa – the presence, absence and architecture of these muscles vary within species more than has been previously recognized.

This work was funded, in part, by the National Science Foundation (IOS-15-57125 and BCS-14-40599).

Speed-related changes in cheiridial posture and pressure distribution

ROSHNA E. WUNDERLICH

Biology, James Madison University

The hands and feet serve as the interface between primates and the complex substrates on which they travel. Despite assumptions about how hands should respond to changes in speed, previous studies have observed that the hands of terrestrial monkeys become less digitigrade and increase palmar contact area to decrease pressure, at higher speeds, while the feet become more digitigrade. Here we further test this concept by examining changes in hand and foot contact area, peak force, pressure, and limb kinematics resulting from variations in speed and substrate slope in 3 *Lemur catta* (*Lc*) and 3 *Varecia rubra* (*Vr*). As speed increases on a horizontal substrate, *Lc* exhibits reduced palm and sole peak pressures, increased palm and sole contact areas, and increased digital pressures. *Vr* exhibits no speed-related changes in pedal force or pressure but does show increased palm pressures reflecting an unloading of the manual digits and less digitigrade posture. *Lc* exhibited increased palm and sole peak pressures and contact areas with increasing speed on inclines and declines, but *Vr* exhibited stable forelimb pressures on the slopes. In *Vr* these moderations of peak force are accommodated by limb kinematic modification. These patterns may reflect the habitual locomotor patterns in *Lc* that are more terrestrial than *Vr*. This study highlights the complex ways that primates adjust hand and foot use in response to their anatomy, changes in speed and substrate, and their habitual locomotor pattern and adaptations.

ABSTRACTS

The genetic history and adaptive evolution of Tibetan highlanders

SHUHUA XU

Population Genomics, CAS-MPG Partner Institute for Computational Biology

It was a long journey for human to conquer the Tibet Plateau where the average elevation is beyond 4,500 meters and the oxygen pressure is much lower than at sea level. We estimated that the genetic origin of the Tibetan highlanders could be traced back to around 40,000 to 60,000 years ago, in the middle-late Paleolithic. The early migrants to the plateau had extensive genetic admixture with each other, and had further gene flows with the latecomers, leading to the admixed descendants with very complex genetic makeup. Taking advantage of the whole-genome deep sequencing data, we constructed a map of adaptive genetic variants in Tibetans. We further prioritize these identified adaptive genetic variants, and found that the top signal is *TMEM247*, a transmembrane protein coding gene. Especially, a missense variant (rs116983452) located in *TMEM247* showed rather high frequency specifically in Tibetans. The frequency of *TMEM247*-rs116983452-T is strongly and positively correlated with altitude, and is carried by around 94% Tibetans, but is in low frequency or absent from non-Tibetan populations. It is so far the most differentiated missense variant between Tibetans and the lowlanders. By statistical modeling, we found that *TMEM247*-rs116983452 shows greater effect size and better predicts the phenotypic outcome than any *EPAS1* variants in the association with adaptive traits in Tibetans, but interactions were also observed between *TMEM247*-rs116983452 and *EPAS1* variants, indicating that multiple variants may jointly deliver the fitness of the Tibetans on the Plateau, where a complex model is needed to elucidate the adaptive evolution mechanism.

This work is supported by the CAS Strategic Priority Research Program (XDB13040100 to S.X.), the National Natural Science Foundation of China (NSFC) grant (91731303, 31525014, and 31771388 to S.X.).

Genome-wide analysis on adult cephalic morphology in Okinawa and Ishikawa, Japan

KYOKO YAMAGUCHI¹, KAE KOGANEBUCHI², TAKEHIRO SATO³, TAKAYUKI KANNON³, HIROMASA TSUJIGUCHI³, KAZUYOSHI HOSOMICHI³, ATSUSHI TAJIMA³, KEN YAMAMOTO⁴, HAJIME ISHIDA², HIROYUKI NAKAMURA³ and RYOSUKE KIMURA²

¹School of Biological and Environmental Sciences, Liverpool John Moores University, ²School of Medicine, University of the Ryukyus, ³Graduate School of Medical Sciences, Kanazawa University, ⁴School of Medicine, Kurume University

The genetic influences on normal variation in cephalic morphology remain unclear, especially in non-European populations. Finding the

genetic basis of cephalic morphology in non-European populations such as East Asian would play an important role in reconstruction of skulls from DNA for extinct species of genus *Homo*. Therefore, we conducted two genome-wide association studies (GWAS) on head size and shape in Japan using DNA microarray data of 767 adults (429 males, 338 females) in Okinawa Island and 301 adults (158 males, 143 females) residing in Ishikawa. The meta analysis of the two GWASs suggested an association between a single nucleotide polymorphism (SNP) located within *HTR2A* on chromosome 13 and head circumference measured with a tape measure, after controlling for sex, height, BMI, and genomic principal components ($P = 4.25E-07$). *HTR2A* encodes a neurotransmitter and mutations in this gene are reported to be associated with schizophrenia and obsessive-compulsive disorder. As the skull development is strongly linked to the brain development, it is worth investigating the association with the polymorphisms in this gene and brain size in the future. Our study on adult head size and shape showed inconsistent results with the previous studies, and showed the importance of conducting studies in East Asia for reconstruction of skulls from DNA for extinct species that is closely related East Asians.

Intra-tooth $\delta^{18}\text{O}$ range of fossil suids indicate an increase in rainfall seasonality/aridity in the Koobi Fora Formation, early Pleistocene

DEMING YANG¹ and KEVIN T. UNO²

¹IDPAS, Stony Brook University, ²Division of Biology and Paleo Environment, Lamont-Doherty Earth Observatory of Columbia University

Stable isotope intra-tooth sampling has been used to reconstruct diet and rainfall seasonality. Recent studies showed a strong correlation between intra-tooth oxygen isotope ($\delta^{18}\text{O}$) range of equid teeth and intra-annual $\delta^{18}\text{O}$ range in precipitation in eastern Africa, which is correlated with aridity. Similar to equids, fossil suids are water-dependent animals with high-crowned teeth. Their intra-tooth $\delta^{18}\text{O}$ range likely reflect rainfall seasonality/aridity.

We sampled third molars of *Notochoerus scotti* and *Metridiochoerus* spp. from three early Pleistocene members of the Koobi Fora Formation (~2.1 – 1.4 Ma). We compared intra-tooth $\delta^{18}\text{O}$ range between different suid species and through time.

Fossil suid intra-tooth $\delta^{18}\text{O}$ range falls between ~1‰ to 4‰, which is similar to that of extant warthogs in Kenya (~2‰ to 5‰). There is no difference in the $\delta^{18}\text{O}$ range between the suids *Notochoerus scotti* and *Metridiochoerus andrewsi*. *Metridiochoerus compactus* has significantly higher range than *Metridiochoerus andrewsi* but not *Notochoerus scotti*. When combining data from all taxa, there is an increase in intra-tooth

$\delta^{18}\text{O}$ range from ~1.9 to 1.7 Ma and again from ~1.7 to 1.5 Ma. The intra-tooth $\delta^{13}\text{C}$ values in all taxa are relatively invariant, suggesting that diet likely did not influence the observed $\delta^{18}\text{O}$ changes.

Our results indicate an increase in rainfall seasonality/aridity from ~1.9 to 1.5 Ma in East Turkana. An increase in paleosol carbonate $\delta^{18}\text{O}$ values from the region over this time interval supports this interpretation. More intra-tooth profiles will help to discern spatial and temporal factors that may influence intra-tooth variation in $\delta^{18}\text{O}$ values.

This research is supported by the Leakey Foundation, the University of Utah, and the Turkana Basin Institute.

Using thin plate splines to statistically compare force curves produced by western lowland gorillas (*Gorilla gorilla gorilla*)

GABRIEL S. YAPUNCICH¹, DANIEL SCHMITT¹, ROSHNA E. WUNDERLICH² and ANGEL ZEININGER¹

¹Evolutionary Anthropology, Duke University,

²Biology, James Madison University

Primates have functional differentiation of their forelimb and hindlimb peak vertical and fore-aft (braking/propulsive) forces. However, the timing of peak vertical force within each limb and its coordination with the timing of peak braking/propulsive force remains untested. To evaluate the hypotheses that a) the forelimb experiences a lower loading rate and a later vertical peak than the hindlimb and b) that braking/propulsive forces are lowest within a limb when vertical force is highest, we applied novel thin plate spline models to unfiltered force traces to address questions of differences in overall force curve shape. Vertical and braking/propulsive force curves produced by the forelimb ($n=43$) and hindlimb ($n=19$) were collected for six *Gorilla* individuals at the North Carolina Zoo. Forces were normalized to body mass and stance time. Mean force curves were generated for each limb using thin plate spline models and statistically compared with permutation tests. In the first half of stance phase, mean forelimb vertical force was significantly lower than mean hindlimb vertical force ($p<0.001$) while the forelimb experienced significantly greater mean braking force ($p<0.001$). In the second half of stance, mean hindlimb vertical force was significantly lower than the forelimb ($p<0.001$) while the hindlimb reached its propulsive peak. Thin plate splines have the potential to model and permit statistical comparison of force curves along their entire length. Combined with positional data, these data could be used to evaluate how loading influences anatomy at key points in the locomotor cycle.

This research was funded by NSF BCS 1517561 to AZ, RW, and DS.

ABSTRACTS

The intersectional effects of sex and socioeconomic status on risk of mortality in industrializing England

SAMANTHA L. YAUSSY

Anthropology, University of Nevada, Reno

Intersectionality theory posits that multiple levels of marginalization interact to produce observed patterns of frailty and mortality. To examine how mortality during industrialization was selective with respect to sex and socioeconomic status (SES), this study analyzes data from four skeletal samples from the industrial period (18th-19th centuries) in England: St. Bride's Fleet Street (London, n=221), Coach Lane (North Shields, n=212), St. Peter's Collegiate Church (Wolverhampton, n=122), and New Bunhill Fields (London, n=530). In this study, St. Bride's was considered the high SES sample, and Coach Lane, St. Peter's, and New Bunhill Fields were separately and collectively analyzed as the low SES samples. SES was modeled as a covariate affecting the Siler model of mortality, and sex, in adults, was modeled as a covariate affecting the Gompertz model of mortality. The results indicate that, generally, SES had an effect on the risk of mortality, and sex had an effect on the risk of mortality within the high SES group. High SES individuals were at reduced risk of death compared to low SES individuals, and high SES males faced a significantly lower mortality risk compared to high SES females. Increased risk of mortality among low SES individuals was likely due to the overcrowded and unsanitary living conditions common in the poorer areas of the industrializing cities of England. However, consistent with intersectionality theory, the benefits of high SES were unequally distributed among adults in the high SES sample, suggesting that men were the primary beneficiaries of the protective aspects of high SES.

Grants: NSF (BCS-1649757), SPARC Graduate Research Grant (University of South Carolina)

Beyond "Outreach": Effective Strategies for Engaging At-Risk High School Students in Biological Anthropology

KATRINA YEZZI-WOODLEY¹, JOEL ABDELLA² and KATHERINE ERDMAN³

¹Anthropology, University of Minnesota, ²Biological Science, Gordon Parks High School, ³SASSA in the Classroom, Science and Social Studies Adventures

Our purpose is to create interactive, inquiry-based, student-centered activities that utilize tactile and 3D methods to engage at-risk high school students in the study of human evolution. We use surveys and reflection questions as academic and engagement measures. Our approach sparks students' interest and curiosity as they are able to touch and interact with materials they do not normally have access to. This project is an ongoing collaboration between Science and Social

Studies Adventures (SASSA) and Gordon Parks High School. SASSA is a volunteer organization that connects collegiate researchers with K-12 schools around the Twin Cities metro to respond to the needs of local teachers and students to develop and present educational modules for use in K-12 classrooms. In one of our partnerships with Gordon Parks High School we guide students through an interactive biology unit which focuses on evolutionary theory. The students at Gordon Parks are considered at-risk students, many of whom are overcoming severe obstacles such as homelessness and displacement, making it extremely difficult to focus on classroom learning. Using hands-on laboratory experiences, students are able to interact with materials that illustrate complex ideas in a tactile way. Questions posed to the students promote high level thinking skills that require them to develop and test hypotheses using the materials before them. Through this approach, students are able to see the relevancy of evolutionary theory for understanding the world today and what it means in their own lives.

Climate predicts changes in growth trajectories in modern humans: a mixed model approach

AN-DI YIM¹, LIBBY COWGILL², DAVID C. KATZ³ and CHARLES C. ROSEMAN⁴

¹Department of Anthropology, University of Illinois at Urbana-Champaign, ²Department of Anthropology, University of Missouri, ³Department of Cell Biology and Anatomy, University of Calgary Cumming School of Medicine, ⁴Department of Animal Biology, University of Illinois at Urbana-Champaign

The selective and neutral evolutionary forces (random genetic drift, mutation and gene flow) responsible for diversity in the limb dimensions and proportions of recent humans have been studied primarily for adult morphology. This study examines how various evolutionary forces affect diversity in the developing limbs and in limb ontogenetic trajectories. We used a multivariate mixed effects model approach to quantify the effects of climatic adaptation and population structure (genetic relationships among groups) resulted from neutral evolution on subadult femur and tibia measurements in a global sample (n = 556 from seven groups). For both limb elements, models that take population structure into account generally outperform models without a population structure random term. After accounting for the effects of neutral evolution, we show that the effects of extreme temperatures on the dimensions of femur and tibia follow the prediction of ecogeographic rules throughout growth. Mean annual temperature, however, is a poor predictor for individual bones but may explain variation in intralimb proportion among groups during growth. This study shows that adaptation by natural selection to climate has a substantial effect on growth

trajectories and therefore adult morphology. This important factor should not be overlooked when interpreting postcranial skeletal morphology, even in subadults.

Funding provided by the Wenner-Gren Foundation (Dissertation Fieldwork Grant).

Investigating the relationship between mental foramen number and cross-sectional area

CAITLIN B. YOAKUM and CLAIRE E. TERHUNE
Anthropology, University of Arkansas

The mental foramen houses the mental nerve, a termination of the inferior alveolar nerve (IAN) that supplies all sensation to the lower teeth, jaws, lips, and gums. While significant research has been done on the presence of accessory mental foramen, little research focuses on comparing the overall cross-sectional areas of the left and right mental foramina. This study aims to assess the presence/absence of accessory mental foramen and perform a comparison of the total cross-sectional area between the left and right sides in 54 species of primates (n=154). Within-species significance tests (by sex) showed significant differences in cross sectional area on the left side (*Colobus polykomos*, p=0.013) and in number of foramina present (*Papio anubis*, Right, p=0.004 and Left, p=0.008) in two species. However, because most species had no significant differences between sides (in either number of foramina or cross-sectional area), the sexes were combined to generate species averages. Correlation analyses identified significant correlations between the left and right sides in both number of foramina and cross-sectional area. Finally, a series of phylogenetic generalized least squares analyses (PGLS) comparing foramen cross-sectional area and number of foramina against the corresponding mandibular length showed significant relationships in all cases. PGLS slopes indicated a positive and significant relationship in all cases. These preliminary data are critical for establishing a framework for future work examining the soft tissues running through the mandibular canal.

A thousand new cercopithecoid fossils to fill the Late Pleistocene void

RYAN YOHLER^{1,2}, MARIANNE BRASIL^{1,2}, TESLA MONSON³, CAT TAYLOR^{1,2} and LESLEA J. HLUSKO^{1,2}

¹Integrative Biology, University of California, Berkeley, ²Human Evolution Research Center, University of California, Berkeley, ³Anthropology, Western Washington University

Recent field work in the upper Dawaitoli Formation of the Middle Awash, Ethiopia, led to the recovery of >1,000 Cercopithecidae fossil specimens. The collection represents two faunas, the Faro Daba (n=732; at ~100,000 years old) and Chai Baro Members (n=276; at ~200,000 years old). Given

ABSTRACTS

the remarkably large size of the total collection, we present these new fossils using a populational approach that relies on quantitative analyses and comparison to a sample of 818 extant cercopithecoids spanning 12 genera.

The younger Faro Daba preserves Colobini and Cercopithecini, with a ratio of 1.16. We estimated ontogenetic age for 270 specimens and found that 75% of them were young to middle-aged adults. The sex ratio is ~50:50. Eighteen percent of the assemblage shows taphonomic alterations, the vast majority being carnivore modification, often in conjunction with insect and/or rodent damage. Applying an evolutionary species concept, the Faro Daba assemblage is designated as *Colobus cf. guereza* and *Cercopithecus* (sensu lato) sp. with a mix of affinities to both *C. aethiops* and *C. mitis*.

The Chai Baro assemblage parallels Faro Daba in its age-at-death profile and sex ratio. However, this older horizon differs by preserving significantly less carnivore, rodent, and/or insect damage. The faunal composition also differs taxonomically, with *Papio hamadryas* and *Cercopithecus* (sensu lato) sp. present, with a 1.44 ratio.

These fossils represent an unprecedented addition to the Late Pleistocene fossil record and increase the record for the African Cercopithecini by an order of magnitude. The implications will be discussed.

Convergent adaptation to climate extremes in bear and human nasal anatomy

TODD R. YOKLEY¹, ALEXA P. KELLY² and SCOTT D. MADDUX²

¹Sociology and Anthropology, Metropolitan State University of Denver, ²Center for Anatomical Sciences, University of North Texas HSC

Humans from cold and/or dry environments generally exhibit taller, narrower, and longer nasal passages than humans from more tropical regions. This pattern of variation is widely argued to evince climatic adaptation, as the cold/dry configuration simultaneously narrows the nasal airways and maximizes total mucosal surface area – features that enhance intranasal heat and moisture exchange. Yet, additional research is necessary to test whether this statistically demonstrable pattern of morphology actually reflects evolutionary adaptation to climate. Comparative anatomy represents one effective approach for assessing such adaptive scenarios, as different species encountering similar environmental pressures often converge on functionally similar anatomy. Accordingly, this study specifically investigates potential convergence in nasal anatomy between humans and bears. Dimensions of the nasal passages, including relative mucosa-to-airway area (P/A) and turbinate size, were collected from twenty-four CT scans

of bear crania from Arctic (polar bear, *Ursus maritimus*), temperate (brown bear, *Ursus arctos*), and tropical (sun bear, *Ursus malayanus*; sloth bear, *Ursus ursinus*) locales. Kruskal-Wallis ANOVA results ($X^2 = 10.617$, $p = 0.004$) indicate that, like humans from cold/dry environments, polar bears (P/A = 0.471) exhibit significantly greater mucosa-to-airway ratios compared to bears from both temperate (P/A = 0.326) and tropical environments (P/A = 0.259). Importantly, this clinal distribution in P/A appears primarily attributable to bears from colder/drier environments exhibiting larger maxilloturbinate ($X^2 = 12.054$, $p = 0.002$), a factor also recently demonstrated to contribute to ecogeographic variation in human nasal morphology. These results bolster assertions that climate has influenced nasal variation in both humans and bears.

Using the species-area equation to understand species diversity within the primate order

COLLEEN B. YOUNG

Anthropology, University of Missouri

While over half of all primates inhabit islands throughout the Pacific Ocean, rarely is an island lens used to understand primate diversity. This study explores the species-area equation (MacArthur and Wilson, 1967) in primates on islands in order to understand if and how primate species number is influenced by landmass area. Inferences from the relationship between primate diversity and landmass area can be applied to hominin diversity in the past.

To examine primate species-area dynamics on islands, data on counts and body mass of primate species was gathered using the IUCN RedList (IUCNredlist.org) database. Island area was found using google maps. Ordinary least-squares regressions were explored in R statistical software to identify if primates follow a species-area pattern. Results indicate that primates do show a positive relationship, and generally greater island area results in greater number of species ($r^2=0.21$), making island area an important predictor for the number of primate species. When average body size of a species is used as a predictor there is an equal but opposite influence on number of species per area ($r^2=0.22$): the larger average mass of a species results in fewer species per area. Thus, for primates, both island area and body size of taxa play important roles in predicting the number of species that should be present for a given area ($r^2=0.48$). Hominin paleontologists should consider ecological models in conjunction with phenotypic data in classifying new (and old) hominin species.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship Program under Grant No. DGE-1443129.

Genetic and Epigenetic Insights into Human Girdle Evolution Using the Mouse Model

MARIEL YOUNG¹, LYENA BIRKENSTOCK¹ and TERENCE D. CAPELLINI^{1,2}

¹Human Evolutionary Biology, Harvard University, ²Broad Institute of MIT and Harvard

The human pelvis and scapula have undergone dramatic morphological shifts during hominin evolution. Many phenotypic differences between human and chimpanzee girdles are present perinatally, indicating that natural selection acted on prenatal developmental processes. As girdle development is poorly characterized, we used the mouse model and performed RNA-sequencing to identify genes differentially expressed (DE) in each girdle and their components (i.e., scapula acromion/blade/head-neck; pelvic ilium/acetabulum/pubis-ischium) and ATAC-sequencing to identify regulatory regions differentially accessible (DA) in these tissues. We integrated both datasets to connect regulatory sequences to likely target genes and identify molecular pathways underlying girdle development. As pathway use is generally conserved across mammals in most examined developmental contexts, such knowledge helps inform human scapula and pelvis biology. Our RNA-seq yielded hundreds of DE genes previously known (e.g., *Tbx5*, scapula; *Tbx4*, pelvis) and unknown (e.g., *Pappa2*, scapula; *Sfrp2*, pelvis) in girdles, or between specific components (e.g., *Emx2* in ilium, not pubis). Our ATAC-seq yielded 37,741 putative regulatory elements, 5,283 unique to scapula, 7,001 unique to pelvis, also with elements unique to specific components (e.g., 2,279 elements in ilium). Our approach revealed important genes and regulatory elements involved in human biology and variation. Notably, *Rxfp1*, which encodes a relaxin hormone receptor, was upregulated in the pubis-ischium relative to other components. Given relaxin's effect on pubic symphysis relaxation during parturition, and the presence of accessible sequences nearby, it is a prime candidate to examine for sequence changes in humans. These and other candidates may yield important sequence changes along the human lineage.

This research has been funded in part by a grant from the National Science Foundation (No. BCS-1518596).

The developmental basis for variation in the human shoulder

NATHAN M. YOUNG¹, NEIL T. ROACH² and TERENCE D. CAPELLINI²

¹Orthopaedic Surgery, University of California San Francisco, ²Human Evolutionary Biology, Harvard University

The modern human shoulder exhibits a combination of traits both unique to our lineage and shared with other apes. Notably, the shape of the scapular blade exhibits similarities to *Pan* and *Gorilla*,

ABSTRACTS

while the scapular spine angle is more lateralized, similar to *Pongo* and some arboreal monkeys. Identifying the polarity of these traits is important for reconstructing both the *Homo-Pan* last common ancestor, and the direction of phenotypic changes associated with our lineage's evolution. An important step in this process is to identify the developmental origins of these traits and how they may or may not change during ontogeny. Previously, we demonstrated that primate scapular shape exhibits conserved ontogenetic changes across lineages from infants to adults, suggesting that species-specific differences must have their origins at prenatal timepoints. To investigate the timing of modern human shape traits, we reconstructed three-dimensional shoulder morphology from serial sections of human embryos from Carnegie Stages 18-23 (N=6) and compared them to the adult living hominoid shape space, including humans. We found that the embryonic scapular blade shape is distinctly human-like from the earliest retrievable periods of morphogenesis, and that the spine exhibits a similar orientation. Given the strong congruity between early and later timepoints, these results demonstrate that the locus of variation and target of selection on human shoulder shape is predominantly events early in embryonic morphogenesis, and that later post-natal changes have a relatively weak effect on adult phenotypic outcomes.

This project was supported by the National Science Foundation (BCS-1518596).

Multivariate Comparison of East and Southeast Asian Cranial Morphology

NANDAR YUKYI¹, ELAINE Y. CHU² and M. KATE SPRADLEY³

¹SNA International, Defense POW/MIA Accounting Agency, ²Department of Anthropology, University of Nevada, Reno, ³Department of Anthropology, Texas State University

When dealing with the ancestry estimation portion of the biological profile, biological anthropologists have traditionally simplified ancestry groups into three main categories: Caucasoid, Negroid, and Mongoloid (Rhine 1990). One of the problems with doing so is the oversimplification of the diversity of population groups. The current research focuses on cranial morphologies of East and Southeast Asian individuals. The primary research question of this research will explore if East and Southeast Asians have statistically significant differences in terms of craniometrics.

The samples used in this research include individuals from Vietnam, Burma, Thailand, Hong Kong, Taiwan (including Atayal), Japan (including Ainu), and the Philippines; all data were obtained from Dr. Michael Pietruszewsky or the Howells craniometric database. Statistical methods utilized include the CANDISC procedure, Mahalanobis squared distance, and linear discriminant function analysis in R Studio. Results indicate that

the differences between craniometrics of East and Southeast Asian individuals are statistically significant. According to the first canonical values, there is a clear distinction between the Philippines, North Japan, and Ainu groups and the rest of the groups. According to the second canonical values, there is a clear distinction between the Southeast Asian groups (Vietnam, Thailand, Burma, and Philippines) and the East Asian groups (Hong Kong, Taiwan, and Japan). Based on these results, it is evident that East and Southeast Asian groups should be considered as distinct groups, rather than being grouped together as "Asian." This research has implications for biological human variation research and forensic biological affinity estimation.

Osteoporotic bone fractures and age-related bone loss in human populations inhabiting the Kujawy region in north-central Poland from the Neolithic to early modern Times

ELZBIETA ZADZINSKA¹, WIESLAW LORKIEWICZ¹, JOANNA MIETLINSKA¹, JUSTYNA KARKUS¹, PAULINA BOROWKA¹, MICHAL STUSS², EWA SEWERYNEK² and DAMIAN PLAZUK³

¹Department of Anthropology, Faculty of Biology and Environmental Protection, University of Lodz, ²Department of Endocrine Disorders and Bone Metabolism, Medical University of Lodz, ³Department of Organic Chemistry, Faculty of Chemistry, University of Lodz

The increase in the incidence of osteoporotic fractures and the decrease in age in which these first occur raise the question about historical changes in the patterns of bone loss with age and their biological and cultural determinants in the past. This study analysed bone mineral density (DEXA) and bone fractures in 529 skeletons (267 males and 262 females) representing prehistoric (Neolithic) and historical (early Middle Ages to early modern times) populations from Kujawy. Regular patterns of age related bone loss in men and women were similar to those observed today. In all age groups, Neolithic men and women showed higher BMD as compared to the historical samples (Neolithic women exhibiting no osteoporotic fractures); on the other hand, the latter revealed similar values to contemporary populations in the middle and old age groups. Thus, a major transition in bone maintenance patterns occurred between the Neolithic and the Early Middle Ages. The archaeological populations exhibited a faster rate of bone loss with age: while their initial BMD levels were higher than those in contemporary populations, BMD for the oldest age groups was similar or lower than today. Pronounced sex differences in BMD were found for young adults, which indicates a greater influence of factors limiting peak bone mass and contributing to bone loss in young women, probably associated with reproductive history. The young men exhibited a higher prevalence of

osteoporotic fractures. The factor determining such sex- and age-specific patterns of osteoporotic-type fractures was the greater susceptibility to injuries of the males.

This research was funded by National Science Centre, Poland, grant no. 2016/23/B/NZ8/03145 (OPUS 12).

Flexor digitorum profundus tendon forces in climbing grips

HANNAH ZAEHRINGER, ELEN M. FEUERRIEGEL and PATRICIA A. KRAMER

Anthropology, University of Washington

Morphological evidence suggests that fossil hominins were powerful climbers, despite their obligate bipedalism. Rock climbing has been overlooked as a behavior that may have contributed to the upper limb diversity seen in the fossil record. If and how rock climbing hand biomechanics differs from that of arboreal modes of climbing is, however, unknown. Accurate representation of musculoskeletal geometry is needed to characterize the function of the hand in climbing behaviors, necessitating the use of computational methods to estimate the tendon forces.

The tendon forces of rock and arboreal climbing grips are examined in the third digit using a 3D finite element (FE) model to estimate flexor digitorum profundus (FDP) tendon force in four grips: two rock climbing grips (crimp, slope) and two arboreal grips (hook, power). Finger joint angles for the FE models were acquired from five experienced rock climbers using kinematic analysis. Unit vertical loads plus a shear load due to friction were applied to the phalanges. The percentage change across grips at the proximal, intermediate, and distal segments of the FDP are calculated.

We found that FDP tendon forces are greater in the crimp grip than all other grip types compared, particularly at the distal element. Rock climbing grips create higher forces than do arboreal grips. The crimp grip exhibited increases of >1500%, >900%, and 500% compared to the slope, hook, and power grips, respectively. This preliminary study underscores the need for more detailed biomechanical models of soft tissue dynamics in climbing grips.

Sacral slope and greater sciatic notch shape variation in the developing human pelvis

SARAH M. ZALESKI

Anthropology, University of Florida

This study tests the hypothesis that the position of the sacrum relates to greater sciatic notch (GSN) shape during development of the human pelvis. I assessed GSN variation in 48 females and 50 males aged 0-20 years using decedent computed tomography data from the Center for Forensic Imaging at the University of New Mexico.

ABSTRACTS

I collected three-dimensional landmark coordinate data in Amira and completed geometric morphometric analyses in R Geomorph and Morpho. Sacral slope (SS) was defined by the angle between the first sacral cranial endplate and a transverse plane. Two-block partial least squares analyses tested the relationship between SS and pelvic centroid size and twelve coordinates aligned by Generalized Procrustes Analysis representing GSN shape. Lack of significant covariation patterns cautions interpretations; however, notable trends are apparent. Greater SS is associated with a more posteriorly displaced GSN apex among 0-1.99 year-olds and, conversely, with a notch more evenly proportioned anteroposteriorly among 7-11.99 year and 12-14.99 year cohorts. At intermediate ages (2-6.99 year-olds), greater SS tracks with more shallow apices. Among 15-20.99 years-olds, greater SS is accompanied by posterior GSN buttressing. In a broader age group (7-20.99 years), females show more evenly proportioned GSNs with greater SS and more posteriorly displaced GSN apices with decreased SS. Males show more posteriorly displaced GSN apices with greater pelvic centroid size. Covariation magnitude does not significantly differ between sexes. Observed trends suggest that variation in SS, which may affect how loads are distributed in developing pelvis, relates to GSN shape variation.

Dry Season Behavioral Ecology of Von der Decken's Sifaka (*P. deckenii*) Inhabiting Limestone Karst Forest at Beanka Reserve, Madagascar

ANDREW J. ZAMORA¹, CHARLES RASOLONDRAVOAVY² and SHANNON NELSON-MANEY¹

¹Anthropology, University of Massachusetts,
²Madagascar Conservation Program, Lemur Conservation Fund

Von der Decken's sifaka (*Propithecus deckenii*), is a poorly-studied, endangered lemur endemic to central- and north-western Madagascar's dry deciduous forests. *P. deckenii* populations are notable for often inhabiting unique ecological conditions within forests growing on and among dramatic limestone karst formations, *tsingy*. Here we present data from a 2.5 month long study of the behavior ecology *P. deckenii* living in continuous and fragmented limestone karst forest at Beanka Reserve, located in the northwestern Melaky region.

We habituated and observed four *P. deckenii* groups ranging in size from three to six individuals. Observations occurred between late August-early November 2015, coinciding with the mid-to-late Beanka dry season. We recorded social behavior, feeding, and activity budget records using both continuous focal and instantaneous group scans. Additionally, we regularly recorded the location of the group being observed using a handheld GPS.

We found that *P. deckenii* groups inhabited home ranges averaging 3.3 ha in size, comparable to other western sifaka species. Similar to *P. verreauxi*, *P. deckenii* groups contain one adult male with a dark "chest badge" and these males are behaviorally dominant over other male group members. Male aggression towards females however was almost completely absent. *P. deckenii* individuals depended heavily on young leaves, making up between 50-80% of observed feeding records. Individuals also spent most of their time either feeding (29-38%) or resting (46.1-53.3%), consistent with a largely folivorous diet and potential strategy to minimize energy expenditure. We discuss these and further findings in light of sifaka ecology and evolution.

This work was funded by Rowe-Wright Primate Fund grant #26 awarded by Primate Conservation Inc.

Morphological signatures of hybridization in North American canids: a new model for detecting hybrids in the human fossil record

NATASA ZDJELAR¹, CHRISTOPHER KENDALL¹, LAVANIA NAGENDRAN¹, REBECCA R. ACKERMANN^{2,3} and LAUREN SCHROEDER^{3,4,5}

¹Department of Anthropology, University of Toronto, ²Department of Archaeology, University of Cape Town, ³Human Evolution Research Institute, University of Cape Town, ⁴Department of Anthropology, University of Toronto Mississauga, ⁵Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo

Although there is a growing consensus that hybridization is important in human evolution, our understanding of its impact on the skeleton remains relatively limited. Recent studies of extant mammalian hybrids (e.g. baboons, mice) have identified skeletal effects of hybridization, including a suite of anomalous dental and sutural traits that are present at high frequencies in hybrid populations. However, more research is required to understand the universality of these traits, and therefore their applicability to the human fossil record. Building on these previous studies, we examined a sample of genetically determined canid hybrids, specifically the eastern coyote ("coywolf"), a hybrid between coyotes, wolves, and dogs, to test whether coywolves exhibit a comparable pattern of anomalous non-metric characters. Cranial and mandibular specimens of *Canis latrans* var. ("coywolves"; n=110), *C. latrans* (western coyotes; n=283), *C. lupus* (western grey wolves; n=181), and *C. familiaris* (dogs; n=91) were scored for anomalous traits including supernumerary and rotated teeth, dental crowding, and sutural anomalies. Chi-square tests were conducted to determine whether the hybrids exhibit higher trait frequencies than parental taxa. The results are largely consistent with other studies, indicating that the incidence of dental anomalies, dental crowding, and sutural

anomalies is significantly higher in hybrids. However, differences are not significant for supernumerary teeth and rotated dentition. When these results are combined with previous studies, they suggest that skeletal signatures of hybridization are common to different mammalian taxa across multiple generations, however, some traits like supernumerary teeth may be lost after a few generations.

We would like to acknowledge the Connaught Fund at the University of Toronto for funding.

The role of the manual and pedal fat pads in moderating ground reaction forces and pressure patterns in knuckle-walking African apes.

ANGEL ZEININGER¹, GABRIEL S. YAPUNCICH¹, DANIEL SCHMITT¹ and ROSHNA E. WUNDERLICH²

¹Evolutionary Anthropology, Duke University, ²Department of Biology, James Madison University

African apes use a knuckle-walking hand posture in which the dorsal side of the middle phalanx contacts the ground and a heel strike foot posture in which the heel makes initial contact with the ground. Because ground reaction forces (GRFs) travel directly through cheiridia, osteological features such as middle phalanx robusticity and the absence of a calcaneal lateral plantar process (LPP) have been used to infer locomotion in fossil species. However, the role that the fat pads underlying these bones serve in moderating GRFs in African apes is unexplored, leaving form/function assumptions incompletely tested. For *Pan* and *Gorilla*, we collected video, pressure, and GRFs during walking, and measured phalangeal and heel pad size on anesthetized animals. Three forelimbs and hindlimbs of each species were placed in a custom-built rig in a neutral position and, for the foot, an inverted position, and loaded according to known peak forces. CT and MR imaging showed bone and pad position and deformation. In the hand, the phalangeal pad width:length ratio was greatest in *Gorilla* (0.43 vs 0.34) and the pad compressed and expanded significantly under load. *Gorilla* landed with a non-inverted foot and had a slightly larger heel width:foot length ratio than *Pan*. The heel pad was present extensively beneath and around the lateral calcaneal tuber despite the lack of an LPP. Cheiridial soft tissue plays an important role in distributing force and reducing pressure and complicates the form/function relationship of hand and foot bones.

Research supported by the National Science Foundation Grant BCS-1517561

ABSTRACTS

Atypical, asymmetrical dental wear on a medieval Transylvanian male

KATIE ZEJDLIK¹, JONATHAN D. BETHARD², ZSOLT NYÁRÁDI³ and ANDRE GONCIAR⁴

¹Anthropology and Sociology, Western Carolina University, ²Anthropology, University of South Florida, ³Archaeology, Haáz Rezső Museum, ⁴Archaeology, ArchaeoTek-Canada LLC

Atypical dental wear, in the form of attrition and erosion, was observed in an adult male from the medieval Papdomb archaeological site in Transylvania, Romania. Maxillary dentition presented severe buccal-to-lingual wear on multiple teeth with pulp cavity exposure. In contrast, mandibular dentition showed minimal-to-moderate wear with observable occlusal morphology, limited dentin exposure, and no instances of pulp cavity exposure. Four peri-apical lesions were also observed in the maxillary dentition; no other signs of pathological modification were present. Additionally, there were no signs of biological or behavioral modifications on the post-cranial remains.

No previously documented cases of this pattern of asymmetrical dental wear could be found in the literature. Analysis of the dentition suggests that a combination of acid erosive- and mastication-related attrition could account for these features. Differential diagnosis of these features indicates erosion of the maxillary dentition is not the result of a physiological conditions such as gastrointestinal reflux or chronic vomiting. Additionally, the singular occurrence of the atypical wear pattern among the 223 observable dentitions suggests an individualized activity possibly related to occupation. Finally, the individual's interment near the pulpit of the church intimates a person of status. Craft guilds were recognized through designated seating in medieval churches and medieval occupations related to the production of candles, soap, and pigments for clothing or painting required the production of lye, which could produce erosive fumes. Although, attribution of the origin of these modifications is difficult, an interpretation of occupational hazard is offered as the most reasonable interpretation.

Osteological characteristics of Chinese foot-binding in archaeological remains

WEN ZENG^{1,2,3}, YONGSHENG ZHAO^{1,2,3}, LIN GUO^{1,2,3}, YUNI XIAO^{1,2,3} and DELIANG HE⁴

¹Institute of Cultural Heritage, Shandong University, ²International Joint Research Laboratory of Environmental and Social Archaeology, Shandong University, ³School of History and Culture, Shandong University, ⁴Shandong Provincial Institute of Cultural Relics and Archaeology, Shandong Provincial Institute of Cultural Relics and Archaeology

Foot-binding was a widespread custom in China for hundreds of years. The severity and type of binding varied considerably over time and space.

To examine the morphological consequences of extremely severe foot-binding, this paper uses 35 sets of bound and 33 sets of unbound foot bones, from the remains of women excavated from the Xinzi cemetery in the northern Shandong. Based on macroscopic observation, CT images, and measurements of bound foot bones multiple distinctive consequences of foot-binding were identified. Compared with normal bones, bound foot bones have severely reduced overall size and weight; the shape, proportions, and position of articular surfaces of tarsal bones were extremely variable and differed greatly from these morphological features of unaffected tarsal bones; the density of trabecular mesh was reduced and its structure was altered in all tarsal bones; degenerative osteoarthropathic changes affected articular surfaces of the foot bones even of young individuals. These changes suggest that the biomechanics of bipedal locomotion was considerably affected in all females with severely bound feet.

The Archaeological and Historical Peaks Project of Shandong University and the National Social Science Foundation of China.

Trepanation or Trauma? Differential diagnosis of cranial perforations of an early Iron Age site in Xinjiang, China

XIAOYA ZHAN¹, AI-JIA MU², LIANG CHEN², QUN ZHANG¹, YONG WU³, WANGLIN HU³ and HUI-YUAN YE¹

¹School of Humanities, Nanyang Technological University, ²School of Cultural Heritage, Northwest University, China, ³Xinjiang Institute of Cultural Relics and Archaeology, China

Cranial perforations have attracted academia to explore the mechanisms. Diseases, trepanation, violent activities, and postmortem damages could all penetrate through the cranial bones, leaving perforations varying in number, size, and shape. Careful considerations should be given when diagnosing the cranial perforations. A human skull with two perforations unearthed from Xiaoshankou Cemetery, Xinjiang, China, dating back to the early Iron Age, is the subject of this particular study. Age and biological sex were estimated based on cranial traits and dental wear, following the standards of Buikstra and Ubelær (1994) and White and Folkens (2005). Other than macroscopic observation, microscopic observation and CT scans were performed for more details. This skull presented male features, and closure of cranial sutures and the severe dental wear suggested he was in his late adulthood. Both perforations, one on the left parietal bone and the other on the left side of the occipital bone, were oval in shape with similar size. A possible fracture line was present around the parietal bone. No sign of healing was present. Moreover, neither pathological lesions nor tool's marks presented. The internal beveling of the parietal perforation and the external beveling of

the occipital perforation matched the features of entry and exit wounds of projectile injuries. Thus, we concluded that the perforations were perimortem trauma caused by sharp-ended objects, possibly arrowheads through one shot. This study provides another case of violence in the early Iron Age of Xinjiang and new perspectives on diagnosing cranial perforations in this region.

This research was supported by both NAP-Grant from Nanyang Technological University, Singapore and National Natural Science Foundation of China (No. 41572161).

A bioarchaeological investigation of an obstetric death in Ancient China: Exploring the death and burial of an adult female with an infant at Huigou site

AI ZHANG¹, YAWEI ZHOU¹, QIAN WU², WANFA GU² and QINGLI WEI²

¹History department, Zhengzhou University, ²Culture relics and archaeology, Zhengzhou institute

This article is the first reported case study of an adult female buried with an infant in the Yellow River Basin in Neolithic China. Bone preservation in the tomb is excellent, allowing a detailed evaluation of the remains. The gestational age of the infant is roughly full-term based on the relevant reference. Observations on the adult female's pelvis and comparisons to modern clinical data suggest that restriction in the bony birth canal caused a difficult delivery, leading to the death of mother and infant during or shortly after birth. A hyperplastic lesion on the pubic symphysis may reflect a prior difficult birth that was survived. We think this case enriches the osteological research on female's reproductive health and is of great significance.

The effect of Procrustes superimposition on the quantification of hominin cranial morphology

CHI ZHANG

Department of Anthropology, University of Pittsburgh

In a geometric morphometric analysis (GMA), when the Procrustes superimposition eliminates the effect of orientation in a group of superimposed landmark configurations, the sole criterion is to rotate them until the sum of squared differences between every pair of corresponding landmarks is minimized. On the other hand, descriptive morphology is based on orienting specimens by the Frankfurt plane.

Therefore, this study assesses whether shape differences captured by GMA can be incompatible with observed morphological differences, due to different ways of aligning specimens. For this purpose, four surface semilandmark sets were collected from 3D models of hominin crania for

ABSTRACTS

analyzing the gross morphology of the overall cranium, posterior cranium, temporal bone, and frontal bone. Principal component analysis (PCA) was performed to simplify the process of visualizing shape differences.

Results indicate that some aspects of shape differences revealed by higher-ranked principal components, such as the degree of frontal rise, the direction that the supraorbital region faces, the trajectory of the squamosal suture, and the inclination of the nuchal plane, cannot be directly associated with observed morphological differences. Evaluating the results of the Procrustes superimposition shows that the superimposed landmark configurations are all rotated to different angles. This inconsistent rotation contributes to the incompatibility between aspects of shape differences captured by PCA and observed morphological features. Thus, when using GMA, especially with the aid of PCA, to analyze the overall cranial morphology of hominins, extra attention should be paid to the effect of the Procrustes superimposition.

Models for Population History of the Tibetan Plateau: Toward an Integration of Archaeology and Genetics

PEIQI ZHANG¹, XINJUN ZHANG², XIAOLING ZHANG^{3,4}, XING GAO^{3,4}, EMILIA HUERTA-SANCHEZ⁵ and NICOLAS ZWYNS¹

¹Department of Anthropology, University of California, Davis, ²Department of Ecology and Evolutionary Biology, University of California, Los Angeles, ³Key Laboratory of Vertebrate Evolution and Human Origins of Chinese Academy of Sciences, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences, ⁴CAS Center for Excellence in Life and Paleoenvironment, ⁵Department of Ecology and Evolutionary Biology, Brown University

With an average altitude above 4,500 meters above the sea level, the Tibetan Plateau is among the most challenging environment for early human settlements. The peopling history of the plateau, including the timing of the first human occupation and the consecutive biological and behavioral adaptations to high-altitude, is still poorly understood. Genetics generated inconsistent dates and sometimes even contradictory. Yet, fossil evidence suggest that Denisovans have visited 'the roof of the World' during the Middle Pleistocene while new archaeological discoveries document Upper Paleolithic occupations of the plateau starting from ca. 40,000 years ago. Here, we formulate two comprehensive models (and their respective predictions) based on a critical review of the existing archaeological and genetic data. The models proposed support either a *discontinuous* occupation that the all previous settlers were replaced by most recent migrants or a *continuous* settlement which started from Pleistocene modern human

arrivals; hence, they have contrasted implications and expectations for human subsistence and adaptive scenarios. Although both models acknowledge that hunter-gatherer groups may have migrated early to the Tibetan Plateau, they also raise questions regarding the contribution of such dispersals to the modern Tibetan gene pool. Furthermore, it suggests that a gene flow event between Denisovans and the ancestral population of Han-Tibetan occurred prior to the definitive human settlement on the Tibetan Plateau. Such an archaic admixture might have changed the genetic structure of *H. sapiens* populations and facilitated high-altitude adaptation.

Baldwin Fellowship of the Leaky Foundation

Bone examples of several cases of human *Treponema* in ancient China

YAWEI ZHOU¹, GUOSHUAI GAO¹, XIANGYU ZHANG², BO GAO² and SHUAI XU³

¹History department, Zhengzhou University, ²Cultural relics and archaeology, Xian institute, ³Henan university, Henan

This paper describes a number of human skeletal remains suspected to be infected by treponema during the ancient Chinese dynasty. Funerary objects and radiocarbon dating analysis of bones show that these specimens can be traced back to the 7th century AD and the 15th century at the latest. We use high precision CT fault scanning surface and super depth of field microscope to observe. According to the Standard of Bone Identification of *Treponema pallidum* diseases, the systemic bone lesions of several individuals were compared. Results We believe that these pathological phenomena are more consistent with the syphilis caused by *Treponema pallidum*. The case is also by far the most typical of ancient suspected *Treponema pallidum* diseases found in China.

Molecular archaeological methods to explore the traces of Akhal-Teke in China

SIQI ZHU

School of Archaeology, Jilin University

In the study, the Next-generation sequencing technology and method were used to analyze the ancient DNA of the horse remains unearthed from the Shihuyao tombs in the Han and Tang Dynasties in Xinjiang (about 2200 to 1100 years ago), and six high-quality mitochondrial genomes were obtained. They were divided into two maternal haplogroups by B and D, and we also found two Tang Dynasty samples with original sites of Akhal-Teke. A joint study with ancient and modern samples from other parts of Eurasia confirmed that these two ancient horses have a direct maternal genetic relationship with the Akhal-Teke, and are the earliest blood relatives of Akhal-Teke that have been discovered. Combined

with the literature and archaeological evidence, we initially analyzed the group history of the Akhal-Teke and revealed the great role played by the ancient Silk Road in their dissemination. These provide us with new insights into the history of the domestication and spread of horses such as Akhal-Teke, the cultural exchanges between the East and the West, and the important position that Xinjiang has in it.

Pan paniscus or Pan troglodytes? The case for a divergent Pan troglodytes

ADRIENNE ZIHLMAN

Anthropology, University of California Santa Cruz

The genus *Pan* separated into two species as recently as one million years ago, subsequent to a shared evolutionary history of 3 to 4 myrs. The question is: which species deviated the most from the parent population? A widely held assumption, that *Pan troglodytes* represents the core population, is based mainly on behavioral (e.g. social, tool-using, hunting) evidence; integration of anatomical evidence particularly from *Pan paniscus* has been neglected.

A counter to the *Pan troglodytes* default position presented here is based on evidence from both skeletal and soft tissue. Data derive from dissections on 18 adult *Pan*, and skeletal data from an additional 20 *paniscus* and 25 *troglodytes* representing two subspecies. Some cranial-facial and dental features distinguish the two species statistically, though body mass and cranial capacities do not. Body composition (e.g. bone, muscle, skin) shows little intraspecific variation among females or among males. Comparison of *paniscus* and *troglodytes* females matched for age and body mass illustrate that the few statistically significant dimensions reflect differences in trunk and limb proportions. Females compared to their species males, in *paniscus* show no statistical differences in skeletal dimensions, whereas male *troglodytes* depart from females.

Results of these four-way anatomical comparisons show *troglodytes* males as the outliers, supporting the hypothesis that *troglodytes* and not *paniscus* is the divergent species. Extending these comparisons to *Gorilla* and australopiths gives a clearer picture of evolutionary history and possible selective pressures that account for divergent *troglodytes* anatomy and behavior.

New insights into health, diet and disease in the Tyrolean Iceman

ALBERT R. ZINK and FRANK MAIXNER

Institute for Mummy Studies, Eurac Research

The Tyrolean Iceman, commonly known as ötzi, is the world's oldest glacier mummy and one of the best investigated ancient human remains in the world. Since the discovery of the 5,300-year-old Copper Age individual in 1991, in the Eastern

ABSTRACTS

Italian Alps, a variety of morphological, biochemical, and molecular analyses have been performed that revealed important insights into his origin, his life habits, and the circumstances surrounding his demise.

In more recent studies, the mummy was subjected to cutting-edge modern research methodologies currently focusing on highthroughput sequence analysis of ancient biomolecules (DNA, proteins, lipids). Thereby, genetic evidence for a virulent *Helicobacter pylori* strain was detected in his stomach and a comparative whole-genome analyses of the 5,300-year-old bacterium revealed new and important insights into the evolution of this pathogen.

Moreover, by using a combined multi-"omics" approach, we obtained a molecular fingerprint of the Iceman's diet preceding his death. The analysis revealed a remarkably high proportion of fat in his diet, supplemented with dried wild meat, cereals and with traces of toxic bracken. The detection of the Iceman's stomach content further provided the unique opportunity to gain first insights into the intestinal flora of a Copper Age individual. Initial results seem to confirm a loss of diversity in modern populations with a westernized lifestyle. Here, we present the findings of our current studies on the Iceman and discuss its implications for the understanding of living conditions, health and disease in ancient societies.

Investigating cell-type specific shifts in metabolic gene expression between human and chimpanzees

TRISHA M. ZINTEL^{1,2}, JASON PIZZOLLO^{1,2} and COURTNEY C. BABBITT¹

¹Biology, UMass Amherst, ²Molecular and Cellular Biology Graduate Program, UMass Amherst

The human brain is more energetically costly than that of other primates, utilizing ~ 20% of all of the body's metabolic resources, while chimpanzee brains use less than 10%. Previous work on whole brain tissue have consistently determined significant differences in metabolism between species. A cell-type specific comparison is necessary to understand distinct cellular contributions to interspecific differences in neurological function. Here, we conducted a cell-type specific investigation of neural differences between humans and chimpanzee by conducting RNA-Seq on neural progenitor cells (NPCs), neurons, and astrocytes generated from induced pluripotent stem cells (iPSCs) from both species. Differential expression (DE) analyses demonstrate that the greatest proportion of genes exhibiting DE are between species' astrocytes (12.2% of all expressed genes), followed by NPCs (8.57%), and neurons (5.8%). Categorical enrichment analyses of genes exhibiting DE show that all three neural cell types display interspecies gene expression enriched for metabolic processes, driven primarily by higher

expression of metabolic genes in human cells. Gene set enrichment analyses reveal that human neurons and astrocytes are enriched for greater glucose transport while chimpanzee neurons and astrocytes exhibit greater lactate transmembrane transport. We also determined cell-type by species differences in gene expression for nuclear- and mitochondrially-encoded subunits of the protein complexes important for oxidative phosphorylation. This work circumvents the technical and ethical hurdles of investigating rare cell types in primates to provide exciting insight into the cell type specific metabolic changes that were necessary to support evolution of the human brain.

Funding Citation: National Science Foundation

Strontium isoscapes and hard tissue provenience in southern Africa to reconstruct hunter-gatherer social and exchange networks

ANDREW M. ZIPKIN¹, ERICH C. FISHER², HAYLEY C. CAWTHRA³, GWYNETH GORDON⁴, MARTIN HIPONDOKA⁵, PETRUS LE ROUX⁶, CURTIS W. MAREAN^{1,7}, KELLY J. KNUDSON^{1,8} and POLLY WIESSNER¹

¹School of Human Evolution and Social Change, Arizona State University, ²Institute of Human Origins, Arizona State University, ³Geophysics and Remote Sensing Unit, Council for Geoscience, ⁴School of Earth and Space Exploration, Arizona State University, ⁵Department of Geography, History and Environmental Studies, University of Namibia, ⁶Department of Geological Sciences, University of Cape Town, ⁷African Centre for Coastal Palaeoscience, Nelson Mandela University, ⁸Center for Bioarchaeological Research, Arizona State University

The radiogenic strontium isotope ratio $87\text{Sr}/86\text{Sr}$ has been used in physical anthropology and archaeology for studying mobility and migration, resource exploitation and landscape use, and more recently, social and exchange networks. Increasingly, researchers construct spatially explicit, landscape-scale models of $87\text{Sr}/86\text{Sr}$ variation (i.e., isoscapes) to identify the region of origin for human and faunal remains. We report on a multi-year project to build strontium isoscapes from the South African southern coast northward to the Great Karoo and in the Namibian Kalahari Desert, and to reconstruct hunter-gatherer social networks using provenience of ostrich eggshell beads.

We refined an existing isoscape in the south coast of South Africa and extended it to include an additional ~40,000 sq km. The new isoscape used elevation and geological group as predictive variables for Empirical Bayesian Kriging interpolation of plant $87\text{Sr}/86\text{Sr}$ results. The isoscape exhibits an $87\text{Sr}/86\text{Sr}$ range of 0.7092-0.7236 and absolute mean prediction error of 0.0011, with

the most radiogenic predicted values found in the Swartberg Mountains. North of the Swartberg, predicted isotope ratios exhibit partial equifinality with the study area south of the mountains.

The Kalahari study area facilitates validation of our provenience methods with multiple proxies for bioavailable $87\text{Sr}/86\text{Sr}$. Modern hunter-gatherer ostrich eggshell beads show an $87\text{Sr}/86\text{Sr}$ range of 0.7168-0.7336, comparable to porcupine enamel in the region. We also incorporate paired plant and soil sample analysis to test the limits of a single proxy approach to bioavailable Sr isoscape construction. These isoscapes are applicable to anthropological, forensic, and environmental science studies in the region.

Isoscape survey in Namibia and geochemical analyses at Arizona State University were supported by Wenner-Gren Foundation grant # 9801 (Zipkin).

Developmental Plasticity and Life Course Among Unidentified Migrants and Modern Americans: Implications of Childhood Stress on Predispositions to Vertebral Pathology

CAROLINE L. ZNACHKO¹, MICHELLE D. HAMILTON² and JAMES T. WATSON³

¹Anthropology, University of Tennessee Knoxville, ²Anthropology, Texas State University, ³Arizona State Museum, University of Arizona

Stress episodes experienced during early life development have the potential to increase adulthood morbidity. Developmental plasticity of vertebral neural canal (VNC) anteroposterior (AP) and transverse (TR) diameters can serve as indicators of stress experienced in early childhood and adolescent periods respectively. Schmorl's nodes (SNs), which have historically been assumed to be indicative of injury associated with manual labor, have more recently been shown to correlate with vertebral morphology and wear and tear stress. The purpose of this research was to elucidate the relationship between embodiments of developmental stress and predispositions to adult morbidity in the vertebrae. VNC AP and TR diameters and SNs among unidentified presumed migrant forensic cases in Arizona ($n = 32$) and Texas ($n = 104$) were assessed along with modern Americans from a documented collection ($n = 76$). ANOVA results show VNC AP and TR diameters were significantly different between samples ($p = 2.1\text{E-}13$; $p = 4.85\text{E-}14$), with modern Americans exhibiting larger VNCs throughout the spinal column. The presence of SNs was significantly correlated to larger AP and TR diameters in the thoracic but smaller AP and TR diameters in the lumbar vertebrae (p -values dependent on the individual vertebrae). Results indicate that the spinal column can be utilized to understand embodiments of stress under a life course perspective

ABSTRACTS

and that differences in the biosocial environment during early life development carry lifelong implications for vertebral morphology and individual morbidity.

This research was funded by the Grady Early Endowment Fellowship and the Graduate College Research Support Fellowship at Texas State University.

Incorporating community feedback and ethical concepts of personhood into bioarchaeological practice: Informing excavation, curation, and analysis at the cemetery of the Mississippi State Asylum with contextualized feedback from the community of practice

MOLLY K. ZUCKERMAN, ANNA J. OSTERHOLTZ
and L. KATE MCCLELLAN

**Department of Anthropology and Middle Eastern
Cultures, Mississippi State University**

Excavations (2012-2013) at the cemetery of the Mississippi State Asylum (MSA), Jackson, MS (AD 1855-1935) uncovered the remains of sixty-eight individuals who died while patients at the Asylum. Associated publicity has elicited numerous contacts from members of the MSA's community of practice (CoP)(patient and staff descendants, members of neighboring communities). These, and the circumstances that the cemetery is both a potter's field and a primarily African American cemetery, create an opportunity for open consideration of the ethical issues surrounding both the excavation of cemeteries for economically and politically marginalized communities with active CoPs, and the memorialization of institutionalized patients. Many CoP members have provided informal feedback (e.g., via public outreach, e-mail). Some are primarily focused on details related to their relative's admission/ discharge, while others have emphasized the importance of aDNA-based positive identification of the remains, memorialization of the patients, and a relational concept of personhood for the remains, associating them with the identity of the MSA patients and family histories. Additional, anticipated formal CoP feedback (e.g., snowball sampling, online surveys, focus group interviewing) will survey culturally appropriate memorialization, family histories of staff and patient experience and burial, exhumation, storage, analysis, and topics of interest about the MSA. This feedback will guide excavation, curation, and analytical protocols and procedures (e.g., destructive analysis). It will also be used to develop bioarchaeological research questions on the MSA that are attuned to ethical issues surrounding the Asylum, and similar cemeteries, and enable community-engaged scholarship on both the current and anticipated, larger MSA assemblage.

ABSTRACTS

and that differences in the biosocial environment during early life development carry lifelong implications for vertebral morphology and individual morbidity.

This research was funded by the Grady Early Endowment Fellowship and the Graduate College Research Support Fellowship at Texas State University.

Incorporating community feedback and ethical concepts of personhood into bioarchaeological practice: Informing excavation, curation, and analysis at the cemetery of the Mississippi State Asylum with contextualized feedback from the community of practice

MOLLY K. ZUCKERMAN, ANNA J. OSTERHOLTZ
and L. KATE MCCLELLAN

**Department of Anthropology and Middle Eastern
Cultures, Mississippi State University**

Excavations (2012-2013) at the cemetery of the Mississippi State Asylum (MSA), Jackson, MS (AD 1855-1935) uncovered the remains of sixty-eight individuals who died while patients at the Asylum. Associated publicity has elicited numerous contacts from members of the MSA's community of practice (CoP)(patient and staff descendants, members of neighboring communities). These, and the circumstances that the cemetery is both a potter's field and a primarily African American cemetery, create an opportunity for open consideration of the ethical issues surrounding both the excavation of cemeteries for economically and politically marginalized communities with active CoPs, and the memorialization of institutionalized patients. Many CoP members have provided informal feedback (e.g., via public outreach, e-mail). Some are primarily focused on details related to their relative's admission/ discharge, while others have emphasized the importance of aDNA-based positive identification of the remains, memorialization of the patients, and a relational concept of personhood for the remains, associating them with the identity of the MSA patients and family histories. Additional, anticipated formal CoP feedback (e.g., snowball sampling, online surveys, focus group interviewing) will survey culturally appropriate memorialization, family histories of staff and patient experience and burial, exhumation, storage, analysis, and topics of interest about the MSA. This feedback will guide excavation, curation, and analytical protocols and procedures (e.g., destructive analysis). It will also be used to develop bioarchaeological research questions on the MSA that are attuned to ethical issues surrounding the Asylum, and similar cemeteries, and enable community-engaged scholarship on both the current and anticipated, larger MSA assemblage.

