

PROGRAM OF THE  
**90<sup>TH</sup> ANNUAL MEETING OF THE  
AMERICAN ASSOCIATION OF PHYSICAL  
ANTHROPOLOGISTS**  
APRIL 7 – 28, 2021

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To be held

**ONLINE**

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# MESSAGE FROM THE VP & PROGRAM CHAIR

## **2021 Abstract Issue**

This volume consists of accepted abstracts submitted for presentation at the 90th Annual Meeting of the American Association of Physical Anthropologists held entirely online due to the COVID-19 pandemic. A total of 458 abstracts were submitted by the October 15, 2020 deadline. Each abstract was subjected to peer-review by two members of the program committee, with reviews completed by December 1, 2021. The committee recommended rejection for less than 1% of the abstracts. Authors of accepted abstracts were notified on January 2, 2021. Two abstracts had been withdrawn by January 27, 2021

The 2020 AAPA abstract issue includes 455 peer-reviewed scientific papers, which will be presented in either video or poster format at the annual meeting. 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 by our partner organizations in some form or another, the Paleopathology Association (PPA), the Human Biology Association (HBA), the American Association for Anthropological Genetics (AAAG), and the Dental Anthropology Association (DAA). Abstracts are presented alphabetically by the last name of the first author.

The abstracts illustrate the remarkable breadth of our discipline, covering a range of research topics and approaches, and with global reach and incredible time depth. A total of 8 invited symposia included 82 abstracts. Contributed abstract submissions totaled 373. Broken down by subfield, these include Bioarchaeology (~23.6%), Primatology (~20.6%), Paleoanthropology (~12.9%), Human Biology (~13.9%), Functional Anatomy and Tissue Biology (~10.5%), Genetics and Genomics (~9.9%), Forensics (~7%), and Education in Biological Anthropology (~2.4%).

## **Acknowledgements and Appreciation**

My sincere thanks to everyone who helped organize the 2021 meetings. We are immensely grateful to the 44 talented, generous, and dedicated members of our Program Committee, who conducted and completed reviews thoughtfully, thoroughly, and expeditiously. We also thank the 23 members of the Program Committee who additionally took on the task of organizing the contributed session in lieu of the advance team who handled this task in prior years.

The 2021 annual meeting is unlike no other in AAPA's history. Many people stepped up to create an entirely new format and keep our scientific community together in the midst of the global pandemic. Thanks are due to our extraordinary business partners, Lori Strong and her team (from Burk & Associates), as well as Ed Hagen (our webmaster and app developer). Our program assistant, Catherine Taylor, has been invaluable, as have the Officers and other members of the Executive Committee. A very special thanks goes to AAPA President Anne Grauer and AAPA President Elect Steve Leigh for their leadership in envisioning and supporting this new meeting format in an incredibly challenging year.

Leslea J. Hlusko  
AAPA Vice President and Program Chair



# ABSTRACTS

## How High School Biology Teachers Can Engage Students Through Online Learning Using Human Evolution

JOEL D. ABDELLA<sup>1</sup> and KATRINA E. YEZZI-WOODLEY<sup>2</sup>

<sup>1</sup>Science, Gordon Parks High School, <sup>2</sup>Department of Anthropology, University of Minnesota, Twin Cities

Area Learning Centers, such as Gordon Parks High School, serve students who are at risk of not meeting high school graduation requirements and are dealing with systemic stressors such as institutional racism and limited socioeconomic standing. Distance learning as a result of Covid-19 exacerbates the struggles these students wrestle with daily. Interactive, tactile learning activities are essential for these young scholars and distance learning is not conducive to this approach. Given this context, why should students care about human evolution? And, how can we use human evolution to build students' personal investment in their education? We address these questions through a three phase process. During the first phase we interview students to assess their current understanding of human evolution and their desire to explore the topic further. During phase two, students work with 3D models to build phylogenies based on observed cranial features of fossil hominins. During the third phase we revisit the interview questions. We evaluate changes in the level of interest and understanding by comparing the answers from both interviews. We quantify investment by calculating attendance rates, assignment submission rates, and online engagement. We compare these data from the unit on human evolution to previous educational units taught during this academic year. We gauge the effectiveness of our approach and reflect on the factors that affected the results. This project is synthetic in nature and these data are designed to initiate conversations and a deeper exploration of ways in which educators can reach all young scholars.

*Science and Social Studies Adventures has provided funding for us to attend this conference. This is a volunteer driven project.*

## The Role of Genetic Variants in the Evolutionary Origins of Human Socio-Communicative Behavior

AZEEZA V. ABDULRAUF<sup>1,2</sup>, MARTIN HUDSON<sup>1</sup>, SUSAN SMITH<sup>1</sup> and JARED P. TAGLIALATELA<sup>2,3</sup>

<sup>1</sup>Molecular and Cellular Biology, Kennesaw State University, <sup>2</sup>Ecology, Evolutionary, and Organismal Biology, Kennesaw State University, <sup>3</sup>Research, Ape Cognition and Conservation Initiative

Single nucleotide polymorphisms (SNPs) have been associated with individual variability in socio-communicative behavior in humans. Specifically, SNPs in three genes - OXTR, AVPR1A, and FOXP2 - are associated with recognizing and regulating emotion, understanding the emotions

of others, and communications skills. Surprisingly, putative associations in the species most closest related to us, bonobos, chimpanzees, and gorillas have received relatively little scientific attention. All three genes of interest, OXTR, AVPR1A, and FOXP2, are present in the three species of African apes, and contain at least two SNPs in each species. One of the aims of this study was to determine if reference and alternate alleles are shared among the three species and humans. To accomplish this, we used the University of California Santa Cruz Genome Browser to locate each SNP, and the reference and alternate alleles were documented. Initial results have revealed that humans, for at least some loci, do share the same reference allele as bonobos, chimpanzees, and gorillas; however, there are locations where humans differ from the great apes. The reference allele for great apes at these locations are the same as the alternate allele found in humans suggesting that the alternate allele could be an ancestral allele. These data are considered in relation to species-specific differences in mating systems and socio-communicative behavior among the three species. These data provide insight into how SNPs can affect differences in socio-communicative behavior at both the individual and species levels.

## Sexual behaviors and reproductive endocrinology of subadult female woolly monkeys before emigrating from their natal groups

LAURA A. ABONDANO<sup>1</sup>, TONI E. ZIEGLER<sup>2</sup>, KELSEY M. ELLIS<sup>1,3</sup> and ANTHONY DI FIORE<sup>1,4</sup>

<sup>1</sup>Department of Anthropology, University of Texas at Austin, <sup>2</sup>Wisconsin National Primate Research Center, University of Wisconsin-Madison, <sup>3</sup>Department of Anthropology, Miami University, <sup>4</sup>College of Biological and Environmental Sciences, Universidad San Francisco de Quito

Sex-biased dispersal is one mechanism that may help animals avoid inbreeding with kin. In many species, reproductive maturity does not occur until after females have dispersed into new groups, where they can mate with unrelated males. In this study we investigated the relationship between sexual behaviors and endocrine patterns of subadult female woolly monkeys, a species characterized by female-biased dispersal. We recorded sexual behaviors of two subadult female woolly monkeys (*Lagothrix lagotricha poeppigii*) for approximately 2-4 months prior to their dispersal from their natal groups and used fecal extracts to quantify concentrations of the ovarian hormone metabolites (pregnanediol-3-glucuronide [PdG] and estrone-3-glucuronide [E1G]) to assess their reproductive status. Both subadult females showed significant increases in ovarian hormone levels between 4 and 9 days before they disappeared from their natal groups, but only one of them displayed sexual behaviors

around the time when both PdG and E1G concentrations were elevated. These increases in ovarian hormone levels prior to emigration may be indicative of the onset of puberty. Although sample size is limited, these results differ from those reported for other atelin primates (i.e., muriquis [genus *Brachyteles*] and spider monkeys [genus *Ateles*]), where adolescent females tend to disperse before they begin to display sexual behaviors or show evidence of ovarian cycling. We suggest that a high degree of home range overlap and frequent encounters between animals from neighboring groups may expose pre-dispersal subadult female woolly monkeys to chemical signals from novel extra-group males, which may induce the onset of puberty before females emigrate.

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

## Re-examining population differences in permanent tooth eruption

ARIELA MARIE A. ADAME, LAURA E. CIRILLO and KYRA E. STULL

Anthropology, University of Nevada, Reno

Dental eruption is known to be more variable than dental development because it is commonly considered more impacted by the environment. An individual's ancestry, socioeconomic status, and sex have all been proposed as factors that may contribute to difference in eruption timing and pattern. To explore these potential differences further, data from the left side of the permanent dentition was compared from contemporary individuals from four diverse geographic locations: Brazil, France, Netherlands, and the United States. Dental eruption was scored using Bengston's (1935) descriptive stages from radiographs and computed tomography scans of individuals between the ages of 8 and 15 years old for a total sample size of 387 individuals. Kruskal-Wallis comparison revealed temporary, statistically significant differences in three mandibular and four maxillary teeth. However, when a Dunn's test was applied and p-values were adjusted with the Benjamini-Hochberg method, there was no consistent trend in which country, tooth, or age was significantly different. Rather, the most distinct difference was only temporarily seen in the mandibular second molar of the United States population at ages 8 and 9. This project proposes that despite some statistical significance, there is no meaningful, interpretable difference in dental eruption between these populations and explores the assumptions of within and between group difference in bioanthropological research based on geographic location and socioeconomic status.

## ABSTRACTS

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

MAYOWA T. ADEGBOYEGA<sup>1</sup>, SARA JHANJAR<sup>1</sup> and TIMOTHY D. WEAVER<sup>1,2</sup>

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

The pubic symphysis is a secondary cartilaginous joint – a fibrocartilage and hyaline joint – that connects the left and right pubic bones to complete the anterior margin of the pelvic aperture. It is 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 inter-pubic 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 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).

We investigated the morphology of the inter-pubic space between the two pubic bones in adult modern humans from 105 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, and BMI, and to use that information to improve on the accuracy of fossil pelvic reconstructions. Our results have revealed a negative covariance between age and symphyseal thickness but no significant relationship between symphyseal thickness and BMI. Sexual dimorphism was a major driver of variation in our dataset, but its influence is diminished in the older age categories.

### Aunties over Grandmas? Maternal and Paternal aunts provide the majority of extra-household childcare among Tsimane forager-farmers

SARAH ALAMI<sup>1</sup>, EDMOND SEABRIGHT<sup>2</sup>, THOMAS S. KRAFT<sup>1</sup>, HILLARD KAPLAN<sup>3</sup> and MICHAEL GURVEN<sup>1</sup>

<sup>1</sup>Anthropology, University of California, Santa Barbara, <sup>2</sup>Anthropology, University of New Mexico, <sup>3</sup>Economic Science Institute, Chapman University

Consanguineal relatives are important providers of support in many species. A distinguishing feature of human kinship systems is the recognition and maintenance of cooperative relationships with affinal relatives. This cultural aspect of kinship provides opportunities for women to expand their social support networks, and is particularly important for understanding patterns of post-marital

residence. Here, we explore observed allocare of children under the age of ten among ambilocal Tsimane forager-farmers. We find that 32% of recorded active childcare was undertaken by people other than the parents. The majority of allocare is provided by older sisters (38%), followed by maternal aunts (11%) and paternal aunts (9%). Matrilocal residence increases the odds of a child receiving allocare relative to patrilocality (OR=1.5). However, this result is largely driven by a higher number of female kin in matrilocal families, suggesting women with fewer sisters than their husbands may benefit from living closer to affinal kin. We discuss the role that women's social support networks may have played in the evolution of marriage systems.

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### Physical Activity and Bone Remodeling: Agriculture in early Colonial San Gregorio Atlapulco

EDGAR ALARCÓN TINAJERO<sup>1,2</sup> and JORGE A. GÓMEZ-VALDÉS<sup>3</sup>

<sup>1</sup>Department of Anthropology, University of Georgia, <sup>2</sup>Center for Applied Isotope Studies, University of Georgia, <sup>3</sup>Laboratorio de Bioarqueología, Posgrado en Antropología Física, Escuela Nacional de Antropología e Historia, INAH

Sixteenth century European colonization in North America brought about challenges for indigenous communities via epidemic disease, demographic decline, interpersonal violence, and environmental disruption. In the densely populated Valley of Mexico, indigenous communities reassessed agricultural strategies in the decades after sustained European contact and settlement. San Gregorio Atlapulco, one of many agricultural towns, coalesced from smaller hamlets and maintained traditional wetland agriculture – the chinampa system. This research uses cross-sectional properties from bone of adult individuals (ages 19-57, n=44) as indicators of individual physical activity and community subsistence practice. Repetitive and intense physical activity strains bone in patterned ways influencing cellular resorption and redeposition. Over time, bone remodeling produces cross-sectional properties in diaphyses that vary according to activity patterns. Ten cross-sectional properties from five humerus and femur diaphyses are calculated from periosteal measurements to evaluate the effects of repetitive activity that included agriculture, hunting, fishing, and food preparation. Linear discriminant analysis of calculated properties separates San Gregorio individuals from more than 600 individuals of twenty-two comparative European communities. Cross-sectional ratios of the distal humeri are most significantly different between San Gregorio and all European populations

sampled (means 1.0 and 1.12 respectively,  $p < 0.001$ ). Based on this analysis, it is inferred that San Gregorio farmers experienced mechanical strain different from most Europeans studied due to use of traditional hand tools and wetland agriculture rather than plows and draft animals. This study highlights persistence in farming methods during a turbulent time for native communities in North America.

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### Sexual dimorphism in metatarsal robusticity in a modern donated skeletal collection

MALORIE E. ALBEE

Department of Anthropology, The Ohio State University

Although previous studies have established that metatarsal robusticity is sexually dimorphic, the explanations for this dimorphism have largely only considered genetic and biodemographic causes. However, men and women also experience cultural differences that might affect metatarsal morphology, including sex-linked disparities in workforce and social participation that have changed considerably over the last 100 years. This study documents temporal differences in sexual dimorphism by comparing metatarsal robusticity between sexes via two-sample t-test for 71 adults (28 born pre-1950, 43 born post-1950) from the William M. Bass Donated Skeletal Collection. Robusticity was measured as a ratio between the diaphyseal diameters and bone length, and the effects of age, body mass, and occupation on robusticity were accounted for via ANCOVA. To test the hypothesis that metatarsal robusticity is more sexually dimorphic in individuals born before 1950, the sample was divided by period and the previous analyses were repeated for each period. The entire-sample results indicate that even when covariates are included, metatarsal robusticity is statistically different between sexes for the first ( $p=0.0021$ ) and third ( $p=0.0119$ ) metatarsals. In the pre-1950 sample, only first metatarsal robusticity is statistically significant between sexes ( $p=0.0236$ ), and this difference remains significant ( $p=0.0179$ ) when accounting for covariates. In the post-1950 sample, there are no significant relationships between metatarsal robusticity and sex. These findings indicate that the sexual dimorphism of the metatarsals, particularly the first metatarsal, may reflect sex-specific cultural influences previously unexplored in the modern human foot, perhaps related to period trends in footwear and activity patterns outside of occupation.

## ABSTRACTS

### Finding the Blood Tax: Using multi-tooth strontium isotope analysis for evidence of the Ottoman child tribute system in Europe

KATHRYN GROW ALLEN<sup>1</sup> and ERIN BLINCOE<sup>2</sup>

<sup>1</sup>Anthropology, SUNY Potsdam, <sup>2</sup>Anthropology/Sociology, Eastern Oregon University

The Ottoman Empire, one of history's most influential Islamic states, expanded into Southeast Europe during the Early Modern period. Evidence indicates both migrations of non-European Muslims and the conversion of Europeans to Islam contributed to the biological makeup of these communities. Notably, a system called *Devşirme* resulted in significant conversions. As a blood tax system, *Devşirme* took the oldest male child from European families. These children were converted and trained, permanently in service to the Sultan. Our study explores the identification of tribute children from an Ottoman cemetery in Romania using strontium isotope analysis.

Using enamel samples from the former military garrison of Timișoara, we explore the possibility that tribute children can be identified using variable timing of enamel development corresponding to historically-documented tribute events. According to written accounts, tribute boys were taken between the ages of 8-10y and sent to Istanbul for conversion and training. They were then stationed around the Empire. The formation of permanent dental enamel typically concludes between 8-10y. The exception are third molars, with enamel development starting at 7-8y, but continuing into teen years. Consequently, dental enamel in most tribute children would have developed before removal from their homes, except the third molar, whose strontium signature may highlight a relocation. The third molars of five Ottoman males were compared to earlier molars. Of the five males, two displayed results indicative of a relocation consistent with *Devşirme*. This study displays the potential for multi-tooth strontium analysis in highlighting cultural practices involving adolescent relocation.

*This material is based upon work supported by the National Science Foundation under Grant No. 1642007 and an Eastern Oregon University Foundation Grant.*

### A candidate mechanism for hominin brain expansion: NF1, DHEA/S, and the ERK/MAPK cell signal cascade

ANDREA J. ALVESHIRE<sup>1</sup> and VINCENT M. RICCARDI<sup>2</sup>

<sup>1</sup>Sociology and Anthropology, Western Illinois University, <sup>2</sup>Director, The Neurofibromatosis Institute

Previous hypotheses have linked reduced levels of apoptosis, required for hominin brain expansion, with increased cancer risk; however, the biological pathways that may have facilitated this developmental shift remain unclear. Recently, a primate-specific cellular "kill switch," catalyzed

upon inactivation of the "genome guardian" *TP53* in the presence of adequate DHEA/S, has been proposed. Derived high DHEAS levels in anthropoid primates are substantially higher in humans. Increasing DHEAS has been linked to prefrontal brain development and found to correlate with longevity. The uniquely-human, autosomal dominant genetic disorder, NF1, is catalyzed by a germline/embryonic mutation in the *NF1* gene, and is characterized by benign tumors of the nerve sheath (neurofibromas) associated with secondary, somatic mutations in the wild-type allele, with progression inversely correlating to the lifetime DHEA curve. NF1 is associated with a constellation of additional physical, cognitive, and behavioral traits that have also been used to distinguish humans and other hominins from one another and from chimpanzees. The *NF1* gene product, neurofibromin, down-regulates Ras, which activates the cellular proliferation/differentiation ERK/MAPK signal transduction cascade. *TP53* mutations are common in malignancies, but rare in benign neurofibromas.

We have identified a fixed, derived, human neurofibromin variant predicted to elicit a modest increase in overall phosphorylation potential and to slightly up-regulate Ras activation of the ERK/MAPK pathway. Evidence from humans and other primates suggests that the "kill switch," combined with uniquely-high human DHEA/S levels and two wild-type human *NF1* alleles, may provide the enhanced "genome guarding" necessary for maintenance of this human-optimized cellular proliferation/differentiation pathway.

### Early life adversity predicts DNA methylation levels in wild adult baboons

JORDAN ANDERSON<sup>1</sup>, AMANDA LEA<sup>2,3</sup>, MERCY AKINYI<sup>4</sup>, TAWNI VOYLES<sup>5</sup>, SUSAN ALBERTS<sup>1,4,5</sup>, ELIZABETH ARCHIE<sup>6</sup> and JENNY TUNG<sup>1,4,5,7</sup>

<sup>1</sup>Evolutionary Anthropology, Duke University,

<sup>2</sup>Lewis-Sigler Institute for Integrative Genomics, Carl Icahn Laboratory, Princeton University,

<sup>3</sup>Ecology and Evolution, Princeton University,

<sup>4</sup>Institute of Primate Research, National Museums of Kenya, <sup>5</sup>Biology, Duke University, <sup>6</sup>Biological Sciences, University of Notre Dame, <sup>7</sup>Duke Population Research Institute, Duke University

The early life environment strongly predicts fitness outcomes in many primate species. Despite its importance, we know little about the molecular mechanisms that link early life experiences to later life traits. To address this gap, we investigated the relationship between early life experience and DNA methylation in a population of wild baboons in Kenya. We analyzed data on whole blood DNA methylation levels from 312 samples (271 unique individuals at 246,048 CpG sites). We show that established sources of early adversity in this population (drought, high density, low social status, social isolation, maternal loss, competing younger sibling) are also associated

with DNA methylation in adulthood (30,544 early adversity-associated CpG sites, 10% false discovery rate). However, these effects were specific to or magnified in individuals born in low quality, low resource habitats, such that over half of these sites (n=15,401) exhibit early adversity-early life habitat interactions. The strongest effects of early adversity were associated with early life drought or high group density, both of which can exacerbate resource limitation. Early adversity-associated sites were enriched in DNA sequence with likely functional consequences, including gene bodies (Fisher's Exact Test p-value=8.11 x 10<sup>22</sup>, odds ratio=1.13) and metabolism-related pathways. Together, our results support the hypothesis that early life adversity shapes fitness outcomes through changes in DNA methylation, either because they are stable over the life course or because they are indicators of early life-associated physical condition. They thus highlight specific molecular mechanisms and genomic loci likely to respond to environmental selection pressures during early life.

### Functional Morphology of the Large-Bodied Colobines from the Turkana Basin during the Plio-Pleistocene

MONYA ANDERSON

Anthropology, Texas A&M University

There are at least 4 recognized large-bodied colobines present in the Turkana Basin during the Plio-Pleistocene: *Cercopithecooides williamsi*, *Cercopithecooides kimeui*, *Paracolobus mutiwa*, and *Rhinocolobus turkanensis*. With the exception of *R. turkanensis*, all forms display postcranial morphology consistent with some degree of terrestriality. Many of these fossil forms are known from sites containing hominin fossils as well as a diversity of mammalian fauna including other large-bodied monkeys like *Theropithecus*. The presence of colobinans in fossil assemblages has been oft-cited as evidence for the presence of forested environments which has influenced models of human evolution such as bipedalism in early hominins like *Ardipithecus ramidus*.

Here I present the results of analyses of the functional morphology of these large-bodied colobines along with a description of an unpublished partial skeleton from the Omo Valley, Ethiopia. Qualitative methods include descriptions of preservation and functionally relevant skeletal features of the fossil colobines relative to extant and other fossil comparators. Quantitative methods include 126 linear metrics, 54 functionally relevant indices, and body mass estimates. The comparative cercopithecoid sample includes postcranial elements from 607 specimens: 309 extant colobines, 180 extant cercopithecines, 97 fossil cercopithecines, and 21 fossil colobines.

# ABSTRACTS

The fossil colobines are morphologically distinct from the terrestrial cercopithecines and from each other in their functional morphology suggesting a range of variation in locomotor mode not present in extant African cercopithecids. The presence of so many large-bodied and terrestrial primates emphasizes the importance of accurate comparative functional analyses for paleoenvironmental reconstructions that may affect models for human evolution.

*This research was supported by Texas A&M University, the University of Oregon, and the National Science Foundation (Proposal No. 1650923).*

## Drivers of gene regulatory variation in red colobus

TANNER J. ANDERSON<sup>1</sup>, NOAH D. SIMONS<sup>2</sup>, KIRSTIN N. STERNER<sup>1</sup> and NELSON TING<sup>1,3</sup>

<sup>1</sup>Anthropology, University of Oregon, <sup>2</sup>Evolutionary Anthropology, Duke University, <sup>3</sup>Institute 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. Here we build upon a previous study that tested the relationship between SIV infection and host immune responses at the molecular level using whole blood transcriptome data from 29 Ugandan red colobus. Previous analysis in this system asked whether infection status was related to mean within-group gene expression. Here we extend those analyses by controlling for relatedness and viral load using linear mixed-effects modeling to ask 1) whether infection status predicts overall gene expression patterns, 2) whether social status predicts overall gene expression patterns, and 3) whether social status and SIV infection interact to influence gene expression patterns. 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, consistent with previous analyses. Our preliminary results also suggest that SIV infection might interact with social status to influence gene expression patterns. This expanded analysis will provide a more nuanced understanding of the relationship between infection status, viral load, the social environment, and gene expression in an important wild primate model.

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## Norm Compliance in Common Pool Resource Management: Experimental Evidence from Pemba

JEFFREY ANDREWS and MONIQUE BORGERHOFF MULDER

Human Behavior, Ecology and Culture, Max Planck Institute of Evolutionary Anthropology

Why do individuals inculcate norms that are not in their self interest to do so? Enforcement intended to ensure compliance to institutional norms is often insufficient to fully induce behavioral change. Yet empirically, even in the face of insufficient monitoring/punishment individuals will often comply with costly, but weakly enforced rules and regulations even when it is in their best interest not to. Part of the answer to this question involves a norm psychology that provides psychic utility and in turn motivates compliance to previously learned norms. Here we present both a theoretical model for the evolution of such psychology and results from common pool resource games run in Pemba Tanzania. Our results show that compliance is a function of trade-off between resource dependence, and time discounting – those who are dependent and future oriented inculcate norms and comply and those who are dependent and present biased do not comply.

*Max Planck Society for Evolutionary Anthropology*

## Evolutionary dental trends in Primates; insights from Evo-Devo-Dental Anthropology

CASSY M. APPELT, ELSA M. VAN ANKUM, DENVER F. MARCHIORI and JULIA C. BOUGHNER

Anatomy, Physiology & Pharmacology, University of Saskatchewan

Primate dentitions develop and evolve under the regulation of cell processes to generate different dental formulae, asymmetry between upper and lower formulae, and specialized tooth forms. Here we explore and theorize about these underlying cellular and developmental processes. Our interdisciplinary meta-analysis integrated data and literature across physical anthropology, cellular biology, and evolutionary developmental biology, including our own research using a mouse mutant for the p63 gene. We found that prosimians show more variation across dental formulae compared to anthropoids. Also, across primates, lower teeth appear more labile in number and form, and morphology appears more varied in ante-molar teeth versus molars. We posit that primate dental formula evolves via changes in the odontogenic homeobox code that patterns the nascent lamina of the deciduous dentition. These changes implicate tooth signaling centres as well as differentiation, proliferation, migration and compaction of odontogenic cells. Referring back to the p63 mouse model of craniodental development, our results in primates support the hypothesis that stronger developmental and functional integration of the midface constrains dental macroevolution in the upper dentition compared to the lower. We propose the Linchpin Hypothesis, that deciduous precursors are requisite for the formation of permanent successional (ante-molar) teeth but not additional (molar) teeth. Evolutionary losses in dental formulae likely occur via a myriad of changes in the cellular dynamics

of odontogenesis. More studies of diphyodont, heterodont animal models are needed to clarify the cell processes evolving under strong selection for diet and other para-functions in primates including humans and fossil relations.

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## Demographic and cost analysis of a retired NIH research chimpanzee population

DREW M. ARBOGAST<sup>1</sup>, JOHN J. ELY<sup>2,3,4</sup>, W. SCOTT MCGRAW<sup>1</sup> and DOUGLAS CREWS<sup>1</sup>

<sup>1</sup>Department of Anthropology, The Ohio State University, <sup>2</sup>Founder, MAEBIOS, <sup>3</sup>Department of Veterinary Sciences, UTMD Anderson Center, Keeling Center for Comparative Medicine, <sup>4</sup>Department of Anthropology, Center for the Advanced Study of Human Paleobiology, George Washington University

Reliable demographic data are essential for informing proper management strategies, guiding age-appropriate veterinary care, and forecasting population trends. Such information is particularly critical for long-lived taxa such as non-human primates. Little is known about the demographic structure of the recently retired meta-population of chimpanzees (*Pan troglodytes*) supported by the National Institutes of Health. We analyzed twenty-five years of data from the captive former biomedical research chimpanzees to generate life tables and perform a survival analysis. Results show that life expectancy at birth is greater for females ( $x=29.9$  years) than for males ( $x=26.6$  years). The current intrinsic rate of increase is approximately  $-5.18\%$ , indicating an on-going decline in the size of the nonbreeding meta-population. This was expected due to the breeding moratorium and normal age-related mortality. The model predicts population extinction within the next 25 years, by approximately the year 2045. According to the most recent NIH Chimpanzee Management Report, the average individual daily maintenance cost is \$38.71. Given our analyses, we estimate a lifetime expense of approximately \$422,462 per female and \$375,835 per individual male. Assuming twenty-five years until population extinction, this translates to a total cost of \$65.9 million. These estimates are useful for budgetary purposes and for establishing management timelines. Such estimates are important elements of responsible and practical management programs geared toward retired populations of taxa with long lifespans.

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# ABSTRACTS

## Investigating the health status of 19<sup>th</sup> century African Americans: multi-sited evidence from Texas

SAMANTHA M. ARCHER<sup>1</sup>, LAUREN C. SPRINGS<sup>2</sup> and DEBORAH A. BOLNICK<sup>1,3</sup>

<sup>1</sup>Department of Anthropology, University of Connecticut, <sup>2</sup>Department of Anthropology, University of Texas at Austin, <sup>3</sup>Institute for Systems Genomics, University of Connecticut

Throughout the 19<sup>th</sup> and early 20<sup>th</sup> centuries, African Americans in Texas had heterogeneous life experiences, particularly during Texas Reconstruction and early Jim Crow. From the beginning of Anglo American settlement in Texas to the end of the Civil War, nearly 250,000 enslaved African Americans were brought to Texas. Structural racism and the threat of racist retaliation in post-bellum Texas meant that Black Texans endured limited access to resources and opportunities. However, African Americans in postbellum Texas also found moments of possibility: by 1900, over 30% of Black Texans owned land and hundreds of Freedmen communities flourished.

To investigate the health status of African Americans during this period, we analyzed bioarchaeological data from five predominately African American historical cemeteries with burials from 1839 to 1914. This dataset includes 1,320 individuals from multiple livelihoods in rural and urban settings. We compared biological markers of health stress among individuals interred in these cemeteries, demonstrating the heterogeneity of lived experiences and their associated health outcomes. For example, while there is no clear association between incidence of linear enamel hypoplasias (LEH) and urban vs. rural lifeways, frequencies of LEH increased over time in the 19<sup>th</sup> and 20<sup>th</sup> centuries. A significantly higher incidence of skeletal trauma was also associated with entry into the Texas penal system during the era of convict leasing. These results demonstrate heterogeneity in lived experience. We employ theoretical paradigms from the bioarchaeology of violence to contextualize our findings and correct overgeneralizations made about the lived experiences of emancipated African Americans in Texas.

## Growth analysis of South African Mixed Ancestry infants

LIESL M. ARENDSE<sup>1</sup>, DESIRÉ BRITS<sup>2</sup>, ESTELLE V. LAMBERT<sup>1</sup> and VICTORIA E. GIBBON<sup>1</sup>

<sup>1</sup>Human Biology, University of Cape Town, <sup>2</sup>Human Variation and Identification Research Unit, School of Anatomical Sciences, University of Witwatersrand

The South African National Demographic and Health Survey (2016) showed 27% of South African children under five years were stunted and 13.5% overweight/obese, according to WHO Multicentre Growth Reference standards. The

aim of this study was to document infant growth, against this international reference standard, in a cohort of 0–18 month old South Africa children of Mixed Ancestry. Mothers were recruited from 3 clinics (2 public, one private) and 163 (male=73, female=90) infants were divided into three age groups. Standard nutritional anthropometry was conducted (length-for-age, weight-for-age, weight-to-length-for-age and head circumference-for-age z-scores). The 0-5.9 month age group, for both sexes, aggregated between +0.50 and -1.5 for length (57%) and weight (69%) z-scores. Boys aged 6-18 months tended to aggregate below +0.50 for length (63%) and/or weight (72%) z-scores, but had higher z-scores for head circumference (65%). Girls aged 6-18 months tended to aggregate above -0.50 for length (60%) and weight (68%) z-scores. Only 2.5% of infants fell below 2 standard deviations (SD) for length-for-age or stunted. Further, only 4.3% were above 2 SD for weight-for-age and would be considered overweight/obese. 52% (85/163) of head circumference z-scores data fell between -0.50 and +1.00. Results for the 0-5.9 month cohort indicate a downward deviation for length/weight from the WHO's growth median whereas head circumference z-scores for all infants (0-18 months) indicate a positive deviation from the WHO's median. Further work is needed to determine if the WHO growth reference is an appropriate standard for Mixed Ancestry infants in South Africa.

*This work is based on the research supported in part by the National Research Foundation of South Africa (Ref:SFH170630246904); University of Cape Town Financial Aid; and Siri Johnson Bursary.*

## The trabecular structure of the proximal ulna in hominoids

JULIA ARIAS-MARTORELL<sup>1,2</sup>, CHRISTOPHER J. DUNMORE<sup>2</sup>, MATTHEW M. SKINNER<sup>2,3</sup> and TRACY L. KIVELL<sup>2,3</sup>

<sup>1</sup>Paleoprimatology and Paleoanthropology, Institut Català de Paleontologia Miquel Crusafont, Edifici ICTA-ICP - Universitat Autònoma de Barcelona, Barcelona, Spain, <sup>2</sup>School of Anthropology and Conservation, University of Kent, Canterbury, UK, <sup>3</sup>Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany

The proximal ulna has been used to explore locomotor behaviour in extant and fossil hominoids through the study of its external morphology that reflects both phylogenetic history and function. Conversely, trabecular bone can remodel in response to loads experienced in life and thus reflect locomotor joint postures. Therefore, we analysed variation in trabecular structure of the proximal ulna (using a whole-epiphysis approach) to test if corresponds to observed locomotor postures of the elbow across extant apes (*Gorilla gorilla* [n=4], *Pan troglodytes* [n=3], *Symphalangus syndactylus* [n=3]) and New and Old World monkeys (*Ateles* sp [n=4], *Alouatta* sp.

[n=2], *Macaca fascicularis* [n=2], *Papio hamadryas* [n=2]). Variations in bone volume fraction (BV/TV) indicate that suspensory *Symphalangus* have high BV/TV superiorly in the trochlear notch and the posterosuperior olecranon, corresponding with an elbow loaded in extension. *Pan* have high BV/TV in the radial notch and the mediosuperior trochlea, suggesting relatively high mediolateral forces crossing the elbow during knuckle-walking; however, *Gorilla* have concentrations restricted to the centre of the trochlea, perhaps indicating a more central/columnar loading of the elbow during knuckle-walking. The BV/TV pattern of the habitual pronograde quadrupeds *Macaca*, *Papio* and *Ateles* (and to a lesser extent, *Alouatta*) is a large, high BV/TV concentration encompassing most of the olecranon and the superior trochlea, which may respond to their long olecranon impinging on the humerus during quadrupedal stance phase. Overall, the results show that proximal ulnar trabecular structure corresponds with habitual posture loading and can provide novel information for investigating locomotor behaviours in fossil primates

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## Muscle attachment sites influence cut mark morphology

MIRANDA ARMOUR-CHELU

Cut marks are one of the most important categories of evidence for identifying hominin utilization of animal tissues but the interpretation of butchery traces remains problematic despite extensive study. One recurring theme is whether the marks created by filleting meat from bone as opposed to disarticulation of joints can be differentiated. Both of these activities leave traces in the metaphyseal region (proximal/distal shaft) of long bones and it has been concluded that each can be distinguished on the basis of cut mark morphology, such as cut mark depth, length or direction.

Muscle attachment sites or entheses differ anatomically and are defined as being fibrous or fibrocartilaginous. Fibrous entheses cover broad areas of the bone shaft and are connected to the periosteum whilst fibrocartilaginous entheses are found at epiphyses and apophyses, are smaller in transverse section and the tendon separate from the bone, except at the physical site of attachment.

This study documents cut mark morphology in relation to muscle attachment sites, drawing on two data sets, (museum collection and dissections of white-tailed deer). Multiple cut marks were identified and while they all derived from the removal of muscle from long bone shafts, different morphologies of cut marks were observed. It was difficult to detach the brachialis muscle, (multiple, short nonaligned cut marks), compared with the

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triceps or quadriceps (long, oblique, parallel cut marks). It is suggested that cut mark morphologies are affected by differences in the toughness/thickness of connective tissues at the interface between bone and epimysium.

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### Care analysis on human skeletal remains from a post-medieval London Cemetery

PATRICIA N. ARNETT

Department of Anthropology, University of Alabama

Providing care to individuals that are affected by illness and injury is one of the most common human behaviors, yet the mechanisms of care which include social support tend to be overlooked for working-class and prison populations. The characteristics of the care provided by these groups can reflect the motivation and commitment of the caretakers among the underprivileged, low social status members of society. This may be especially so for the working class of 17-19th century London, whose remains are analyzed by this project. Through the examination of the St. Brides lower churchyard cemetery population consisting of 544 individuals who were of low socioeconomic status, this study addresses how social support in terms of care may be the mediator for physiological effects of this group. The goal of this study is to determine how many individuals were affected by pathologies and traumas that required care provisioning, including but not limited to severe osteoarthritis, surgical intervention, Pagets disease, fractures, and breaks. After this has been addressed, the next goal is to identify how these pathologies and traumas would have impacted both the individuals requiring care and those providing it. Of the individuals being studied (544), 175 are subadults and the remaining 369 are adults (194 male, 125 female). Only 1.5% of the total population presents with no pathological conditions and over half the population (~65%) presents with at least 3 identifiable pathologies. The high rate of pathological conditions suggests that those that are providing care may also require care. This raises important considerations about caregiving practices of the working class of 17-19th century London.

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### Maternal low social-status, increased fetal developmental instability in males, and offspring sex-ratio in *Macaca mulatta*

JUAN PABLO ARROYO and LORENA MADRIGAL

Applied Anthropology, University of South Florida

Trivers-Willard hypothesis predicts mothers to produce lower proportions of male offspring under challenging conditions. Maternal hormonal-stress-responses can result in increased developmental instability and interfere with sexually dimorphic development in-utero. 2D:4D ratio, an indicator of prenatal androgen exposure, is

a sexually dimorphic trait established in-utero, associated with adult condition. This study examined in *Macaca mulatta*, the impact of maternal social-status on offspring developmental instability in-utero; assessed by offspring 2D:4D and sex-ratio. Low-ranking mothers produced lower proportions of male offspring ( $n=9$ ) than female offspring ( $n=22$ ),  $\chi^2(1) = 5.45, p = .020$ ; and lower proportions of male offspring (29%) than high-ranking mothers (52.1%),  $\chi^2(1) = 17.04, p < .001$ . High-ranking mothers had an increased likelihood (166%), and low-ranking mothers a reduced likelihood (-62%) of producing male offspring,  $B = -0.98, OR = 0.38, p = .034$ . Among males, dominance-rank explained 13% of the variance in 2D:4D,  $F(1,41) = 6.18, p = .017, R^2 = 0.13$ ; and high-rank predicted higher 2D:4D,  $B = 0.01, t(41) = 2.49, p = .017$ . Low-rank increased the likelihood (293%) of higher bilateral asymmetry of 2D:4D,  $B = 1.37, OR = 3.93, p = .045$ . Low received-aggression increased the likelihood (109%) of high 2D:4D,  $B = 0.73, OR = 2.09, p = .035$ . Findings suggest that maternal low-status may result in higher fetal developmental instability and reduced masculinization in male offspring, as assessed by low 2D:4D, higher bilateral asymmetry, and sex-ratio. Male fetal development appears to be more vulnerable to detrimental conditions of maternal low-status.

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### Investigating Social Age Changes in the Roman Empire through Dietary Stable Isotopes

L. CREIGHTON AVERY, MEGAN B. BRICKLEY and TRACY L. PROWSE

Anthropology, McMaster University

Childhood is a biological and social phenomenon, but investigation of social age in bioarchaeology is limited by currently available methodologies. We use seriated stable isotope analysis of tooth dentine to investigate dietary change as a proxy for social age changes in males and females ( $n=13M, 17F$ ) buried at the Imperial Roman Michelet Necropolis, France (c. 350-450 CE). Thirty second permanent molars (217 seriated sections) were used to identify dietary changes between the ages of 2.5 and 15 years.

Results demonstrate relative homogeneity for  $\delta^{13}C$  and  $\delta^{15}N$  values for males and females between the ages of 2.5 and 14 years ( $p > .050$ ). At 15 years, however, males exhibit significantly lower  $\delta^{15}N$  values than females ( $p = .008$ ;  $\delta^{13}C$  values are not significantly different).

Literary sources suggest that middle class males began formal apprenticeships around 15 years old. The lower nitrogen values observed in this study may therefore reflect a dietary change that accompanied this shift, as they transitioned from childhood to adolescence. Females, however, exhibit little to no dietary change between 2.5 and 15 years, suggesting that social age changes did

not encompass dietary changes, or that social age changes in the female life course occurred later than 15, perhaps in line with their first marriage, in their late teens or early twenties. The results of this study help further understand biological and social transitions in the Roman Empire, as well as the utility of stable isotopes to identify social age changes in the past.

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### Ethical considerations and community engagement experiences of the Afromexico Genomics Project

MARIA C. AVILA ARCOS<sup>1</sup>, GERARDO SANCHEZ ROMERO<sup>2</sup>, ANDRES MORENO-ESTRADA<sup>3</sup>, CARLOS D. BUSTAMANTE<sup>4,5</sup> and MARCUS W. FELDMAN<sup>6</sup>

<sup>1</sup>International Laboratory for Human Genome Research, National Autonomous University of Mexico, <sup>2</sup>Mutua Investigación e Innovación Social SC, <sup>3</sup>Laboratorio Nacional de Genómica para la Biodiversidad, CINVESTAV, IPN, <sup>4</sup>Department of Genetics, Stanford University, <sup>5</sup>Department of Biomedical Data Science, Stanford University, <sup>6</sup>Department of Biology, Stanford University

During the Trans-Atlantic Slave Trade, approximately 250,000 enslaved Africans were forcibly brought to New Spain. A legacy of this involuntary population movement is the presence of more than 3 million Mexicans who self-identify as "Afro-Mexicans", who were finally officially recognized in the Mexican constitution in 2019. The Afromexico Genomics Project collaborated with Afro-Mexican communities to characterize their genetic ancestry using dense genome-wide genotyping. Participants in the study were 380 people who self-identified as either Afro-descendants, indigenous or have a mixed heritage from three Mexican states. To complement the genome-wide genotype data, we collected genealogical data and self-identification information. We engaged with the communities through informative talks and brochures and returned the genetic ancestry results to participants. We carried out ethnographic interviews to learn about their expectations for the project as well as additional interviews after returning the genetic ancestry results to investigate the impact of these on their self-identification. We observed that the participants were deeply interested in the research and expressed their gratitude for the return of the ancestry results, which made them feel valued and recognized. The study was carried out with utmost consideration of the vulnerable status of these populations, which include marginalization, discrimination, and limited access to health

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services. Therefore, an additional goal of the project is to contribute to the appreciation of Afro-Mexicans as part of Mexico's mosaic of diversity and help set the stage for health interventions.

*The project has been funded by Stanford Center for Computational, Evolutionary and Human Genomics and UNAM's PAPIIT grant IA206817*

## Comparing population history in the widely dispersed *Homo erectus* and *Homo sapiens* species

KAREN L. BAAB

Department of Anatomy, Midwestern University

*Homo erectus* and recent *H. sapiens* share features of evolutionary history, including major dispersals out of Africa to more temperate and seasonal habitats in Eurasia and Asia, but it is unknown whether this resulted in similar population histories. The current study uses evolutionary quantitative genetics to test the hypothesis that similar, primarily neutral, microevolutionary factors (e.g., genetic drift) shaped cranial morphology in both species.

*Homo erectus* fossils were grouped into six paleodemes (populations), each containing 2-6 individuals and constrained to <130 kyr. The recent human sample ( $n \sim 290$ ), derived from eight populations, was used to calculate population means and the within-population phenotypic covariance matrix ( $P$ ). Analyses were performed separately for frontal and occipital bone shapes quantified by three-dimensional landmarks and semilandmarks. Results indicate higher intraspecific and between-deme variation in frontal and occipital bone shape in *H. erectus* than recent *H. sapiens*. These findings are consistent with a scenario where *H. erectus* did not undergo the same population bottleneck during dispersal as *H. sapiens* and populations were more isolated. Occipital bone shape diverged neutrally among populations in both species, while the frontal bone evolved via selection in *H. erectus* but not *H. sapiens*. Based on analogy with modern humans, evidence for selection on the frontal bone may reflect climate-driven adaptation of the face via integration of the upper face and frontal bone. The results of these analyses highlight both distinct population histories for the two most dispersed *Homo* species and different evolutionary histories for the anterior and posterior vault in *H. erectus*.

## Identification of the deceased: A retrospective review of Forensic Anthropology Cape Town casework

ATHI BALISO<sup>1</sup>, LAURA J. HEATHFIELD<sup>2</sup> and VICTORIA E. GIBBON<sup>1</sup>

<sup>1</sup>Human Biology, University of Cape Town,

<sup>2</sup>Pathology, University of Cape Town

Each year, hundreds of decedents remain unidentified in South Africa – particularly those who are decomposed. In such cases, Forensic Anthropology Cape Town (FACT) at the University of Cape Town can assist with identification in the Western Cape (WC) province. Regional standards for the estimation of post-mortem interval (PMI) in the WC province are lacking and regional-specific data are important due to the significant impact local environmental conditions and climate have on local decomposition rates. To identify areas where regionally-specific forensic taphonomy research should be conducted, patterns related to the location of discovery for FACT cases referred between 2006 – 2018 from Forensic Pathology Services (FPS) were examined. In total, FACT consulted on 172 forensic cases representing 174 individuals. A considerable number of these individuals did not have PMI estimations (32%; 55/174) and several were made without precision. Most decedents (51%; 87/174) were discovered in police precincts from high crime areas, yet a considerable number were also found in low crime and sparsely populated areas (47%; 81/174) popular for recreational activities. Vegetated areas (23%; 40/174) were the most common sites of discovery, followed by the roadside (15%; 29/174), aquatic environments (11%; 20/174) and farms (11%; 19/174). Decedents were discovered exposed (35%; 62/174), covered with items such as bedding or shrubs (14%; 25/174) or buried (10%; 17/174). These data highlight common areas for the discovery of decomposed bodies in the WC province and thus, should be used to guide taphonomic research to better understand local decomposition rates.

*Athi Baliso is the recipient of the VC Research Scholarship Master's; Master's Research Scholarship; UCT Master's Financial Aid; Ada & Bertie Levenstein Bursary; and the NRF Innovation M&D Scholarship.*

## The absence of plexiform bone is not a reliable sole indicator to differentiate human from deer bone

MEIR M. BARAK<sup>1</sup> and ADELIN LE CABEC<sup>2</sup>

<sup>1</sup>Department of Veterinary Biomedical Sciences, Long Island University, <sup>2</sup>PACEA, UMR 5199-CNRS, Université de Bordeaux

Deer bones are frequently found in archeological sites in association with human remains. Differentiating human from deer bone is commonly achieved using external macroscopic landmarks, or histology in case of small fragments. The latter approach is focused on the premise that contrary to Haversian bone in humans, deer bone is predominantly plexiform in nature. To confirm the prevalence of plexiform bone in deer long bones we investigated bone micro-structure and mineralization in two locations (proximal and mid-diaphysis) along the humeri and femora of seven juvenile white-tailed deer. Deer juvenile state was determined by the presence of an active

growth plate, indicating an age between 5 and 20 months. Multiple surfaces from each cortical location were sectioned, polished and inspected under a light microscope. Proximal and mid-diaphysis sections from white-tailed deer humeri were also investigated under scanning electron microscopy. Finally, the samples were crushed, grounded and ashed to quantify their mineral content. Our histological results revealed that while the proximal femur and the femur and humerus mid-diaphyses were predominantly plexiform in nature, the proximal humerus was almost completely remodeled to Haversian bone. These findings were also supported by the ashing results, which showed that proximal locations were less mineralized than mid-diaphyses (i.e. younger bone) and that as a whole the femur was more mineralized than the humerus (i.e. the proximal humerus has the least mineralized bone). These results indicate that the absence of plexiform bone is not a reliable sole indicator to discriminate human from deer bone.

## UnangaꝔ Prehistory in the Western Aleutian Islands - Early Findings

CHRISTOPHER E. BARRETT, JUSTIN C. TACKNEY, LAUREN E. NORMAN, JENNIFER A. RAFF and DENNIS H. O'ROURKE

Anthropology, University of Kansas

The archaeological record in the western Aleutian Islands of Alaska is less developed relative to the greater archipelago. Inconsistencies between molecular and archaeological evidence highlight questions regarding local ecologies and population histories. Available ancient DNA (aDNA) and isotope data describing ancestral UnangaꝔ (Aleut) are largely limited to the Alaskan Peninsula and the central and eastern regions of the Aleutians. Here we describe radiocarbon dates, stable isotopes, and ancient mitochondrial DNA (mtDNA) from the Qaxun (Rat) and Sasixnan (Near) islands in the western Aleutians. Calibrated radiocarbon dates ( $N=16$ ) from human remains range from 2,815-275 cal YBP with younger dates likely being contemporary. Stable isotopes ( $N=10$ ) from purified bone collagen returned average stable carbon values ( $\delta^{13}C$ ) of  $-13.01\text{‰}$ , and average stable nitrogen ( $\delta^{15}N$ ) of  $16.56\text{‰}$ . Mitochondrial lineages observed ( $N=15$ ) include A2a, D2a, A2b1, and D4b1a2a1b.

While sample sizes limit some inferences, these early data situate ancestral western communities among pan-archipelago UnangaꝔ populations. Average  $\delta^{13}C$  values more closely resemble those reported from the peninsula region, while average  $\delta^{15}N$  values are lower than those found on the peninsula or the eastern Aleutians. Lineages A2a and D2a are ubiquitous in living and ancestral UnangaꝔ, while Inuit associated A2b and east Asia associated D4b1a2a1b are not reported in contemporary descendants, except for those with clear maternal ancestry to populations further

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north. These findings provide early insight to the ecology and matrilineal genetic diversity of the western Aleutian Islands and possibly the larger archipelago.

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### Increased secondary sex ratios following natural disasters: Same response shows different adaptive value among species

ALISON M. BEHIE<sup>1</sup>, PATRICIA C. WRIGHT<sup>2,4</sup>, MARY SM. PAVELKA<sup>3</sup>, STEIG JOHNSON<sup>3</sup> and DINA ANDRIANOELY<sup>4</sup>

<sup>1</sup>School of Archaeology and Anthropology, The Australian National University, <sup>2</sup>Department of Anthropology, Stony Brook University, <sup>3</sup>Department of Anthropology and Archaeology, The University of Calgary, <sup>4</sup>Centre ValBio, Centre ValBio Research Station

Variation in secondary sex ratios (SSR) across primates may represent adaptive processes in response to the mother's physiological condition (Trivers-Willard hypothesis) or to the available resource base (local resource competition hypothesis). Many studies have explored these hypotheses in the context of maternal dominance rank and/or resource availability, but none have explored them in reference to natural disasters. This study thus compares SSR in three primate species: Milne's Edward Sifakas (*Propithecus edwardsi*), black howler monkeys (*Alouatta pigra*) and Yucatan spider monkeys (*Ateles geoffroyi yucatanensis*) exposed to natural disasters by comparing SSR in disaster years (first two years of breeding post-disaster) with non-disaster years. In all three species there was an increase in male births in post-disaster years with sifakas showing an increase in SSR from 1.00 in non-cyclone years to 1.63 in post-cyclone years and spider monkeys showing an increase from 1.6 in non-hurricane years to 11 in post-hurricane years. For howler monkeys, the increased SSR increase was due to a spike in male births in the second-year post-hurricane with other years showing more female than male births. Despite all species showing a similar change in SSR, a closer look at their ecologies reveal that they do not all fit one adaptive hypothesis. Rather, howler monkeys support TW, sifakas support LRC and spider monkeys do not meet the predictions of either. These results suggest that there is not one adaptive process that can explain sex determination across all primates even following similar environmental changes.

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### Prevalence of cranial trauma in Upper Paleolithic human fossil remains

JUDITH BEIER<sup>1</sup>, NILS ANTHES<sup>2</sup>, JOACHIM WAHL<sup>1</sup> and KATERINA HARVATI<sup>1,3</sup>

<sup>1</sup>Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoenvironment, University of Tübingen, <sup>2</sup>Animal Evolutionary Ecology, Institute of Evolution and Ecology,

University of Tübingen, <sup>3</sup>DFG Center for Advanced Studies "Words, Bones, Genes, Tools", University of Tübingen

Patterns of trauma reveal insights into human lifestyles and behaviors and can serve as a proxy for the stresses sustained by past populations. In this study, we characterized patterns of cranial trauma prevalence in Upper Paleolithic skeletal remains (ca. 40,000-10,000 BP). It has been suggested that during this time, climatic and environmental changes exposed human populations frequently to elevated stress levels, prompting biocultural adaptations of survival strategies to buffer environmental conditions. Our sample comprised 234 specimens, corresponding to 1285 single cranial elements, with and without traumata from 101 Eurasian sites. We used generalized linear mixed models with a Markov chain Monte Carlo algorithm to assess cranial trauma prevalence in relation to age-at-death, sex, and time period (before and after the Last Glacial Maximum [LGM]), while accounting for the differential preservation of the fossil remains. We found a predicted mean cranial trauma prevalence of 0.07 (95% CI 0.003-0.19) for skeletal elements, and of 0.26 (95% CI 0.08-0.48) for specimens, each when remains were >75% complete, which corresponds to the trauma prevalence described for Mesolithic and Neolithic samples. Males and females were exposed to slightly different injury risks, as indicated by a slightly higher trauma prevalence among male remains. Both sexes exhibit more trauma in the >30 years old age group. The trauma prevalence of the two sexes and age groups of samples from before and after the LGM were similar, suggesting no time period-specific trauma patterns that would reflect the environmental stressors likely accompanying the climatic instabilities during the LGM.

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### The Impact of Fine-scale Demography on the Genetic Architecture of Disease in Diverse Populations

GILLIAN M. BELBIN

Internal Medicine, Icahn School of Medicine at Mount Sinai

The impact of fine-scale genetic ancestry on the genetic architecture of disease, and its consequence for population health disparities remains under-explored. We leveraged genomic data for a diverse biobank (BioMe) of >30,000 patient participants from New York City. We explore fine-scale genetic ancestry in the form of Identity-by-Descent (IBD) sharing. IBD represent haplotypes of the genome co-inherited by individuals from a recent shared ancestor. By examining IBD sharing at a population level, it is possible to discern patterns of shared genealogy due to

recent shared demographic history. By employing machine learning approaches to a network of IBD sharing in BioMe, we were able to uncover 17 communities enriched for recent, shared genetic ancestry. These IBD-communities often correlated with fine-scale geographical origin, with many exhibiting genomic evidence of founder effects. We demonstrate significant differences in the fine-scale segregation of known Mendelian variants between IBD-communities, and also significant differences in the distributions and predictive accuracy of polygenic risk scores (PRS) for a number of complex diseases. We also replicate our findings in the UK Biobank, where we uncover a total of 99 distinct IBD-communities from a network of 500,000 individuals; with some communities representing more recent diaspora to the United Kingdom, and others correlating with geographical region-of-origin within the UK. This work demonstrates the importance of exploring fine-scale genetic ancestry to inform precision medicine efforts.

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### Examination of Stress and Anxiety in Pregnancy During COVID-19 Using an Anti-racist Praxis: Insights from the HOPE COVID-19 Study

APRIL J. BELL<sup>1,2</sup>, KAREN A. SCOTT<sup>2,3</sup> and LAURA JELLIFFE-PAWLOWSKI<sup>1,4,5</sup>

<sup>1</sup>CA Preterm Birth Initiative, University of California San Francisco, <sup>2</sup>Department of Obstetrics, Gynecology, & Reproductive Sciences, University of California San Francisco, <sup>3</sup>Department of Humanities & Social Sciences, University of California San Francisco, <sup>4</sup>Department of Epidemiology & Biostatistics, University of California San Francisco, <sup>5</sup>Director, Precision Health & Discovery, University of California San Francisco

There is increasing evidence that some racial and ethnic minority groups in the United States are being disproportionately affected by the 2019 novel coronavirus disease (COVID-19). Inequities in the social determinants of health, such as poverty and healthcare access, affecting these groups are interrelated and influence a wide range of health and quality-of-life outcomes and risks. As the pandemic grows, it is important to understand how pregnant people and infants are being affected since evidence suggests that risks for some adverse pregnancy and infant outcomes are increased (e.g., preterm birth, cesarean section, respiratory distress, and hospitalization), particularly Black and Latinx pregnant people. The HOPE COVID-19 Study is a multi-year, prospective investigation designed to better understand how the COVID-19 impact adverse pregnancy and infant outcomes. It also examines how the pandemic exacerbates existing hardships such as social isolation, economic destabilization, job loss, housing instability, and/or family member sickness or death among minoritized and marginalized communities. Sixty percent of participants reported feeling anxious or on edge in the prior

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two weeks. Most (92%) reported feeling worried about themselves, their families, or their infants becoming infected. Many (68%) felt increased stress about losing a job or a decrease in family income. A smaller proportion (22%) had concerns about food insecurity. Our results demonstrate that pregnant people in the United States are experiencing increased rates of stress and anxiety related to COVID-19, placing them at higher risk for adverse birth outcomes.

Seed funding was received from the UCSF California Preterm Birth Initiative, the San Diego Study of Mothers and Infants, the UCSF Newborn Brain Research Institute, and UCSF investigator funds.

### Characterizing wild lemur microbiomes across multiple body regions in southwest Madagascar

RACHEL B. BELL<sup>1</sup>, RICHARD R. LAWLER<sup>2</sup>, JOELISOA RATSIRARSON<sup>3</sup>, JEANNIN RANAIVONASY<sup>3</sup>, REBECCA LEDUC<sup>4</sup> and JASON M. KAMILAR<sup>1,5</sup>

<sup>1</sup>Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst, <sup>2</sup>Department of Sociology and Anthropology, James Madison University, <sup>3</sup>Agroecology, Biodiversity and Climate Change Department, ESSA, University of Antananarivo, <sup>4</sup>Department of Biology, University of Massachusetts Amherst, <sup>5</sup>Department of Anthropology, University of Massachusetts Amherst

There is a growing body of research exploring ecological effects on primate gut microbiota, yet comparative studies including microbial communities throughout the host body are lacking due to the challenges of invasively sampling wild primates. Our study explores how anthropogenic disturbance affects the hair, oral, and gut microbiome of wild Verreaux's sifaka (*Propithecus verreauxi*), as well as the gut microbiome of wild ring-tailed lemurs (*Lemur catta*), within Bezà Mahafaly Special Reserve in southwest Madagascar. We analyzed the diversity of 68 microbiome samples after targeting the V4 region of the 16S rRNA bacterial gene for high throughput sequencing. Initial analyses reveal significant microbial community distinctions between body regions, including different sampling locations of hair from the same animal, as well as differences between ring-tailed lemur and Verreaux's sifaka samples. Initial results also suggest that microbiome samples from ring-tailed lemur individuals who frequent human camps were significantly different from samples in all other habitat types. Our research addresses how host species identity and body region interact with the effects of anthropogenic disturbance on the microbiome and is among the first comparative analyses of microbiota from multiple body regions in wild primates. Comparative microbiome research, such as the interspecific analysis here, can parse out the roles of the environment and host phylogeny in determining microbial community structure. Additionally, analyzing microbial communities

in multiple regions of the wild primate body can expand our knowledge beyond the well-characterized gut-microbiome studies of primates, and point to additional ways in which microbiomes influence host function and health.

*The University of Massachusetts Amherst Natural History Collections Summer Scholarship, the UMass Amherst Graduate School Predissertation Grant, and the UMass Amherst Graduate School Dissertation Fieldwork Grant provided funding for this study.*

### Sex estimation for forensic human identification: a case report of discordance between anthropological assessment and DNA analysis

TRACY BENNETT<sup>1</sup>, VICTORIA E. GIBBON<sup>2</sup>, LAURA D. TAYLOR<sup>1</sup> and LAURA J. HEATHFIELD<sup>1</sup>

<sup>1</sup>Pathology | Division of Forensic Medicine and Toxicology, University of Cape Town, <sup>2</sup>Human Biology | Division of Clinical Anatomy and Biological Anthropology, University of Cape Town

The partial skeleton of an adult person was discovered in a field and admitted to Salt River Mortuary, Cape Town, South Africa for post-mortem examination. No visual features or soft tissue were present for identification, and there was evidence of canid scavenging. Forensic assessment to estimate sex was accomplished using the Phenice method, shape of the greater sciatic notch and gracility of the cranium, and all suggested this person was probably female. The clothing included overalls and boxer briefs, which appeared consistent with what a male might wear. This possible contradiction led to the request of DNA analysis to determine biological sex, however, the state as well as a private laboratory were unable to generate a DNA profile. A molar was then submitted to the University of Cape Town where DNA was extracted using a modified phenol-chloroform method. Quantification of the DNA using real time PCR showed amplification of the Y-chromosome target, which suggested the remains were male. This was verified using DNA profiling where the Amelogenin marker showed XY (*i.e.* male). These results highlight the need for revised anthropological data for the modern and diverse South African population, as well as improved molecular protocols to ensure that DNA profiles can reliably be obtained. Many people remain unidentified in mortuaries each year and improving accuracy of sex estimation may contribute towards increased case resolution. This case also demonstrates the importance of interdisciplinary collaboration for accurate and reliable forensic identification.

### Assembling a bioarchaeology of mental illness: Applying a "provisional evolutionary schema of mental disorders" to a 19<sup>th</sup> century asylum context

JACQUELINE M. BERGER

Department of Anthropology, University of South Florida

Biological anthropology continues to expand its horizons through novel and much-needed collaborations; however, gulfs between practitioners do exist, despite similar underlying research interests or goals. In regard to the study of mental illness, Syme and Hagen (2019) offer a new way forward for biological anthropologists. While Syme and Hagen (2019) focus on living populations; bioarchaeologists have much to gain from their presentation of a "provisional evolutionary schema of mental disorders" (PES). Archaeological scholarship addressing institutional contexts, including asylums, has increased over time, and begun to address the intersectionality of marginalized identities, including implications for the postmortem treatment of remains. The present study demonstrates the benefits to be gained by involving bioarchaeologists in the study of mental illness, applying the PES to the Siena Craniological Collection (SCC) from Siena, Italy, specifically the patients of the *L' Ospedale Psichiatrico San Niccolò* (San Niccolò Psychiatric Hospital - SNPH) ( $n=287$ ), as identified by the diagnoses listed in the collection *registri* (catalogs). First, diagnostic trends from the SNPH were reinterpreted using primary historical sources, and compared to modern diagnostic rates for Italian in-patient populations. Results indicate a highly significant difference ( $\alpha = 0.05$ ) in diagnoses prevalence between the SNPH and modern Italian patients ( $\chi^2 = 251.47$ ,  $df = 27$ ,  $p < 0.001$ ). These results were then reinterpreted using the PES, showcasing the benefit of the PES in site-specific approaches to mental illness in a bioarchaeological context. From these findings, the "bioarchaeology of mental illness" as a framework for future study is proposed.

*Support for research analysis and writing provided by the University of South Florida - Department of Anthropology Dissertation Completion Fellowship.*

### The taphonomic context of Late Pleistocene and Early Holocene burials at Hora 1, Malawi: implications for the study of forager mortuary practices

ALEX BERTACCHI<sup>1</sup>, JESSICA CEREZO-ROMÁN<sup>2</sup>, JESSICA C. THOMPSON<sup>1</sup>, ALAN MORRIS<sup>3</sup> and POTIPHAR KALIBA<sup>4</sup>

<sup>1</sup>Department of Anthropology, Yale University, <sup>2</sup>Department of Anthropology, University of Oklahoma, <sup>3</sup>Department of Human Biology, University of Cape Town, <sup>4</sup>Malawi Ministry of Tourism, Culture and Wildlife

Research at archaeological sites traditionally described as "Later Stone Age" (LSA) has begun to highlight the variability of Late Quaternary

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mortuary practices among African foragers. However, the interpretation of mortuary contexts requires an understanding of site formation processes and potential post-depositional disturbances. We contribute to these discussions with a sample of five individuals from the Hora 1 site in northern Malawi and associated faunal remains. Three adult burials date to the Early Holocene, while two infant burials are Late Pleistocene in age. Two of the adults are inhumations, while the other is the intentional burning of a woman showing evidence for perimortem defleshing, with selective curation of bones after burning. The latter represents the first report of such mortuary practice in an LSA context. All individuals are missing some elements, and in two cases these are the same elements of the hands, feet, and lower limbs.

Here we offer an analysis of the context and state of preservation of the five individuals. Particularly, we leverage the taphonomic study of the fauna from the site to show that: 1) the absence of specific human elements is not explained by post-depositional fragmentation or recovery bias, possibly indicating intentional removal; 2) defleshing of human remains is qualitatively different from mammal butchery, suggesting a non-nutritional explanation for this practice; 3) most of the faunal remains in stratigraphic association with the burned individual are unburnt, thus excluding the possibility that the human remains were burned accidentally during site maintenance activities.

*Fieldwork and laboratory analyses were funded by Emory University, the Wenner-Gren Foundation for Anthropological Research (Grant #9437), the National Geographic Foundation (Grant NGS-53412R-18) and the Augusta Hazard Fund.*

### Contemporary variation in human eccrine sweat gland density

ANDREW W. BEST<sup>1</sup>, DANIEL E. LIEBERMAN<sup>2</sup> and JASON M. KAMILAR<sup>1,3</sup>

<sup>1</sup>Anthropology, University of Massachusetts,  
<sup>2</sup>Human Evolutionary Biology, Harvard University,  
<sup>3</sup>Graduate Program in Organismic 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. After human dispersal from Africa, sweat gland density may have changed to suit local environmental conditions. 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. Using pilocarpine iontophoresis and silicone impressions we found substantial interindividual

variation in active sweat gland density in a sample of 90 human volunteers from diverse geographic ancestries and childhood climatic conditions. This variation was best explained by body surface area, sex, and age. Moderate associations were found between gland density of several body regions and geographic ancestry as estimated by 23andMe test results, and water vapor pressure of childhood climate. These results reveal potential drivers of contemporary variation in an important and relatively unexplored human trait.

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### Exploratory study of existing methods for converting endocranial volume to brain mass

SANAMPREET K. BHULLAR and ROBERT C. MCCARTHY

Department of Biological Sciences, Benedictine University

Researchers studying encephalization in fossil specimens oftentimes convert endocranial volume (ECV) to brain mass, which is then used to calculate an index (e.g., the encephalization quotient, or EQ). Recent studies claim that the isometric relationship between ECV (in cubic centimeters) and brain mass (in grams) means that it is possible to convert one to the other by adjusting for the brain's specific gravity without needing to account for more complex spatial relationships. We tested this claim by comparing three different methods for converting ECV to brain mass (multiplying by the brain's specific gravity, multiplying by the brain mass/ECV index, predicting brain mass from ECV using regression) in four fossil specimens (CGM 85785 *Aegyptopithecus zeuxis*, ARA-VP 6/500 *Ardipithecus ramidus*, Sangiran 17 *Homo erectus*, Amud 1 *Homo neanderthalensis*) that span the size range of interest to many paleoanthropologists. We show that adjusting by the brain's specific gravity or proportional relationship to the endocranial cavity produces unreasonable brain mass estimates at both small and large ends of the size continuum. Existing regression equations predict brain masses unrealistically larger than ECV for ECV values <300 cubic centimeters. Unrealistic brain mass estimates are the product of brain mass data quality issues and mismatches between brain mass and ECV species values that bias our interpretation of brain:body allometry. These problems lead us to advocate for a "piece-meal" approach (choosing equations based on performance across a size range of interest) for narrowly-focused studies but for ECV not to be converted to brain mass in broadly interspecific studies.

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### Personality and Alternative Mating Strategy in Male Japanese Macaques (*Macaca fuscata*)

NICHOLE BIGGS, KYLEN N. GARTLAND and FRANCES J. WHITE

Anthropology, University of Oregon

In a non-human primate social system, males competing for reproductive success may utilize some form of alternative mating strategies to secure reproductive opportunities. Individual-specific behaviors with stable patterns among primates is referred to as personality. Male behaviors such as female directed aggression, and affiliation used to define a personality are also used to define alternative mating strategies therefore we predict concordance in male personality and alternative mating strategies. We examined personality domains to see if they function as alternative mating strategies in semi-free ranging male Japanese macaques (*Macaca fuscata*) at the Oregon National Primate Research Center. We collected 512 hours of focal follow data on 17 adult males. Using principal component analyses, we identified five distinct personality domains. We used genetic paternity data to assess variance in fitness. We used two-way analysis of variance to test for fitness differences among personality domains and dominance ranks. We compared the frequency of live offspring for males by age group and personality domains using G-tests of Independence. There was no significant variation in fitness according to personality domains or dominance ranks ( $F=0.035$ ,  $df=5$ ,  $p=0.8681$ ). There was a dependence of number of offspring on younger males ( $G=21.925$ ,  $df=8$ ,  $p<0.01$ ) for they have higher reproductive success regardless of personality domain. Based on these results, males of all personality domains had equal reproductive success. Furthermore, the degree of fitness benefits by personality domains did not significantly vary from those benefits conferred by high dominance ranks. We conclude that personality reflects alternative mating strategies within this population.

### Genomic insights into Andean high-altitude adaptive phenotypes

ABIGAIL W. BIGHAM<sup>1</sup>, AINASH CHILDEBAYEVA<sup>2</sup>, JENNA L. ISHERWOOD<sup>3</sup>, JULIEN WEINSTEIN<sup>4</sup>, MELISA KIYAMU<sup>5</sup>, GIANPIETRO ELIAS REVOLLENDO<sup>7</sup>, MARIA RIVERA-CHIARA<sup>5</sup>, FABIOLA LEON-VELARDE<sup>5</sup>, FRANK S. LEE<sup>6</sup> and TOM D. BRUTSAERT<sup>7</sup>

<sup>1</sup>Anthropology, UCLA, <sup>2</sup>Archaeogenetics, Max Planck Institute for Science of Human History, <sup>3</sup>Human Genetics, Wayne State University, <sup>4</sup>Anthropology, University of Michigan, <sup>5</sup>Physiology, Universidad Peruana Cayetano Heredia, <sup>6</sup>Pathology and Laboratory Medicine, University of Pennsylvania, <sup>7</sup>Exercise Science, Syracuse University

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Andeans have inhabited the Andean Altiplano (average elevation of 12,000 feet) for up to 11,000 years. This high-altitude environment is characterized by chronic hypoxia that challenges human survival and reproduction. Nevertheless, Andeans have thrived in the hypoxic environment of high altitude, displaying unique adaptations including elevated hemoglobin concentration, elevated arterial oxygen saturation, and a blunted hypoxic ventilatory response. Their ability to overcome the chronic hypoxia of high altitude provides an exceptional opportunity to understand the genetic mechanisms underlying their unique altitude-adaptive phenotypes. To refine our understanding of the Andean pattern of high-altitude adaptation, we recruited three study groups with varying developmental exposures to high altitude including: 1) Quechua ancestry born and raised at high altitude, 2) Second-generation low-altitude down migrants of Quechua ancestry, and 3) First-generation low-altitude down migrants of Quechua ancestry. Pulmonary and hematological phenotypic data were collected from each study participant at the time of enrollment. Using a combination of microarray SNP genotype data, whole genome sequencing data, and RNA sequencing data, we have identified single nucleotide variants (SNVs) that contribute to altitude-adaptive phenotypes. In particular, we identified SNP variation in *EGLN1* that affects the capacity for oxygen transport and/or oxygen uptake during aerobic exercise. Ongoing research is working towards identifying the functional consequence of altitude-adaptive variation. Together, these results provide key insights into the patterns of genetic adaptation to high altitude, shed light on genetic variation contributing to complex phenotypes, and are of potential importance for public health given HIF-pathway involvement with various disease processes.

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### **Paleopathological analysis of an historical urban population from Montréal: Exploring the interactions between vitamin D deficiency and other diseases.**

ROSE-ANN BIGUÉ<sup>1</sup>, ISABELLE RIBOT<sup>1</sup> and CHARLOTTE ROBERTS<sup>2</sup>

<sup>1</sup>Anthropology, Université de Montréal,  
<sup>2</sup>Archaeology, Durham University

Bioarchaeological studies on vitamin D deficiency have mostly been conducted on 19<sup>th</sup> century European skeletal collections and have not so far been explored extensively in Canadian populations. Furthermore, the possible links between vitamin D deficiency and other diseases have been poorly investigated. To fill this gap, this analysis of 54 individuals from the Saint-Antoine cemetery in Montréal (1799-1854) concentrates on exploring the possible link between vitamin D

deficiency during infancy and mortality, biological sex, urban environment and health deterioration later in life. It is possible that industrializing Montréal underwent sanitary and environmental deteriorations which increased the prevalence of vitamin D deficiency. Moreover, clinical studies seem to indicate a link between vitamin D deficiency and various diseases. The methodology is composed of a skeletal inventory, macroscopic and radiographic observations of pathological lesions and a histologic examination of interglobular dentin (IGD) in M<sub>1</sub>. The results indicate a high prevalence of individuals presenting vitamin D deficiency during infancy, with 57.4% (excluding the degree 1 of IGD) to 79.6% (including the degree 1 of IGD). The majority of the episodes occurred at 6-12 months-old and 2.5 years-old. Vitamin D deficiency during infancy was not correlated with demographic parameters, nor with health status deterioration later in life, except possibly for linear enamel hypoplasia and non-specific joint diseases. Fewer but more severe cases of IGD are present in all more recently buried exhumed individuals. This research provides relevant data on vitamin D deficiency patterns and impacts on an historical Canadian population.

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### **Bornean orangutan (*Pongo pygmaeus wurmbii*) patterns of frugivory and the relation to seed dispersal and seed predation**

ANDREA BLACKBURN<sup>1</sup>, TRI WAHYU SUSANTO<sup>2</sup> and CHERYL D. KNOTT<sup>1,3</sup>

<sup>1</sup>Department of Anthropology, Boston University,  
<sup>2</sup>Department of Biology, Universitas Nasional,  
<sup>3</sup>Department of Biology, Boston University

Seed dispersal is important for forest growth, maintenance, and regeneration. Orangutans are large-bodied frugivores with ecological roles as seed predators and seed dispersers. However, little is known about orangutans' ecological roles and how they relate to orangutans' patterns of frugivory. We investigated Bornean orangutans' (*Pongo pygmaeus wurmbii*) ecological roles at the Cabang Panti Research Station in Gunung Palung National Park, Indonesian Borneo. We collected orangutan feces (n=401) and analyzed them for intact seeds (August 2018 to March 2020). We observed orangutan fruit handling behavior for 306 feeding bouts for 53 fruit genera to measure how often orangutans swallow, spit, or predate seeds. We used Ivlev's Electivity Index to analyze fruit preference using long-term feeding data and phenology data (2014-2019). Lastly, we combined fruit preference with fruit handling behavior using the seed dispersal effectiveness framework to identify which fruit taxa were most effectively dispersed. Orangutans dispersed seeds in 71.8% of fecal samples with a mean of 27.9 ±4.5 (SD=0.95) seeds (>2mm) per fecal sample.

Orangutans predated seeds more often than spitting or swallowing seeds (predating= 42.1% of fruit feeding time; spitting= 21.8%; swallowing= 12.5%; mixed behaviors= 10.6%, not observed=12.0%). Additionally, the top five preferred fruit genera, (*Dialium*, *Sindora*, *Scaphium*, *Magnifera*, and *Spatholobus*) were highly predated (0 to 5% of seeds dispersed). We identified *Alangium* and *Tetramerista* as the most effectively dispersed genera, orangutans frequently dispersed and preferred these fruits. We found orangutans are frequent seed predators, but this overlaps with their seed dispersal role, and we describe orangutans' seed dispersal contribution.

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### **Creating an inclusive learning environment for blind and low vision students in biological anthropology laboratory courses**

SAMANTHA H. BLATT  
Anthropology, Idaho State University

Blind and low vision (BLV) students are marginalized and underrepresented in scientific fields and higher education in general. This is not for lack of interest. Throughout schooling, they encounter limited accessible opportunities to experience science or encouragement to pursue life-long scientific literacy. Science is a core requirement at universities, but laboratory courses often normalize visual phenomena exclusively, making them inaccessible to BLV students. Use of assistive technology (AT) and fostering a sense of belonging has demonstrated improved retention and performance of BLV students. However, educators are infrequently trained to accommodate such needs and, in the use, or availability of AT. While BLV inclusivity measures exist in some disciplines with university laboratory courses, standard practices and resources do not exist for biological anthropology. Here I present my experiences and approach, modifications, and technologies used to accommodate a blind student in a mid-sized (40 student) biological anthropology laboratory course for non-majors. Through qualitative, quantitative, and ethnographic assessment of the BLV and sighted students, I will present examples of using a combination of braille, tactile, auditory, haptic, and kinesthetic adaptations to laboratory assignments. Additionally, I will discuss some tips and guiding practices which fostered a sense of belonging, produce attitudinal gains, and enhanced performative success of the BLV student and their classmates in this laboratory course. The tactile nature of many aspects of biological anthropology make it well suited

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to serve as the go-to science course for BLV students, lowering barriers to academic success and introducing anthropological sciences to the blind.

*Supported by a Teaching Innovation Grants from the Program for Instructional Effectiveness, Idaho State University.*

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### Connections between climate, fire, and dietary diversity in remote Western Australia

REBECCA BLIEGE BIRD

Anthropology, Pennsylvania State University

People whose livelihoods are entangled with local ecological communities are likely to feel the effects of climate change most severely, as shifts in rainfall and temperature change resource availability in ways that impinge on food sovereignty. The effects of climate change on food sovereignty are likely not to be felt directly, but rather are more likely to be expressed through mediating factors, such as changes to plant and animal communities. One significant mediating factor, changes to fire regimes, has not been widely explored, even in regions where fire regimes are rapidly changing, causing corresponding shifts to community structure. Here, we use structural equation modelling of fire patterning as revealed in remotely sensed imagery, in conjunction with ethnographic observations of the production and distribution of traditional foods, to assess the impact of climate-driven changes in fire regimes on diet quality in a remote Aboriginal community in the Western Desert of Australia. Our results show that landscape heterogeneity, in the form of fire-created patchiness, substantially increases the per-capita consumption, as well as the diversity of traditional resources consumed on foraging trips in both the wet and dry seasons. Changes to fire patterning are in turn, directly affected by interactions between rainfall and the cost of traveling to new places to hunt and burn. Because cultural burning to improve hunting returns is the primary force creating landscape heterogeneity, as well as serving as an expression of belonging and ritual caretaking of country, being able to burn not only increases dietary quality, it is also central to fostering environmental justice and autonomy in the face of the trauma of settler colonialism.

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### New wisdom from third molars: Strange variation in human molar size, and its impact on eruption and evolution

JULIA C. BOUGHNER<sup>1</sup>, DENVER F. MARCHIORI<sup>1</sup> and GARNET V. PACKOTA<sup>2</sup>

<sup>1</sup>Anatomy, Physiology & Pharmacology, University of Saskatchewan, <sup>2</sup>College of Dentistry, University of Saskatchewan

The inhibitory cascade model (ICM) is a tenet of mammalian molar morphogenesis that predicts that the larger the first molar (M1) is relative to the size of adjacent molars (M2 and M3), the smaller the M3 and the later its initiation. Worldwide, contemporary modern humans frequently present with impacted M3s that, for unclear mechanisms, are at higher risk of impaction when they develop later. Unexpectedly, our radiographic sample of 323 oral quadrants from 99 dental patients presents 13 molar size ratio patterns at different frequencies (e.g., M1>M2>M3 in only 31.6% of cases) that reflect the maxilla versus the mandible. This pattern diversity includes non-linear size progressions (e.g., M1>M2<M3), and up to four patterns in the same person's mouth. Further, we report that M3 size is predicted not by M1 size but by M2/M1 ratio and absolute M2 size. We also report that M1 size does not predict early versus late M3 development, or proper M3 emergence versus impaction. Our findings that contemporary modern humans do not show one stereotypic molar size ratio pattern indicate that molar size is genetically softwired in recent humans, and subject to oral quadrant-specific and jaw-specific effects. This divergence from the ICM implies relaxed selection pressures leading to weaker developmental integration, stability, and canalization of *Homo sapiens* molar sizes and molar proportions that nonetheless does not impact M3 eruption. The lack of one stereotypical molar size pattern for contemporary humans may confound predictions of molar size in fragmented fossil human specimens.

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### Identifying Trans Individuals From Skeletal Remains: Indicators Of Gender Affirming Interventions

ANGELICA BOURGEOULT

Lady Davis Institute of Medical Research, Jewish General Hospital

Despite disproportionate homicide rates of trans-identifying individuals, there are currently no standards for determining whether an individual has undergone gender affirming interventions (GAI) from skeletal evaluation. The purpose of this paper is fourfold: to identify (1) skeletal indicators for identifying trans individuals, (2) associated surgical devices, (3) differentiations between trans and cisgender (cis) surgeries, and lastly, (4) a proposed method for "sexing" trans skeletal remains. In terms of the skeletal impacts of endocrinal GAI, changes in cortical and trabecular areal and volumetric bone mineral density absolute values and z-scores / t-scores, bone mass, area, thickness, and turnover, as well as endosteal and periosteal circumference were analyzed. Pubertal suppression and cross-sex hormonal therapy,

prior to and following gonadectomy, led to significant differences in bone density, morphology, and morphometry between trans individuals and their cis peers. On the other hand, surgical indicators of GAI were determined by analyzing the effects of facial feminization / masculinization surgery and urological / gynecological gender confirmation surgeries. The most reliable surgical indicators in transwomen consist of combined evidence for bone shaving, various osteotomies, and breast implants. The most durable postmortem surgical devices likely to lead to the positive identification of a transman are the combined presence of facial implants and/or bone grafts, and penoscrotal prostheses. The more the presence of extensive bilateral gender affirming indicators, the higher the likelihood of ascribing the correct "sex" to an unidentified trans individual. This research highlights the importance for forensics to remain up-to-date with innovative medical interventions of increasing popularity.

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### Investigation of cuboid elongation and variation in tarsal proportions of early primates

MADISON M. BRADLEY-CRONKWRIGHT<sup>1</sup>, DOUG M. BOYER<sup>1</sup> and JONATHAN I. BLOCH<sup>2</sup>

<sup>1</sup>Evolutionary Anthropology, Duke University,

<sup>2</sup>Florida Museum of Natural History, University of Florida

There has been little inquiry into whether the cuboid contributes to midfoot elongation in primates. To investigate how tarsal proportions within the midfoot vary between primates and their outgroups, we analyzed 22 genera (9 Eocene primates, 9 extant strepsirrhines and 4 outgroup mammals) using multi-level Bayesian modeling. This allowed for an estimate of the effect of calcaneal elongation (distal calcaneus length/total calcaneus length) and calcaneocuboid facet area (a feature correlated with absolute size) on cuboid proportions within the midfoot. While the scaling factor of cuboid length to calcaneocuboid facet area is identical between outgroup mammals and primates (outgroup:  $\beta=0.46$ ,  $sd=0.04$ ; primates:  $\beta=0.46$ ,  $sd=0.03$ ), primates as a group have relatively long cuboids (outgroup:  $\alpha=0.54$ ,  $sd=0.08$ , primates:  $\alpha=0.73$ ,  $sd=0.08$ ). The proportional length of the cuboid in the midfoot is inversely correlated with calcaneal elongation in primates (primates:  $\beta=-0.28$ ,  $sd=0.08$ ), even when controlling for facet area. This relationship between calcaneal elongation and cuboid proportions is not observed in outgroups (outgroup:  $\beta=0.17$ ,  $sd=0.18$ ), however the overall range of calcaneal elongation is reduced in outgroup mammals. Among Eocene genera, *Archicebus* and *Teilhardina* do not follow the pattern of other primates. *Archicebus* and *Teilhardina* have long cuboids that contribute substantially more to the elongation of their midfoot than would be expected for their degree of calcaneal elongation.

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We interpret this result to suggest that initial changes in calcaneal elongation were accompanied by cuboid elongation, which maintained midfoot tarsal proportions. In later prosimians, variation in these bones became decoupled.

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### Ancient positive selection in bonobos (*Pan paniscus*) and chimpanzees (*Pan troglodytes*)

COLIN M. BRAND<sup>1</sup>, FRANCES J. WHITE<sup>1</sup>, NELSON TING<sup>1,2</sup> and TIMOTHY H. WEBSTER<sup>3</sup>

<sup>1</sup>Anthropology, University of Oregon, <sup>2</sup>Institute of Ecology and Evolution, University of Oregon, <sup>3</sup>Anthropology, University of Utah

Bonobos and chimpanzees diverged ~1.88 Ma and, despite being sister taxa, exhibit striking differences in behavior and ecology. Variation in behavior and ecology also occur between the four chimpanzee subspecies. Despite this information, it is not clear which of these differences may have been adaptive, and a knowledge of the genetic basis of these differences is still lacking. A genomic study of signatures of positive selection would yield a set of candidate genes that potentially underlie adaptive phenotypic differences between lineages. In this study we investigate ancient selection across *Pan* taxa. We used genomic data from 71 individuals representing all five *Pan* lineages to identify single nucleotide variants (SNVs) that fell within coding sequences of the chimpanzee genome. Biallelic SNVs were classified as 1) fixed or polymorphic based on allele frequencies within each population and 2) synonymous or non-synonymous estimated from transcripts. We conducted McDonald-Kreitman tests per gene for each lineage, excluding genes with poor read depth across >50% of the gene, and assessed significance using Fisher's exact test. The majority of statistically significant genes were under purifying selection, but we identified 34 genes under positive selection in bonobos, 52 in eastern chimpanzees, 57 in central chimpanzees, 40 in Nigeria-Cameroon chimpanzees, and 19 in western chimpanzees. The identification of positively selected genes in these taxa contributes to better estimating the timing of lineage-specific adaptations, reconstructing the *Pan* common ancestor, and recognizing potential selective pressures for these adaptations during a key time period in chimpanzee and human evolution.

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### Population-based variation in shaft-to-end proportions of modern human limb bones

MARIANNE F. BRASIL<sup>1,2</sup>, TESLA A. MONSON<sup>3</sup> and CAT E. TAYLOR<sup>2,4</sup>

<sup>1</sup>Berkeley Geochronology Center, Berkeley, CA, <sup>2</sup>Human Evolution Research Center, University of California Berkeley, Berkeley, CA, <sup>3</sup>Department of

Anthropology, Western Washington University, Bellingham, WA, <sup>4</sup>Department of Integrative Biology, University of California Berkeley, Berkeley, CA

Many aspects of the human skeleton have been shown to vary allometrically with body size. Particular attention has been paid to limb segment length, articular surface size, and cross-sectional morphology, in part because of their roles in estimating stature and mass, and inferring activity patterns, respectively. Far less attention has been paid to how intra-element proportions vary with body size. We tested the hypothesis that shaft-to-end proportions of modern human limb bones vary allometrically with femoral head diameter (FHD), a proxy for body mass. We examined this relationship in modern humans from five geographic regions, with mean estimated body masses that range between 58-64 kg: southern African (n=34), Egypt (n=32), Jordan (n=39), Portugal (n=30), and California (n=41). We assessed shaft-to-end proportions for the humerus, radius, femur, and tibia using a ratio of distal epiphyseal breadth to midshaft circumference. We quantified the relationship between this ratio and FHD using linear regressions on log-transformed values, and we evaluated differences in the relationships between sexes and between populations via ANCOVA. In all cases, proportions are very weakly correlated with FHD, and the allometric relationship varies by sex and population, only rarely reaching significance (at p=0.05). We did not find sex to be a significant effect for any of the limb bones (p>0.05); in contrast, population had a significant effect on all four proportions (p<0.01). Variation in these proportions across human populations may be underlain by relative independence of the epiphyses and diaphysis during development, which carries implications for the evolution of intra-element proportions.

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### Resiliency and the impact of stress accumulation over the life course in post-medieval London

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

Resiliency in biological and ecological systems is conceptualized as the ability to absorb disturbances, maintaining function even while undergoing changes. This project uses a life course approach together with the concept of resiliency to examine how socioeconomic status mediated the effects of physiological stress in Industrial-era London. The data for this project come from the Wellcome Osteological Research Database (Museum of London); we include data from three post-medieval London cemeteries:

Chelsea Old Church (n=42), and St. Brides Crypt (n=77), both of which served high-status populations, and St. Brides Lower (n=91), which represents a poorer parish in London. ANOVA was used to evaluate the covariance of linear enamel hypoplasia (LEH) and femoral length (as a proxy for achieved adult stature), while T-tests and Fisher's exact tests were used to examine differences in frequencies of each stress marker in four adult age-at-death groups. Neither LEH frequency nor stature was significantly associated with sex, status, or age-at-death. However, overall, individuals with LEH were shorter than those without LEH, and this relationship was significant for males regardless of status. These results highlight the potential for early life stressors (LEH) to alter stress responses later during adolescence (decreased femoral length) as conceptualized in tradeoffs within life history models. However, both biological and cultural buffering may explain the lack of relationship with increased mortality even with experiencing early life stress, in light of weaning practices and the potential for upward social mobility in post-medieval London.

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### Ranging correlates with energy balance among red-tailed monkey (*Cercopithecus ascanius*) groups

MICHELLE BROWN<sup>1,2</sup>, MICHAEL GAFFNEY<sup>3</sup> and MELISSA EMERY THOMPSON<sup>4</sup>

<sup>1</sup>Department of Anthropology, University of California, Santa Barbara, <sup>2</sup>Department for the Ecology of Animal Societies, Max Planck Institute of Animal Behavior, <sup>3</sup>Department of Anthropology, Washington State University, <sup>4</sup>Department of Anthropology, University of New Mexico

Ranging behavior is shaped by many factors, most notably food availability, competition with other individuals and groups, and predation risk. In many species, intergroup competition and resource limitation are particularly intertwined so we predicted that, within a population, groups experiencing resource limitation live in smaller ranges and use these areas more intensively than groups experiencing little or no resource limitation. We tested this prediction with ranging data and urinary C-peptide of insulin (a biomarker of energy balance) from 6 groups of wild red-tailed monkeys in Kibale National Park, Uganda, collected from Jan 2012 – Jun 2015. We first ran a regression model for each group in each observation period to determine whether the intensity of use for individual cells within the range corresponds with the overall size of the home range and distance from the center of the home range, and included both linear and quadratic terms for distance to account for potentially nonlinear relationships. We then ran a model to test whether the resulting coefficients correlated with C-peptide levels. We found that all three factors correlated strongly with energy balance (N = 1,617 urine samples, Wald chi-squared = 460.39, DF = 6, P <

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0.001): energy balance increased with group size and decreased as the range use patterns became more centralized. These relationships indicate that ranging patterns can be used to identify group-level variation in resource limitation, and as such may be a useful tool for rapid assessments of group condition.

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### Directional asymmetry of upper limb bones between males and females in medieval Giecz, Poland

EMMA T. BRZEZINSKI<sup>1,2</sup>, MARK HUBBE<sup>1</sup> and AMANDA M. AGNEW<sup>1,2</sup>

<sup>1</sup>Department of Anthropology, The Ohio State University, <sup>2</sup>Skeletal Biology Research Lab, The Ohio State University

Lateralized behaviors attributed to “handedness” produce observable asymmetry in skeletal elements of the upper limb, which are an important indicator of functional adaptation. The purpose of this research was to characterize directional asymmetry (DA) in upper limb bones in a medieval Polish population in order to identify specific patterns in sexual division of labor.

The sample included clavicles, humeri, and radii representing adult males (n=89) and females (n=53) excavated from the early medieval (11<sup>th</sup>-12<sup>th</sup> c.) cemetery site, Gz4, in Giecz, Poland. Asymmetry generally was found to be greatest in the midshaft, followed by epiphyseal regions, and least in maximum lengths, especially in the humerus and radius. In the humerus, significant sexual dimorphism in %DA was found for maximum length (p=0.033), and epicondylar breadth (p=0.002) with females being more right-biased than males, but not in midshaft circumference (Kruskal-Wallis tests). In the clavicle, there was significant sexual dimorphism in %DA for maximum length with a left-side bias for males (p=0.019), but not for either midshaft circumference or sternal diameter. In the radius, significant differences in %DA were observed in maximum length (p=0.022), midshaft circumference (p=0.024), and distal breadth (p=0.019), with females demonstrating greater right-bias. The general lack of sex differences in midshaft asymmetry, which is most sensitive to mechanical loading, suggests that, though specific behaviors may have been different, upper limb workload may have been similarly demanding between sexes. Sex differences seen in the radius midshaft may reflect variability in functional loading of the forearm distinct from the arm and pectoral girdle.

### Genomic insights into the demographic history of capuchin monkeys

HAZEL BYRNE<sup>1</sup>, PATRICIA IZAR<sup>2</sup>, JESSICA LYNCH<sup>3,4</sup> and TIMOTHY H. WEBSTER<sup>1</sup>

<sup>1</sup>Department of Anthropology, University of Utah, <sup>2</sup>Department of Experimental Psychology, University of São Paulo, <sup>3</sup>Institute for Society & Genetics, UCLA, <sup>4</sup>Department of Anthropology, UCLA

Capuchin monkeys (Cebinae) are broadly distributed across several major biomes in Central and South America, with sympatric gracile (genus *Cebus*) and robust (genus *Sapajus*) forms in the Amazon. Biogeographical studies have suggested that robust capuchins originated in the Atlantic Forest and dispersed to other regions within the past few hundred thousand years, while gracile capuchins originated in the Amazon. The robust species in the Atlantic Forest are well-defined, however, molecular studies have questioned the distinction between robust species currently recognised in the Amazon and savanna-like biomes. To better understand the diversity of capuchins and the speciation process across these distinct biomes, we analysed high-coverage whole genome sequence data for all eight robust species and three gracile species. We then reconstructed their historical demography (PSMC, hPSMC) and assessed their genetic diversity. Our analyses revealed biome- and clade-specific patterns of diversity and changes in ancestral effective population sizes. We uncovered very high genetic diversity in the Atlantic Forest robust capuchins, but low diversity in robust species in the Amazon and savanna-like biomes with very long runs of homozygosity in some species, and extremely low diversity across gracile species. PSMC analyses indicate an identical trend in ancestral effective population sizes across robust capuchins outside the Atlantic Forest until around the past 100,000 years, suggesting very recent divergence between these forms. Hybrid PSMC analyses also suggest post-divergence gene flow between several species of robust capuchins. Together, these analyses lend insight into the speciation and demographic history of capuchin monkeys in the Pleistocene.

### Where the (Pet) Primates Are: Location of Primates for Sale in the United States

SYDNEY N. CAHOON<sup>1</sup> and MELISSA S. SEABOCH<sup>1,2</sup>

<sup>1</sup>Anthropology, University of Utah, <sup>2</sup>Anthropology, Salt Lake Community College

Despite a consensus of veterinarians and primatologists that primates should not be pets, there are over 15,000 pet primates in the US. Regulation of primate ownership is not federally mandated, but managed by states, sometimes even varying from county to county. Restrictions range from a complete ban, to some regulation, to no restrictions. The goal of this project was to understand the pet primate trade in the US, specifically, in

which states they are for sale. Data were collected from six publicly available exotic pet trade websites from June 2019 to June 2020. For each ad, we recorded the type of primate for sale and its location. We found ads for 553 primates for sale in 22 states. Florida had the most primates for sale (45.7%, n= 252), followed by Tennessee (11.8%, n= 65), Texas (11.6%, n=64), Missouri (6.7%, n=37), and North Carolina (5.6%, n=31). Of the 22 states with primates for sale, 3 states (13.6%) require a permit, 15 states (68.2%) have no restrictions for the type of primates that were for sale (only great apes/larger primates are regulated), and 4 states (18.2%) ban all pet primates. Florida, with the most primates for sale, requires a permit. Nine primates were for sale in states that ban primates. The high variability in regulations speaks to the need for federal guidelines. While a complete ban is unlikely, federal permitting could reduce the number of pet primates. While these primates are likely captive-bred, they nonetheless impact the conservation of wild populations.

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### Were Holocene southern African Hunter-gatherers/herders on the coast less active than those inland?

KIMBERLEY J. CAMERON, CHANDRA FINAUGHTY and VICTORIA E. GIBBON

Division of Clinical Anatomy and Biological Anthropology, Department of Human Biology, University of Cape Town

The postcranial skeleton of 105 Holocene southern African hunter-gatherers/herders (sAHGH) were studied for joint surface changes to better understand how subsistence and survival strategies may have impacted activity levels between those living inland vs coastal. Degenerative joint disease was graded according to severity and musculoskeletal markers according to prominence. Activity markers were prominent; considering the small body size of sAHGH, which are likely linked by to their lifestyle. No significant differences were found by sex, suggesting that gender-based divisions of labour may be over emphasised. Considering that males generally have a larger body size, this may suggest that females were more active to bear the same level of activity. Joint surface changes started young but as expected were more prominent in older individuals. Both coastal and inland people had prominent joint surface changes in the forearm and elbow; suggesting a high degree of manufacturing, handling, thrusting/throwing and resource processing. The inland sample had more degenerative joint disease on the upper limb, indicating repetitive actions of the hands and arms. The coastal sample showed more musculoskeletal markers in both the upper and lower limbs,

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but, had fewer signs of degenerative joint disease. A possible explanation is that coastal populations experienced higher biomechanical loading conferring bone strength from leading more active diverse lives. Despite the limited sample size and skewness in the number of coastal individuals, these data demonstrate the dynamic nature of sAHGH and indicate that ecological influences on behavioural patterns are variable.

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### Gut microbial diversity and composition in seven cercopithecids from Tai Forest, Ivory Coast

TESSA H. CANNON<sup>1</sup>, LUKE FANNIN<sup>2</sup>, W. SCOTT MCGRAW<sup>1</sup> and VANESSA HALE<sup>3</sup>

<sup>1</sup>Department of Anthropology, The Ohio State University, <sup>2</sup>Department of Anthropology, Dartmouth College, <sup>3</sup>Department of Veterinary Preventive Medicine, The Ohio State University

Gut microbiota fundamentally contribute to an animal's overall health and immune function. Current evidence indicates that host-microbe interactions have very likely influenced primate evolution, so the determinants of gut microbial composition and diversity, including diet, phylogeny, habitat disturbance, strata use, and social interaction, continue to be actively investigated. Here we report results from an analysis of the gastrointestinal microbial communities derived from fecal samples of seven cercopithecids living in the Ivory Coast's Tai Forest. Study taxa are *Cercocebus atys* (Sooty mangabey), *Cercopithecus campbelli* (Campbell's monkey), *Cercopithecus diana* (Diana monkey), *Cercopithecus petaurista* (Lesser spot-nosed monkey), *Colobus polykomos* (Black and white colobus), *Ptilocolobus badius* (Western red colobus), and *Procolobus verus* (Olive colobus). Preliminary analyses reveal the highest fecal DNA concentrations are found in *C. atys* and *C. campbelli*. Of the Tai cercopithecids, Sooty mangabeys and Campbell's monkeys spend the most time foraging terrestrially and in lower forest strata. Distinct microbial signatures were evident within each primate species, with the greatest similarities in microbiota observed between closely related taxa. Increased microbial diversity was also identified in predominantly folivorous species. Study of gut microbial diversity and composition in the Tai monkeys presents an excellent opportunity to decipher the interactive effects and relative contributions of diet, habitat use, and evolutionary lineage on the gut microbiome in an ecologically complex community of primates.

Fieldwork in Tai Forest was supported by National Science Foundation (BCS 0840110, 0921770, 0922429) and the Yerkes National Primate Research Center.

### The role of population-specific genotype reference panels in genetic association studies

JENNA C. CARLSON<sup>1,2</sup>, NICOLA L. HAWLEY<sup>3</sup>, HONG CHENG<sup>4</sup>, TAKE NASERI<sup>5</sup>, MUAGUTUTIA SEFUIVA REUPENA<sup>6</sup>, RANJAN DEKA<sup>4</sup>, STEPHEN T. MCGARVEY<sup>7,8</sup>, RYAN L. MINSTER<sup>2</sup> and DANIEL E. WEEKS<sup>1,2</sup>

<sup>1</sup>Department of Biostatistics, University of Pittsburgh, <sup>2</sup>Department of Human Genetics, University of Pittsburgh, <sup>3</sup>Department of Chronic Disease Epidemiology, Yale School of Public Health, <sup>4</sup>Department of Environmental and Public Health Sciences, University of Cincinnati, <sup>5</sup>Ministry of Health, Government of Samoa, <sup>6</sup>Lutia i Puava ae Mapu i Fagalele, <sup>7</sup>International Health Institute and Department of Epidemiology, Brown University, <sup>8</sup>Department of Anthropology, Brown University

Genome-wide association studies (GWAS) in isolated populations have furthered our understanding of human biology by elucidating the genetic architecture of complex traits. A key element of GWAS follow-up is the prioritization of genetic variants, which requires dense genotype maps typically obtained by genotype imputation. However, extant imputation reference panels do not adequately capture genetic variation in isolated populations, such as that of Samoa. These panels must be expanded to include haplotypes derived from population-specific whole-genome sequencing (WGS) data for imputation in Samoans to be accurate. Here we demonstrate this necessity through two examples using a Samoan-specific reference panel (SSRP) derived from WGS of 1,195 Samoans.

First, we compared the imputed genotypes for variants on 5q35.1, a known body mass index (BMI) locus, from the SSRP-based imputation to a trans-ethnic imputation that lacked Samoans in the reference panel. We observed discordant imputed genotypes at previously implicated variant, rs373863828 (SSRP-imputation MAF=27.63%, trans-ethnic imputation MAF=21.5%, true MAF=27.66%).

Secondly, we compared GWASs for lipid levels using observed genotypes to SSRP-based imputation. The SSRP-based GWAS identified a genome-wide significant association with rs200884524 ( $p=4.49 \times 10^{-8}$ ). This signal showed weak evidence of association in the GWAS without imputation, as observed genotypes were sparse in this region.

As these examples demonstrate, imputed genotype frequencies are dependent upon the reference panel, and association analyses are more powerful and informative when boosted by population-specific imputation. This work also

highlights the need to include diverse isolated populations in imputation reference panels so that imputed genotypes are not biased by unrepresentative haplotypes.

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### The pectoral girdle of StW 573 ('Little Foot') and its implications for hominin evolution

KRISTIAN J. CARLSON<sup>1,2</sup>, DAVID J. GREEN<sup>2,3</sup>, TEA JASHASHVILI<sup>1,4</sup>, TRAVIS R. PICKERING<sup>2,5,6</sup>, JASON L. HEATON<sup>2,6,7</sup>, AMELIE BEAUDET<sup>8,9</sup>, DOMINIC STRATFORD<sup>8</sup>, ROBIN CROMPTON<sup>10</sup>, KATHLEEN KUMAN<sup>8</sup>, JULIET MCCLYMONT<sup>10</sup>, LAURENT BRUXELLES<sup>11,12,8</sup> and RONALD J. CLARKE<sup>2</sup>

<sup>1</sup>Department of Integrative Anatomical Sciences, University of Southern California, <sup>2</sup>Evolutionary Studies Institute, University of the Witwatersrand, <sup>3</sup>Department of Anatomy, Campbell University School of Osteopathic Medicine, <sup>4</sup>Department of Geology and Paleontology, Georgian National Museum, <sup>5</sup>Department of Anthropology, University of Wisconsin, <sup>6</sup>Plio-Pleistocene Palaeontology Section, Ditsong National Museum, <sup>7</sup>Department of Biology, Birmingham-Southern College, <sup>8</sup>School of Geography, Archaeology and Environmental Studies, University of the Witwatersrand, <sup>9</sup>Department of Anatomy, University of Pretoria, <sup>10</sup>Department of Musculoskeletal Biology, University of Liverpool, <sup>11</sup>TRACES, French National Centre for Scientific Research, Jean Jaures University, <sup>12</sup>French National Institute for Preventative Archaeological Research (INRAP)

The ca. 3.67 Ma adult skeleton known as 'Little Foot' (StW 573), recovered from Sterkfontein Member 2 breccia in the Silberberg Grotto, is remarkable for its morphology and completeness. Clavicles and scapulae of StW 573 offer opportunities to assess morphological and functional aspects of a nearly complete *Australopithecus* pectoral girdle. The StW 573 pectoral girdle combines features that are intermediate between those of humans and other African apes: a long and inferomedially-inflexed clavicle, suggesting a relatively high and dorsally-positioned scapula; enlarged supraspinous fossa size and shape; a relatively cranially-oriented glenoid fossa; and non-human, ape-like reinforcement of the axillary margin by a stout ventral bar. The StW 573 scapulae are smaller than those of some australopiths (e.g., KSD-VP-1/1 or KNM-ER 47000A), but larger than others (e.g., A.L. 288-1, Sts 7, or MH 2). The StW 573 scapula is similar in size to the australopith StW 431 partial scapula and also shares similar structure along its axillary margin and inferior angle. Overall, morphology of the StW 573 pectoral girdle presents numerous features that are selectively advantageous for arboreal positional behaviors, but relatively fewer of the derived adaptations toward manipulatory function that have been attributed to penecontemporaneous representatives of *Australopithecus afarensis* (i.e., KSD-VP-1/1). Considering morphologies

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of incomplete pectoral girdles from middle/late Miocene apes and consensus views on the adaptiveness of arboreal positional behaviors incorporating abducted glenohumeral joints in early Pliocene hominins, we hypothesize that the StW 573 pectoral girdle configuration is a reasonable model for that of the human-African ape last common ancestor.

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### Humans and chimpanzees exhibit divergent patterns of gut microbial diversity in early life

RACHEL N. CARMODY<sup>1</sup>, ASPEN T. REESE<sup>1,2</sup>, SARAH R. PHILLIPS<sup>3</sup>, LEAH A. OWENS<sup>4</sup>, EMILY M. VENABLE<sup>1</sup>, KEVIN E. LANGERGRABER<sup>5,6,7</sup>, ZARIN P. MACHANDA<sup>8,9</sup>, JOHN C. MITANI<sup>10,6</sup>, MARTIN N. MULLER<sup>3,9</sup>, DAVID P. WATTS<sup>11,6</sup>, RICHARD W. WRANGHAM<sup>1,9</sup>, TONY L. GOLDBERG<sup>12,13,4</sup> and MELISSA EMERY THOMPSON<sup>3,9</sup>

<sup>1</sup>Department of Human Evolutionary Biology, Harvard University, <sup>2</sup>Society of Fellows, Harvard University, <sup>3</sup>Department of Anthropology, University of New Mexico, <sup>4</sup>Department of Pathobiological Sciences, University of Wisconsin-Madison, <sup>5</sup>School of Human Evolution and Social Change, Arizona State University, <sup>6</sup>Ngogo Chimpanzee Project, <sup>7</sup>Institute of Human Origins, <sup>8</sup>Department of Anthropology, Tufts University, <sup>9</sup>Kibale Chimpanzee Project, <sup>10</sup>Department of Anthropology, University of Michigan, <sup>11</sup>Department of Anthropology, Yale University, <sup>12</sup>Global Health Institute, University of Wisconsin-Madison, <sup>13</sup>Department of Zoology, Makerere University

Gut microbial communities change markedly over human development, transitioning from low-diversity, high-variability states at birth to high-diversity, typically stable states in adulthood. Throughout the life course, gut microbes ferment complex carbohydrates, help resist pathogen colonization, and modulate the immune system. However, humans are unique among primates in that we wean early onto exceptionally digestible diets, mature slowly, and exhibit high lifelong investments in somatic maintenance. These adaptations suggest that lifetime trajectories of human-microbial relationships could differ from those of closely related primates. To test this idea, we analyzed 618 fecal samples from 166 wild chimpanzees aged 8 months to 67 years in the Kibale National Park, and compared patterns of gut microbial maturation with those established for humans. We found that gut microbial alpha-diversity ( $p < 0.001$ ), composition ( $P < 0.001$ ), and change over time ( $p = 0.006$ ) varied significantly with age. Notably, gut microbial signatures in infants  $< 2$  years old ( $n = 9$ ) were distinct across all metrics. Infant chimpanzee and infant human guts were enriched in similar taxa (e.g., *Bifidobacterium*, *Streptococcus*, *Bacteroides*,

*Rothia*, *Collinsella*; all  $p < 0.05$ ) and, like humans, chimpanzee gut microbial communities exhibited higher interindividual variation in infancy versus later in life ( $p < 0.001$ ). However, in stark contrast to human infants, chimpanzee infants harbored extremely high-diversity (speciose) gut bacterial communities compared to older conspecifics (all  $p < 0.01$ ). Interspecific differences in lactation, diet, and immune function may contribute to divergent early life gut microbial diversity in humans and chimpanzees. Future work will illuminate the phenotypic consequences of these early life differences and whether the human pattern is derived.

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### Soil-transmitted helminth infections are associated with lower levels of inflammatory cytokines among the Shuar of Amazonian Ecuador – Implications for COVID-19 outcomes in helminth endemic areas

TARA J. CEPON-ROBINS<sup>1</sup>, THERESA E. GILDNER<sup>2,3</sup>, MELISSA A. LIEBERT<sup>4</sup>, SAMUEL S. URLACHER<sup>5,6</sup>, FELICIA C. MADIMENOS<sup>7</sup>, LAWRENCE S. SUGIYAMA<sup>8</sup> and J. JOSH. SNODGRASS<sup>8</sup>

<sup>1</sup>Anthropology, University of Colorado Colorado Springs, <sup>2</sup>Anthropology, Washington University in St. Louis, <sup>3</sup>Anthropology, Dartmouth College, <sup>4</sup>Anthropology, Northern Arizona University, <sup>5</sup>Anthropology, Baylor University, <sup>6</sup>Child and Brain Development Program, CIFAR, <sup>7</sup>Anthropology, Queens College, <sup>8</sup>Anthropology, University of Oregon

Soil-transmitted helminths (STHs) manipulate host immune systems to increase parasite survivability, leading to immunosuppression and reduced inflammation. A leading cause of death from the ongoing COVID-19 pandemic – caused by SARS-CoV-2 – is the cytokine storm, an uncontrolled inflammatory response to the virus. COVID-19 outcomes are highly variable depending on age and pre-existing health conditions. 24% of the world's population suffer from chronic STH infections, the majority in developing countries. Understanding how immunoregulatory effects of STH infection may alter COVID-19 outcomes is critically important from both scientific and public health perspectives. Here, we test relationships between STH infection and cytokine storm-related inflammatory cytokines among Indigenous Shuar of Amazonian Ecuador. We hypothesize that STH infection will be associated with reduced circulating levels of inflammatory cytokines. Stool and dried blood spot (DBS) samples were collected among 113 Shuar adults (ages 15-86 years) between 2011 and 2014. Two STH species (*Ascaris lumbricoides*, *Trichuris trichiura*) were identified from stool. Pro-inflammatory cytokines interleukin-6 (IL-6) and C-reactive Protein (CRP) were measured from DBS. Models controlled for age, sex, and BMI. *Ascaris*-infected participants

had lower CRP levels than uninfected participants ( $p < 0.05$ ). Further, relationships between cytokines varied based on infection. For uninfected participants, IL-6 was positively associated with CRP ( $p < 0.05$ ). While not significant, this relationship was reversed in *Ascaris*-infected participants. Because IL-6 triggers CRP production, these findings suggest that STH infection reduces downstream systemic inflammation. The immune response to STHs may alter pro-inflammatory cytokine profiles, with implications for COVID-19 severity in STH-endemic regions.

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### The relative contribution of skeletal and dental indicators for the precision of juvenile age estimations

MARIANNA S. CERVANTES and HUGO F.V. CARDOSO

Archaeology, Simon Fraser University

Precise age estimation of juveniles in forensic anthropology is essential to aid in identification. Both skeletal and dental elements are employed in searching for precise results. This study examines which skeletal and dental indicators provide the greatest relative precision in a known sex and age sample of 89 individuals between 0 and 12.9 years of age. Diaphyseal lengths and both deciduous and permanent tooth lengths were collected as estimators of chronological age. Linear regression analysis with classical calibration was used to develop single bone and single tooth age estimation models. The prediction errors of each model were used as a measure of the precision of skeletal and dental elements. Principal Component Analysis (PCA) was performed to determine which skeletal and dental variable contributed the most to the relationship with age. PCA tests were run on each long bone compared to each dental element, identifying relative correlations with the PC1. In younger individuals, it was found that dental variables were generally more precise, but long bones outperformed some later forming dental elements. In older individuals, early forming dentition has the greatest precision of all measures, but some long bones are more precise, outperforming some later forming dental elements. The regression results are generally consistent in the PCA analyses, in that dental variables seem to contribute most more often than skeletal variables to the relationship with age. This study confirms the precision of early-forming dental elements in age estimation and provides insight into the relative precision of specific dental and skeletal elements.

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## Residential Data on Child Maya Sacrificial Victims: Strontium Isotope Testing of Deciduous Molars

AMY M. CHAN

Anthropology, California State University, Los Angeles

The role of children in Maya human sacrifice has become an increasingly important topic in bioarchaeological research as 68 percent of the individuals from the Mexican Cenote of Sacrifice assemblage from Chichen Itza was determined to be juvenile. The Midnight Terror Cave (MTC), Belize assemblage also produced large numbers of juveniles. Strontium isotope testing of permanent molars from MTC found that as many as a third of the individuals may have come from outside the Belize River Valley. The 16<sup>th</sup> century inquisitional records, however, suggest that the ideal age for victims is six. Thus, the analysis of permanent teeth does not provide information on this younger cohort.

To determine location of origin for younger victims, two deciduous molars were tested for Strontium isotope signatures. The molars were aged according to eruption, photographed, cast in molding material, and sent to a stable isotope lab. The isotope ratios indicated that the victims came from outside of the Belize River Valley. The two children came from the Northern Lowlands and the Central Maya Area respectively. The younger victims of MTC could have been procured through gifting between guardians and *caciques*, purchase, or kidnapping while the infants were more likely carried by their mother or women acting as wetnurses. This confirms the ethno-historic accounts of Maya child sacrifice and provides a more detailed understanding of the pre-sacrifice process.

Funding provided by California State University, Los Angeles Graduate Resource Center

## A content analysis of bioarchaeological articles in the American Journal of Physical Anthropology from 2007 to 2018

COLLEEN M. CHEVERKO<sup>1</sup>, MADELYN K. GREEN<sup>2</sup> and MARK HUBBE<sup>2,3</sup>

<sup>1</sup>Division of Biomedical Sciences, Edward Via College of Osteopathic Medicine-Louisiana,

<sup>2</sup>Department of Anthropology, The Ohio State University, <sup>3</sup>Instituto de Arqueología y Antropología, Universidad Católica del Norte

The introduction, development, and application of social and biological theories that transcend the biocultural approach have gained considerable attention in bioarchaeology over the past decade. This study reports the results of a survey of 562 bioarchaeologically-focused articles published in the *American Journal of Physical Anthropology* from January 2007 to December 2018. Ten theoretical frameworks were explored using a critical text analysis. 25.8% of papers published

during this 12-year period engaged with one or more of these frameworks, with ranges for individual frameworks encompassing 0 to 11.6% of articles. In addition to raw frequencies of each framework, theoretical engagement by publication type (i.e., hypothesis test, methodological, case studies, and theoretical/review papers), data type (i.e., violence/trauma, mobility, health/stress, diet, and activity), and methodology (i.e., microscopic skeletal, macroscopic skeletal, aDNA, and biogeochemistry) were explored. The rate of theoretical engagement was higher in hypothesis tests and theoretical/review papers than the other two categories ( $p < 0.05$  for these comparisons). However, the rate of theoretical engagement was roughly equivalent by data type and methodology ( $p > 0.05$  in all pairwise comparisons). We also explore interactions between citation rate and use of theory over the 12-year period to explore the importance of theoretical engagement on future impact to the field. These results suggest that bioarchaeology studies, irrespective of their methodological focus, have benefited from the inclusion of multidisciplinary theoretical frameworks over the 12-year period, establishing a promising trajectory for future studies and publications in bioarchaeology in the current decade.

## States of Exception, Structural Vulnerability, and Resiliency: The Global Maternity Care COVID-19 Task Force Project

MELISSA CHEYNEY<sup>1</sup> and SARASWATHI VEDAM<sup>2</sup>

<sup>1</sup>Anthropology, Oregon State University, <sup>2</sup>Midwifery, University of British Columbia

Over the last decade, dismal maternal mortality rates, especially for racial and ethnic subpopulations across the low-to-high-resource-nation continuum, have highlighted health systems' shortcomings. Globally, early in 2020, these deficiencies began to collide with the COVID-19 crisis— a combination that heightened and exposed existing inequalities, systems failures, and fractures in service delivery. The COVID-19 pandemic abruptly altered the maternity landscape everywhere as overtaxed systems struggled to mount effective, well-organized responses to the crisis in all but a handful of communities. In April of 2020, a global task force formed with the goal of developing a template for the reorganization of community midwives, health workers, and rapid response units to safely triage maternity care. During this panel, we will share stories from the field that highlight not only the gendered structural vulnerabilities the pandemic exposed, but also the extraordinary ways communities came together to push back against the authoritarian regimes and states of exception that failed to meet the needs of their citizens at nearly every turn. A focus on community responses at the intersections of maternity care and COVID-19 reveal the resiliency potential of community-led

responses and offer several critical lessons for the state apparatus. As we anticipate additional waves of the pandemic, it is critical that we see and elevate not just the structural vulnerabilities that have determined patterns of mortality and suffering, but also the agency, innovation and brilliance that have shaped community-led responses on the ground for them, we argue, hold the keys to effective future preparedness.

## Infant and Children Feeding Practices in the Precolonial Caribbean: A cross cultural analysis

YADIRA CHINIQUE DE ARMAS<sup>1</sup> and JASON LAFFOON<sup>2</sup>

<sup>1</sup>Anthropology, The University of Winnipeg,

<sup>2</sup>Archaeology, Leiden University

Feeding practices, including breastfeeding and weaning, of infants and children in the Antilles were highly variable and influenced by an emergent symbiosis of biology and culture. In this paper, we analyzed published stable isotope data derived from bone collagen and teeth enamel ( $\delta^{15}\text{N}$ ,  $\delta^{13}\text{C}_{\text{coll}}$ ,  $\delta^{13}\text{C}_{\text{en}}$ ) in non-adults and adults from 24 Antillean and Mesoamerican populations to examine the diversity in weaning and post-weaning food choices among circum-Caribbean groups. Based on the WARN Model parameters, the age at the start of weaning ( $t_1$ ), and the duration of the process ( $t_2 - t_1$ ), was variable among Caribbean populations making it difficult to identify clear patterns. In general terms, statistically significant differences in dietary practices were identified between Antillean and Mesoamerican populations likely related to the higher importance that maize had for Mayan people. Within the Antilles, statistically significant differences were identified between groups for carbon and nitrogen, supporting that a greater diversity in dietary practices existed than previously acknowledged. Infants and children from the Antilles had a mixed and variable diet where  $\text{C}_3$  based resources were more abundant. Differences between non-adult and adult populations indicated that infants and children had a diet where some typical adult food was not included (or at least not in the same proportions). This observation suggests that a more refined approach, taking into account different lines of archaeological and bioarchaeological evidence, and recognizing the role of individual variability, is necessary to understand cross-regional differences in subsistence strategies and food consumption patterns.

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### The influence of climate and population structure on East Asian skeletal morphology

ELIZABETH O. CHO<sup>1</sup>, LIBBY W. COWGILL<sup>1</sup>, GREGORY E. BLOMQUIST<sup>1</sup> and KEVIN M. MIDDLETON<sup>2</sup>

<sup>1</sup>Department of Anthropology, University of Missouri, <sup>2</sup>Department of Pathology and Anatomical Sciences, University of Missouri

The impact of differing climate conditions on the proportions of the human body have been widely studied, particularly in regard to Bergmann's and Allen's rules. While trends vary clinally across Africa and Europe and appear more muted in the Americas, an evaluation of ecogeographic body proportions throughout Asia is largely absent. Additionally, studies often focus solely on contrasting cranial or postcranial traits between populations, but few include the evaluation of both regions together, which has led to conflicting findings. Although past research tended to consider body form differences primarily in regard to varying magnitudes of directional selection due to climatic factors, recent publications have highlighted the increasingly complex relationship between the skeleton, climate, neutral evolutionary forces and population history. For this study, linear measurements of the cranium, mandible, pelvis, limbs, hands, and feet were collected on individuals (N=957) from multiple populations throughout Asia (Mongolia, China, Korea, Japan, Taiwan, Thailand, and the Philippines) to allow for the evaluation of morphological variation of the body as a whole. Genetic variation data from appropriately matched living populations was used to account for the influence of neutral evolutionary forces and population history on skeletal proportions. Both skeletal and genetic data were combined with weather data from each location for analysis using a mixed-effects model. The results of this analysis indicate that different areas of the body have variable relationships to climate. This further emphasizes the need to view organisms as integrated wholes as opposed to discrete regional or anatomical units.

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### Development & Social Dynamics regarding Dispersal in wild Javan gibbons (*Hylobates moloch*)

AHYUN CHOI<sup>1</sup>, JAE CHUN CHOE<sup>2</sup> and ANI MARDIASTUTI<sup>3</sup>

<sup>1</sup>Interdisciplinary Program of EcoCreative, Ewha Womans University, <sup>2</sup>Division of EcoScience, Ewha Womans University, <sup>3</sup>Department of Forest Resources Conservation and Ecotourism, IPB University

As immature individuals grow, intra-group competition may increase because of limited food resources and mates in the natal group, resulting

in age-related changes in social behavior and offspring's dispersal in group-living animals. To test how social dynamics, which are related to intra-group competition, changes according to development of offspring, we investigated relationships between parents and offspring in three groups of wild Javan gibbon (*Hylobates moloch*) in Gunung Halimun-Salak National Park, in West Java, Indonesia. For two years (Nov 2016~Aug 2017, Jan 2019~Nov 2019), we collected behavioral data through focal sampling with six offspring as focal individuals, which resulted in a total of 1,888 observation hours. When we compared offspring by their age classes, subadults received more aggression in feeding context, spent more time feeding alone, spent less time in close proximity (<1m) to the adults while co-feeding, and approached less frequently toward the feeding adults. Also, subadults received more aggression and stayed farther from the same-sex adult and spent less time in grooming with the same-sex adult. Our results indicate that intra-group competition increases with offspring's age and makes subadults peripheralized from adults in Javan gibbons. We argue that increased food and mate competition may motivate subadults to disperse. Further longitudinal studies and genetic analyses will be necessary to understand more about the dispersal mechanism and its consequences at the population level in Javan gibbons.

This work was supported by Amorepacific, National Geographic Society, and The Biodiversity Foundation.

### An Allometric Approach to Digit Ratios in Non-Human Primates

AUDREY M. CHOI<sup>1,2</sup>, CASSANDRA M. TURCOTTE<sup>1,2</sup> and SUSAN C. ANTÓN<sup>1,2</sup>

<sup>1</sup>Center for the Study of Human Origins, New York University, <sup>2</sup>Anthropology, New York Consortium in Evolutionary Primatology

Although likely significant, the role prenatal androgens play in an organism's development is difficult to study because in-utero hormone levels are typically unknown. Because prenatal androgen exposure may facilitate limb patterning in vertebrates, a popular proxy for estimating prenatal androgen exposure is the 2D:4D digit ratio, which compares the length of the second and fourth manual digits. Evidence suggesting that 2D:4D ratio variation is sexually dimorphic and correlated with hormonal disorders has led researchers to use the ratio to infer the involvement of prenatal androgens in the manifestation of various traits and behaviors. However, research on human samples indicates that digit length scales allometrically with overall hand size and that the 2D:4D ratio is therefore not an informative metric. No study thus far has investigated whether this allometric relationship also exists in non-human primates, which are similarly targeted as subjects of 2D:4D ratio research. To fill this gap, we measured the second and fourth

proximal phalangeal lengths of eighteen male and thirty-three female adult rhesus macaques from the free-ranging colony on Cayo Santiago, Puerto Rico. Modelling the relationship between second and fourth phalanx lengths revealed that male and female rhesus macaques share an allometric line with a non-zero intercept. Furthermore, 2D:4D ratios decrease as overall finger lengths increase because of disproportionate increases in fourth digit length. Our results indicate that the 2D:4D ratio in macaques is mathematically skewed by this allometric pattern and thus a poor tool with which to infer prenatal androgen exposure without detailed attention to size adjustment.

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### How secondary males help or hinder primary males in two baboon societies

SHAHRINA CHOWDHURY<sup>1,2,3</sup> and LARISSA SWEDELL<sup>2,3,4</sup>

<sup>1</sup>Anthropology, Brooklyn College, CUNY, <sup>2</sup>Anthropology Program, Graduate Center, CUNY, <sup>3</sup>New York Consortium in Evolutionary Primatology, NYCEP, <sup>4</sup>Anthropology, Queens College, CUNY

Reproductive skew among males varies greatly across primate societies, as do reproductive strategies, ranging from exclusion strategies in one-male groups to aggressive competition in multi-male groups. Here we compare costs and benefits of diverse reproductive strategies in males of two closely related primates, using data from seven years of observations on hamadryas baboons (*Papio hamadryas*) in Ethiopia and two years on chacma baboons (*P. ursinus*) in South Africa. Hamadryas leader males appear to monopolize access to females in their OMUs despite the presence of followers. Chacma males queue for dominance, which accords putative priority of access to females to alpha males. We found that hamadryas leaders had longer tenures compared to chacma alpha males, and although both males had similar hourly copulation rates, hamadryas leaders obtained >90% of copulations with females in their OMUs, while chacma alpha males obtained only ~20% of copulations with females in their troop. Moreover, the presence of followers in hamadryas OMUs was associated with higher reproductive success for leader males, which was not the case for chacma alpha males. Thus, while followers enhance the fitness of hamadryas leaders, subordinate males have the opposite effect on chacma alpha male fitness. We found differences in patterns of aggression, suggesting that costs derive in both systems from the presence of subordinate males and aggressive competition. Overall, it appears that hamadryas leader males achieve higher

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reproductive output with fewer associated costs compared to chacma alpha males, but chacma males benefit from a more equitable distribution of reproduction.

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### Differences in growth and body composition between rural and urban Maya children from the Yucatan Peninsula: The importance of early-life conditions

LAUREN CHRISTOPHER<sup>1</sup>, HUGO AZCORRA<sup>2</sup>, FEDERICO DICKINSON<sup>3</sup>, KAREN KRAMER<sup>4</sup>, INES VARELA-SILVA<sup>5</sup> and AMANDA VEILE<sup>1</sup>

<sup>1</sup>Anthropology and Public Health, Purdue University, <sup>2</sup>Centro de Investigaciones Silvio Zavala, Universidad Modelo, <sup>3</sup>Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional, <sup>4</sup>Anthropology, University of Utah, <sup>5</sup>School of Sport, Exercise and Health Sciences, Loughborough University

Early-life conditions and exposures shape childhood growth, vary over space and time, and are subject to global nutritional and epidemiologic transitions. To identify these dynamic patterns, we compared early-life exposures and child anthropometry in two Yucatec Maya samples: children from rural farming and urban wage laborer families. The Maya samples vary in prenatal and household sanitary conditions as well as obstetric practices which affect growth. We collected anthropometry (height, weight, BMI, triceps skinfold) from a cross-section of 6-year-old schoolchildren (n=140). Data were collected once annually from 2011-2015 (urban, n=74 total) and from 2010-2017 (rural, n=66 total). We 1) compared rural/urban anthropometric differences, 2) modeled prenatal, obstetric and household-sanitation proxy variables (birth weight, birth mode, household crowding) to test their associations with anthropometry, and 3) analyzed secular trends in mean anthropometry across the duration of data collection. Despite having similar birthweights, urban Maya children were significantly heavier, taller, and had higher triceps skinfolds and BMI compared to rural children. The cesarean delivery rate was 47% (urban) versus 21% (rural). Birthweight was positively associated with BMI, height and weight. Birth mode was not associated with any anthropometric outcome. Crowding was negatively associated with child BMI, height and weight, with a greater effect seen in rural children. The mean height of rural Maya six-year-olds increased slightly but significantly from 2010-2017; no other secular trend was

observed. Maya children have different growth outcomes in urban and rural environments, and early-life conditions influence the growth trajectories of rural and urban children in different ways.

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### Associations of psychosocial stressors and resilience factors with DNA methylation at stress-related genes in Latinx mothers and children in a changing political climate

ELIZABETH S. CLAUSING and AMY L. NON  
Anthropology, University of California, San Diego

Psychosocial stressors can become embodied to alter biology throughout the life course in ways that may have lasting health consequences. Immigrants are particularly vulnerable to high burdens of stress, which have heightened in the current sociopolitical climate. This study is an investigation of how immigration-related stress may impact the epigenetic markers and health of Latinx immigrant mothers and children, considering recent increases in divisive rhetoric and anti-immigrant policies in the U.S. We compared DNA methylation at stress-related candidate genes (*SLC6A4* and *FKBP5*), generated via bisulfite pyrosequencing, in Latina immigrant mothers and their children with interview data in Nashville, TN from two time points spanning the 2016 presidential election. Surveys were conducted with immigrant mothers and their children (aged 5-13) between 2015 and 2016 and again in 2018. We analyzed perceived psychosocial stressors, mental health, and resilience factors in relation to DNA methylation at two stress-related genes in mothers and children (n's range from 80 pre-election to 36 post-election). We found small but significant longitudinal decreases in *FKBP5* methylation (mean difference=1.084; p-value=0.009) in only mothers. At both time points, mothers had significantly higher mean methylation at *SLC6A4* than children (p<0.001). Immigrant-related stress and fear of parent deportation associated with increased *SLC6A4* methylation in children, though other stressors and resilience factors showed inconsistent directions of effect. Social support appears protective (lower *SLC6A4* methylation) only for children with undocumented mothers pre-election (p<0.02). More research is needed to determine the role of these epigenetic differences for documenting embodiment of stress across generations.

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### Inequities in Personalizing Medicine: A Pharmacogenomics Perspective

KATRINA G. CLAW

Division of Biomedical Informatics and Personalized Medicine, University of Colorado

The integration of genomic technology into health care settings has the potential to transform health-care through increased personalization of medical decisions. In particular, pharmacogenomics research on drug disposition and response can tailor and improve medication regimens for all patients by informing tests of function altering variation in drug metabolism and transport genes. Unfortunately, Indigenous peoples remain underrepresented in genomic and health research despite having a higher prevalence of heart disease, cancer, diabetes and stroke than any other population. Effective strategies to create research partnerships between tribal communities and genomic researchers are often lacking, yet such partnerships are needed for trustworthy research. As such, Indigenous populations are less likely to benefit from personalized medicine if they are not represented in studies that ascertain genotype-phenotype relationships that can lead to improved drug treatment efficacy.

We review what is currently known about pharmacogenetic variation in Indigenous populations and evaluate three case studies in which pharmacogenetic research with Indigenous populations were conducted. We highlight the importance of including Indigenous populations in future pharmacogenetic studies for implementation of personalized drug therapy, and discuss strategies for ethical engagement and collaboration in genomic research with Indigenous communities. The inclusion of Indigenous and other underrepresented communities in genomic research has the potential to expand our understanding of genomic influences on health and improve clinical approaches for all populations.

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### Evolution of the Primate Prefrontal Cortex Transcriptome

CHRISTOPHER G. CLAYPOOL<sup>1,2</sup>, TRISHA M. ZINTEL<sup>2,3</sup>, JASON PIZZOLLO<sup>2,3</sup>, JASON M. KAMILAR<sup>4</sup>, JOHN J. ELY<sup>5</sup>, MARY ANN RAGHANT<sup>6</sup>, WILLIAM D. HOPKINS<sup>7</sup>, PATRICK R. HOF<sup>8,9</sup>, CHET C. SHERWOOD<sup>10</sup>, AMY L. BAUERNFEIND<sup>11,12</sup> and COURTNEY C. BABBITT<sup>2</sup>

<sup>1</sup>Organismic & Evolutionary Biology, University of Massachusetts Amherst, <sup>2</sup>Department of Biology, University of Massachusetts Amherst, <sup>3</sup>Molecular and Cellular Biology, University of Massachusetts Amherst, <sup>4</sup>Department of Anthropology, University of Massachusetts Amherst, <sup>5</sup>Alamogordo Primate Facility, Holloman Air Force Base, <sup>6</sup>Department of Anthropology, School of Biomedical Sciences, and Brain Health Research Institute, Kent State University, <sup>7</sup>Department of Comparative Medicine,

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Michale E. Keeling Center for Comparative Medicine, The University of Texas M D Anderson Cancer Center, <sup>8</sup>Nash Family Department of Neuroscience and Friedman Brain Institute, Icahn School of Medicine at Mount Sinai, New York, <sup>9</sup>New York Consortium in Evolutionary Primatology, <sup>10</sup>Department of Anthropology and Center for the Advanced Study of Human Paleobiology, The George Washington University, <sup>11</sup>Department of Neuroscience, Washington University School of Medicine, <sup>12</sup>Department of Anthropology, Washington University in St. Louis

Exceptional cognitive abilities characterize the great apes. In the human brain, the prefrontal cortex (PFC) region allows for higher cognitive functions such as language, forethought, and complex behaviors. Volumetrically, all great apes have an expanded PFC and humans show exceptional expansion. The transcriptome of the PFC is well characterized within hominid development, but little is known about how humans compare to other closely related species of ape (other than chimpanzee) or how the PFC transcriptome varies across the primate family. To explore this, we sampled the anterior-most frontal pole in human and 9 other primates, performed RNA-Seq, and analyzed differential expression (DE). Representing 5 hominoids, 3 cercopithecoids, and 2 platyrrhines, this is an unprecedented collection of  $n=22$  samples across primates. Multidimensional scaling plots of hominid transcripts show that differences between great apes and lesser apes are the primary drivers of DE (orangutan and gorilla cluster together, separate from siamang) and differences between human and chimpanzee are the secondary drivers. Biological coefficient of variation plots for pairwise dispersions between hominoids show that the largest deviation is between human and chimpanzee. Significant ( $p < .01$  with Benjamini-Hochberg FDR) functional enrichments show several differences in cellular and biological functions between great and lesser ape and between human and other ape, however, the only pairwise comparison that found significant differences in molecular functions was between human and chimpanzee. These findings reveal conserved genotypes in primates, derived genotypes in great ape lineages, and adaptive phenotypes in human PFC evolution.

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## An infant vertebral column of *Homo naledi*

ZACHARY COFRAN<sup>1</sup>, HEATHER M. GARVIN<sup>2</sup>, DAVORKA RADOVIČIĆ<sup>3</sup>, MARINA C. ELLIOTT<sup>4</sup>, BECCA PEIXOTTO<sup>5</sup>, OLIVIA MATZ<sup>2</sup>, SCOTT A. WILLIAMS<sup>6</sup>, JOHN HAWKS<sup>7</sup> and LEE R. BERGER<sup>4</sup>

<sup>1</sup>Anthropology Department, Vassar College,

<sup>2</sup>College of Osteopathic Medicine, Des Moines

University, <sup>3</sup>Department of Geology and

Paleontology, Croatian Natural History Museum,

<sup>4</sup>Evolutionary Studies Institute and Centre for

Excellence in Palaeosciences, University of the

Witwatersrand, <sup>5</sup>Center for the Exploration of the

Human Journey, Perot Museum of Nature and Science, <sup>6</sup>Department of Anthropology, New York University, <sup>7</sup>Department of Anthropology, University of Wisconsin-Madison

*Homo naledi* is represented by abundant remains from Rising Star Cave in South Africa, dating to 236–335 kya. The fragmentary and commingled nature of most specimens hinders understanding of this species' biology, especially growth and development. Here we report unpublished immature vertebral remains from the 2013 excavations of the Dinaledi Chamber, and attempt to reject the hypothesis that these remains represent a single individual, using provenience, developmental, and osteometric data.

The immature vertebral specimens include ~60 fragments comprising mostly neural arches and pedicles, and represent all vertebral regions. Specific vertebral levels cannot be assigned to all fragments; however, these remains represent minimally three cervical, twelve thoracic, five lumbar, and one sacral elements, indicating a minimum of one individual. Sufficiently preserved laminae are all fused, while neurocentral junctions of two cervical pedicles are unfused, consistent with an age of 1–3 years when compared with modern humans. Because of this developmental consistency, close spatial association, and lack of clearly duplicated elements, we cannot reject the hypothesis that these vertebrae come from a single individual.

Immature lamina heights are at the low end of variation for modern humans aged 1–3 years. Thoracic lamina heights average ~43% the size of adult *H. naledi* from Dinaledi, while lumbar laminae are ~52% the size of the Lesedi "Neo" adult's measurements. Articular facet dimensions are ~50% the size of adult *H. naledi*. New developmental datasets and analytical approaches are needed to uncover the full implications for *H. naledi* growth and development.

## Evolution of Investment in Immatures in Adult Male Japanese Macaques (*Macaca fuscata*)

NOA COHEN, KYLEN N. GARTLAND and FRANCES J. WHITE

Anthropology, University of Oregon

Adult male investment in immatures is uncommon in non-human primates and varies from costly infant-carrying in callitrichids to affiliation in cercopithecines. Several evolutionary hypotheses can explain the variation in care behaviors. The paternal investment hypothesis (PIH) proposes that adult males use kin detection to direct care towards genetically-related immatures. The mating effort hypothesis (MEH) proposes that adult males direct care towards immatures to influence female mate choice. We conducted 512 hours on focal males in semi-free ranging Japanese macaques (*Macaca fuscata*)

at Oregon National Primate Research Center (ONPRC). Males varied in immature-directed behaviors from minimal interaction to frequent immature-carrying. We constructed hypothesis models based on the MEH, PIH and null hypothesis using generalized linear mixed models with a Gaussian distribution, including male ID as a random effect. We used multi-model inference testing to assess which model best explained variation in this behavior between adult males and determined the best model(s) using a  $\Delta AIC < 2$ . Our preliminary results showed the  $\Delta AIC$  for MEH as 3.73, PIH as 3.95 and the null as 0.00. Only the null was a significant model based on  $\delta AIC$ , suggesting that variation in this behavior is best explained by individual difference rather than differences in paternity relationship or mating success. However, non-significance in our evolutionary models demonstrates that although investment does not result in higher reproductive success than non-investing males, it was not significantly lower. Therefore, investment in immatures may be an alternate way to achieve the same reproductive success as non-investing, aggressive, dominant males.

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## Pore Extractor 2D: An ImageJ plugin for identification, classification, and regional characterization of cortical pores on histological bone images

MARY E. COLE<sup>1</sup>, SAMUEL D. STOUT<sup>2</sup> and AMANDA M. AGNEW<sup>2,3</sup>

<sup>1</sup>Biology, The University of Akron, <sup>2</sup>Anthropology, The Ohio State University, <sup>3</sup>Skeletal Biology Research Lab, The Ohio State University

Localized mechanical strain and age-associated declines in cellular function alter the percentage, distribution, and morphometry of cortical bone porosity. In archaeological, forensic, and biomedical contexts, cortical pore morphometry is used as a proxy for changes in mechanical use, bone quality, and bone fragility. The prevalence of such studies is limited by the time required to manually annotate hundreds to thousands of pores on a histological cross-section. Our previous work (Cole and Stout, 2015) developed a semi-automatic workflow for identifying pore regions-of-interest (ROIs) on histological cross-sections. We have now formalized this workflow as a free, open-source ImageJ (NIH) plugin with fully automated analytical components.

The sub-plugins of Pore Extractor 2D include:

1) Pore Extractor: Pore borders and lumens are separately extracted through global thresholding and merged as ROIs. In an update of the previous workflow, these initial pore ROIs are morphometrically filtered through user-selected despeckling, morphological opening, and smoothing cycles as well as size and circularity thresholds.

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2) Pore Modifier: This is a new toolkit for modifying pore ROI sets through superimposition on the histological image. Tools include one-click selection of missed pores by modulating wand tolerance, quick toggling for ROI labels, and easy savepoints.

3) Pore Analyzer: This new, fully automated routine includes a) Classification of individual pore type as cortical or "trabecularized", b) Regional subdivision of rib cross-sections into cutaneous / pleural halves and limb cross-sections into anatomical quadrants, and c) Summary statistics for percent porosity and pore area and shape descriptors, subdivided by anatomical region and pore type.

### Testing new trait definitions and scoring procedures for subadult sex estimation

STEPHANIE J. COLE, ELAINE Y. CHU and KYRA E. STULL

Department of Anthropology, University of Nevada - Reno

This presentation will inform attendees about a new method for estimating subadult sex that utilizes the most commonly relied upon adult morphological sex traits of the skull and pelvis, but with reworked trait definitions and scoring procedures that are more appropriate for use with immature remains. The skull traits include: mastoid process, glabella, supraorbital margin, nuchal crest, and mental eminence. The pelvic traits include: ventral arc, pubis shape, subpubic contour, medial aspect of the ischiopubic ramus, obturator foramen, greater sciatic notch, and pre-auricular sulcus. Intra- and inter-observer agreement between one and two observers with high and moderate levels of sex estimation experience, respectively, were evaluated using Cohen's quadratic weighted kappa and a sample of 10 individuals from the Subadult Virtual Anthropology Database. Results indicate substantial to perfect agreement ( $k = 0.65-1.00$ ) for intra-observer analyses for all traits. Inter-observer analyses were more variable, with agreement for most traits ( $n = 7/12$ ) being substantial ( $k = 0.66-0.722$ ). Inter-observer agreement was highest for glabella ( $k = 1.00$ ) and lowest for ventral arc ( $k = 0.27$ ), which is a likely consequence of this trait being underdeveloped in subadults and difficult to discern on CT images. Despite modest agreement for some traits, discrepancies never exceeded more than a 2-stage difference between observers and account for only 8.3% of all observations. Trait modifications are currently underway and will be tested by additional observers. New classification formulae will then be developed for inclusion in the freely available databases, MorphoPASSE and KidStats.

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### A pilot study of qualitative and quantitative methodologies for commingled remains

SARAI COLON, EMILY R. BROOKS, THERESA M. DE CREE, SAMANTHA LAFRANCE, LUIS CABO-PEREZ and LESLIE FITZPATRICK

Department of Applied Forensic Sciences, Mercyhurst University

There are numerous methods employed to assist forensic anthropologists and bioarchaeologists in determining the minimum number of individuals (MNI) and sorting commingled remains. This study seeks to compare three methods: visual pair matching, osteometric sorting, and X-ray Fluorescence (XRF) Spectrometry analysis. The authors aim to compare methodology and accuracy. Individuals with varying levels of expertise participated in a blind study. The sample was a known, modern collection of 56 skeletal elements, which was selected from the Mercyhurst University's Osteological Collection by a third party. It is hypothesized that visual pair matching will have the greatest error rate due to its subjectivity and dependency on experience. The quantitative methods will have lower error rates due to the objectivity of metric data. XRF sample results will be processed at a later date, but its use is hypothesized to be highly dependent on the variability of the sample. Participants correctly analyzed that the MNI of the sample was 4. Preliminary results show that the majority of the participant's measurements in the osteometric sorting method were within the accepted 2mm range, resulting in nearly identical groupings of the remains. Visual pair sorting showed a significant difference in results. The 56 elements were from 8 individuals, element grouping ranged from 1 to 12 elements. One participant organized the sample into 22 groups, 12 of those groups contained only one element, producing a statistically significant error rate. The second participant had 7 groups with grouping accuracy ranging from 57%-100%. Preliminary results support the hypothesis.

### Morphological integration of the human lower appendicular skeleton with respect to locomotion and biomechanics

MARK A. CONAWAY and NOREEN VON CRAMON-TAUBADEL

Anthropology, Buffalo Human Evolutionary Morphology Lab, University at Buffalo

The extent to which morphological integration is driven by functional constraints is as-yet unverified. Here we explore the integration of the human lower limb from a functional perspective. Landmark data were collected from 3D surface scans of 60 adult human and chimpanzee os coxae, femora, tibiae, fibulae, scapulae, and humeri as well as adult crab-eating macaques (*Macaca fascicularis*) as an outgroup. Integration of homologous elements, as well as functionally-defined *a priori* modules of the lower limb

were quantified in two ways. First, the Integration Coefficient of Variation (ICV) was calculated using interlandmark distances and distributions of values generated using a resampling protocol. Additionally, integration was calculated using a Partial Least Squares (PLS) analysis. Comparison of ICV distributions was performed via pairwise Mann-Whitney U tests with Bonferroni correction. Comparison of rPLS values was carried out via comparison of effect sizes.

The hominoid taxa included here presented lower integration among developmental homologs, when compared to the macaque outgroup, which is consistent with previous research. Further, the human sample returned significantly higher integration values for functional modules of the lower limb when compared to the macaques, as well as *Pan*. Additionally, the human knee and hip were found to be highly integrated. These results provide further evidence for the evolutionary "de-coupling," of the hominoid appendicular skeleton. Results also suggest that the integration in the human leg is, at least partially, a result of constraints imposed due to the evolution of bipedalism. However, further research with specific biomechanical variables is necessary to confirm this.

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### Evaluating the craniofacial feeding biomechanics in *Homo floresiensis* using the finite element method

REBECCA W. COOK<sup>1</sup>, ANTONINO VAZZANA<sup>2</sup>, RITA SORRENTINO<sup>2,3</sup>, STEFANO BENAZZI<sup>2,4</sup>, AMANDA L. SMITH<sup>5</sup>, DAVID S. STRAIT<sup>6</sup> and JUSTIN A. LEDOGAR<sup>1</sup>

<sup>1</sup>Department of Evolutionary Anthropology, Duke University, <sup>2</sup>Department of Cultural Heritage, University of Bologna, <sup>3</sup>Department of Biological, Geological and Environmental Sciences, University of Bologna, <sup>4</sup>Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology,

<sup>5</sup>Department of Organismal Biology and Anatomy, University of Chicago, <sup>6</sup>Department of Anthropology, Washington University in St. Louis

*Homo floresiensis* is a small-bodied hominid from Flores, Indonesia that exhibits primitive craniofacial features, such as a robust mandibular corpus, thick mandibular symphysis, and presence of superior and inferior transverse tori. These features are shared with "buttressed" australopithecines and are suggested to be adaptations to high masticatory stresses. However, *H. floresiensis* also exhibits marked craniofacial gracilization and short first molars more similar to that of later *Homo*, indicating a reduction in high magnitude occlusal loading relative to more robust hominid species. This discrepancy makes it difficult to infer feeding behavior in this species. This study uses finite element analysis

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to examine feeding biomechanics in *H. floresiensis*. Using a reconstruction of the holotype specimen (LB1), masticatory loads scaled from chimpanzee muscle forces were applied to simulate P<sup>3</sup> and M<sup>2</sup> biting. von Mises stress and strain data were compared to a sample of chimpanzees, modern humans, and australopiths (MH1, Sts 5, OH5). With few exceptions, the microstrain magnitudes in LB1 resemble the elevated strains observed for modern humans, and in some areas exhibit chimpanzee-like levels of increased strain. LB1 therefore appears to be relatively weak in relation to most australopiths and more comparable to modern humans. Distractive forces were observed during molar biting, suggesting risk for temporomandibular joint dislocation and therefore a decreased capacity for forceful biting. These results support a modern human-like model of craniofacial gracilization and may suggest a switch to softer foods in *H. floresiensis*.

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### Socioecological Predictors of Respiratory Illness in Western Lowland Gorillas (*Gorilla gorilla gorilla*)

KRISTENA E. COOKSEY<sup>1</sup>, CRICKETTE SANZ<sup>1,2</sup>, JEAN M. MASSAMBA<sup>2</sup>, THIERRY FABRICE EBOMBI<sup>2</sup>, PROSPÈRE TEBERD<sup>2</sup>, ESPOIR MAGEMA<sup>2</sup>, GASTON ABEA<sup>1,2</sup>, GAETON MBEOUTI<sup>2</sup>, JUAN S. ORTEGA PERALEJO<sup>2</sup>, IVONNE KIENAST<sup>2</sup>, COLLEEN STEPHENS<sup>1</sup> and DAVID MORGAN<sup>3</sup>

<sup>1</sup>Anthropology, Washington University in St. Louis,

<sup>2</sup>Congo Program, Wildlife Conservation Society,

<sup>3</sup>Fisher Center for the Study and Conservation of Apes, Lincoln Park Zoo

Socioecological factors have previously been linked to incidences of respiratory illness in primates. Due to their phylogenetic relatedness to humans, great apes are particularly susceptible to anthropogenic respiratory infections. Respiratory illness is the second leading cause of death in mountain gorilla populations but remains relatively understudied in western lowland gorillas. We explore potential socioecological predictors of respiratory illness across four groups of western lowland gorilla (*Gorilla gorilla gorilla*) in northern Republic of Congo. A total of 17,592 observational health assessments were conducted during daily follows in the Goulougo and Djeke Triangles from March 2015 to October 2019. We detected several respiratory episodes within the focal population and observed 828 incidences of respiratory symptoms identified as coughing and sneezing. We observed an average of 7.98 incidences/month (on 9.8% of total observation days) and 7.45 incidences/month (on 2.8% of total observation days) at Goulougo and Mondika, respectively. We propose there is a correlation between the presence of respiratory illness with

other indications of altered health profiles as there are periods where both were present. Based on the observed dynamics of disease spread, we consider plausible ways in which these respiratory infections transfer both within and between groups. Additionally, we suggest identifying key variables impacting respiratory infection transmission, as it can be pivotal in mitigating future respiratory outbreaks. In an effort to contribute to reduce rates of respiratory infections in gorillas, we provide recommendations for best practices and management protocols, in both the wild and captive setting.

Arcus Foundation, Cincinnati Zoo, Indianapolis Zoo, Houston Zoo, Columbus Zoological Park, Nouabale-Ndoki Foundation, U.S. Fish and Wildlife Service

### A geometric morphometric analysis of cranial ontogenetic integration in non-human hominids

MARIANNE J. COOPER, EVAN A. SIMONS and NOREEN VON CRAMON-TAUBADEL

Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo

Investigations of patterns of integration and covariation can inform possible constraints on routes of morphological evolution and are therefore critical in studies of hominid cranial form. Previous geometric morphometric studies of great apes have found high levels of integration in the three established cranial modules – face, basicranium, and neurocranium – and similar patterns of integration among species. However, these studies have largely focused on adult cranial integration and many exclude *Pongo*. This study examines patterns of ontogenetic integration among these three modules in an ontogenetic series (from fully erupted deciduous dentition to fully erupted adult dentition) of 252 specimens of *Pongo pygmaeus* (n = 54), *Gorilla gorilla* (n = 59), *Pan paniscus* (n = 63), and *Pan troglodytes* (n = 76), using 43 three-dimensional cranial landmarks. These data were separated into face, basicranial, and neurocranial modules and landmarks within each module were superimposed separately using generalized Procrustes analysis. The degree of morphological integration among the cranial modules was compared using two-block partial least squares analysis. Results indicate high levels of integration between the face and neurocranium (r-PLS = 0.838, p = 0.0001), the face and basicranium (r-PLS = 0.7567, p = 0.0001), and the basicranium and neurocranium (r-PLS = 0.8695, p = 0.0001) over the course of ontogeny, with no significant differences among age groups or species. This study builds upon prior research and indicates that the similar patterns of integration previously observed in these cranial modules in adults are also found throughout the segment of ontogeny measured here.

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### 3D Modeling isolated cranial remains in Alaska: Reducing handling time and improving osteological analyses

EMILY S. CORLEY, KAELYN SCHENKENBERGER, TED PARSONS and RYAN HARROD

Anthropology, University of Alaska Anchorage

Unearthing of human remains in Alaska is a growing concern given melting permafrost and growth of transportation and public infrastructure throughout the state. Identification of isolated crania is periodically performed at the Bioarchaeology Lab at the University of Alaska Anchorage. Most of the remains eroding out of the ground are culturally affiliated with Alaska Native groups, found in coastal or riverine areas, and often have been exposed to the elements for a significant amount of time. Working with weathered, fragile crania requires that they be minimally handled to reduce further damage. Additionally, minimally invasive analyses are preferred when evaluating affiliated remains. Current techniques used in Alaska rely on observable characteristics and measurements. However, this can require extensive handling of the remains and the use of metal tools that can cause damage. Our intent is to illustrate how photograph-based and RGB-D modeling techniques require less handling of the remains and can allow researchers to perform the same osteological analyses. Models were created under controlled laboratory conditions using unaffiliated teaching crania. Studies have suggested that both techniques can quickly create easily stored, high-quality digital models suitable for detailed study, available for later retrieval and reanalysis. Three crania were scored independently by three trained researchers using standard physical evaluation methods, 3D modeled and scored again. We argue 3D models reduce handling of human remains and intra- and inter-observer error rates. When working with culturally affiliated remains, permission is obtained before modeling and models are only kept long enough to perform osteological analyses.

### Predicting individual heights in Pre-Historic Europe using polygenic scores

SAMANTHA L. COX<sup>1,2</sup>, HANNAH MOOTS<sup>3</sup>, JAY T. STOCK<sup>4,5</sup>, ANDREJ SHBAT<sup>6</sup>, CHRISTOPHER B. RUFF<sup>7</sup> and IAIN MATHIESON<sup>1</sup>

<sup>1</sup>Department of Genetics, Perelman School of Medicine, University of Pennsylvania, <sup>2</sup>Physical Anthropology Section, Penn Museum, University of Pennsylvania, <sup>3</sup>Department of Anthropology, Stanford University, <sup>4</sup>Department of Anthropology, Western University, <sup>5</sup>Department of Archaeology, Max Planck Institute for the Science of Human History, <sup>6</sup>Institute of Anatomy, First Faculty of Medicine, Charles University, <sup>7</sup>Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

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Direct evidence from ancient DNA provides an opportunity to separate the genetic and environmental bases of change in complex traits. We previously showed that population level polygenic predictions of stature in ancient Europeans are consistent with changes in skeletal statures. However, the validity of polygenic scores for predicting individual polygenic traits remains untested. To this end, we collected statures and femur lengths from skeletal remains with published ancient DNA ( $n=154$ , dating from 33,000-850 BP). A polygenic score (PRS) for height predicts 6.9% of the variance in femur length ( $p=0.015$ ), when accounting for sex, genome-wide ancestry, and date. This is consistent with expectations based on the predictive power of height PRS in present-day populations and the low coverage of the ancient samples. The PRS explains more of the variance in femur length than climatic factors, including average daily temperature ( $P=0.599$ ) and annual precipitation ( $P=0.307$ ). We used genotype imputation to increase effective coverage of the data. We find that imputation improves performance for samples that are already relatively high coverage, but not for low coverage samples (2-fold increase in variance explained for samples with greater compared to less than median coverage of 0.61). Imputed data generally performs best with more restrictive PRS construction (i.e. fewer SNPs) whereas unimputed data favors more permissive settings. Overall, our results indicate that polygenic scores for height are as valid in ancient as present-day individuals, and justify the use of PRS to investigate evolutionary trends, although the prospects for accurate individual-level prediction are limited.

### Idiosyncratic variation in ectocranial and endocranial morphology in 6-8.0 year old humans

JESSICA M. CRONIN<sup>1</sup>, JANE VANNAHEUANG<sup>2</sup>, ANA M. SHAUGHNESSY<sup>3</sup>, GARY D. RICHARDS<sup>4</sup> and REBECCA S. JABBOUR<sup>5</sup>

<sup>1</sup>Department of Integrative Biology, UC Berkeley, <sup>2</sup>Department of Public Health, UC Berkeley, <sup>3</sup>Department of Molecular and Cell Biology, UC Berkeley, <sup>4</sup>Department of Biomedical Sciences, A.A. Dugoni School of Dentistry, University of the Pacific, <sup>5</sup>Department of Department of Biology, Saint Mary's College of California

Ectocranial and endocranial shape differences are a product of functional constraints which are only partially shared between these regions. Given these differences, we assess both the degree of shape difference between the ectocranium and endocranium and degree of cranial symmetry in human juveniles.

Our sample comprises 38 crania with ages between 5.8-7.9 years. Developmental ages are based on dental calcification patterns and comparisons to the Schour and Massler aging system. Using CT scans, we collected 35 3D

endocranial landmarks on isosurfaces and, using a Microscribe, 160 landmarks on the external neurocranium. The latter point total was subsequently reduced to 42 landmarks. To assess the degree of shape difference, we performed a Principal Components Analysis (PCA) on Procrustes-aligned shape variables in Morphologika. We also assessed the degree of right/left symmetry.

Shape change along PC1 describes a dolichocephaly-brachiocephaly trend, while a trend towards anteroposterior shortening and height increase is described along PC2. Each individual with similarity between their ectocranial and endocranial shape expresses a right/left cranial base flexion symmetry and anteroposterior 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 their ectocranial and 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 neurocranium.

### Prehispanic mobility in the Northern Maya Lowlands by means of Sr isotope analysis

ANDREA CUCINA<sup>1</sup> and ALLAN ORTEGA MU-OZ<sup>2</sup>

<sup>1</sup>School of Anthropology, Universidad Autonoma de Yucatan, <sup>2</sup>Physical Anthropology, INAH Center Quintana Roo

Human mobility in Prehispanic Maya times was usually inferred by the presence of foreign material culture. However, exchange of ideas and material culture is not bound to faithfully witness the biological interaction between sites and the mobility patterns of single individuals. This analysis focuses on unpublished and published data on <sup>87</sup>Sr/<sup>86</sup>Sr ratios from nine archaeological sites in the Northern Maya Lowlands during Classic (AD 250-900) and Postclassic (AD 900-1521) times. Results indicate that approximately 20% of individuals were foreigners, with minor differences between sexes. The majority of the individuals were adults, yet also a limited number of juveniles and infants were foreigners. Dynamics of residential mobility and the geographical range of places of origin were very heterogeneous, differing from site to site, and between chronological periods. They mirror sites' importance within the coastal or inland trade corridors, as well as within the sphere of influence and political hegemony of City-States, in particular during the Classic period. Most of the foreigners originated within the northern territories of the Yucatan Peninsula; however, coastal sites (like Xcambó) show strong interactions with regions as far away as Tabasco and Veracruz. Interestingly, in Classic period times there is little or no evidence of individuals being born along the coast and having been interred in inland sites,

suggesting two independent coastal and inland networks. Last, the presence of infants and juveniles also suggests that mobility patterns were not only related to trade networks, but that also kinship and family relationships likely triggered movement of entire families.

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### Paleoecology and Biochronology of Early Pleistocene sites in southern Romania

SABRINA C. CURRAN<sup>1</sup>, CLAIRE E. TERHUNE<sup>2</sup>, ROMAN CROITOR<sup>3</sup>, VIRGIL DRAGUSIN<sup>4</sup>, DAVID L. FOX<sup>5</sup>, NIKI GARRETT<sup>6,7</sup>, TIMOTHY GAUDIN<sup>8</sup>, LYDIA B. IRONSIDE<sup>9</sup>, ALEXANDRU PETCULESCU<sup>4</sup>, BRIANA POBINER<sup>10</sup>, CHRIS ROBINSON<sup>11</sup>, MARIUS ROBU<sup>4</sup>, IOAN TANTAU<sup>12</sup>, PETER UNGAR<sup>2</sup> and LARS WERDELIN<sup>13</sup>

<sup>1</sup>Department of Sociology and Anthropology, Ohio University, <sup>2</sup>Department of Anthropology, University of Arkansas, <sup>3</sup>The Mediterranean Laboratory of European and African Prehistory, Aix-Marseille University, <sup>4</sup>Department of Biology, Geology, and Environmental Science, Emil Racovita Institute of Speleology, <sup>5</sup>Department of Earth & Environmental Sciences, University of Minnesota, <sup>6</sup>Department of Anthropology, University of Minnesota, <sup>7</sup>Immunogenetics, National Marrow Donor Program, <sup>8</sup>Biology, Geology and Environmental Science, University of Tennessee at Chattanooga, <sup>9</sup>Health Science Center, University of North Texas, <sup>10</sup>Human Origins Program, Smithsonian Institution, <sup>11</sup>Bronx Community College and the Graduate Center, City University of New York, <sup>12</sup>Department of Geology, Babeş-Bolyai University, <sup>13</sup>Department of Palaeobiology, Swedish Museum of Natural History

The early Pleistocene of Eurasia is marked by significant climatic, environmental, and faunal shifts and is the time during which *Homo* first appears in the Eurasian fossil record. To better characterize the environments that were available to these hominins, accurate data regarding the faunal composition of eastern European sites are necessary, as this is the region through which *Homo* is hypothesized to have dispersed into Europe. Here we present revised taxonomy, updated biochronology, and a multiproxy paleoenvironmental reconstruction for sites in the Oltet River Valley of southern Romania. We report several new taxa (e.g., *Pachystruthio*, *Smutsia*) and expand the known biogeographic range for other taxa (e.g., *Puma pardoides*). Our biochronological assessment of this updated taxonomy is consistent with previous reports, though with some refinement. We suggest the highly fossiliferous Grauncceanu site is Late Villafranchian (~2.2–1.9 Ma) and compositionally similar to the sites of Saint-Vallier (France) and Vatera (Greece). Similarly, the La Pietris assemblage was likely deposited >1.7 Ma. The younger site of Fantana lui Mitilan was deposited after 1.8 Ma, and perhaps as recently as 1.1 Ma. Grauncceanu and La Pietris are reconstructed as being primarily open, though with some nearby woodlands and significant water resources, and

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Fantana lui Mitilan is reconstructed as slightly more closed, though still relatively open in nature. These results are similar to reconstructions for other early Pleistocene Eurasian sites, including ones with and without hominins, suggesting that hominins were likely not inhibited from dispersing across Eurasia due to environmental constraints at this time.

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### Association of hypertension with dietary habits and lipid profile parameters among Dhimal adults from Darjeeling in West Bengal, India

SUDIP DATTA BANIK

Human Ecology, CINVESTAV-IPN

Poor socioeconomic conditions, dietary habits and metabolic alterations are associated with hypertension.

**Objective:** To find the association of hypertension with dietary habits and lipid profile parameters namely, triglycerides (TG), low density lipoprotein cholesterol (LDL-C), high density lipoprotein cholesterol (HDL-C), total cholesterol (TC) and non-HDL-C among adults in a population of poor socioeconomic background in India.

**Methods:** In a cross-sectional study, participants were 94 adults aged 30-59 years (50 men and 44 women) representing Dhimal community with poor socioeconomic background from Darjeeling, West Bengal. Relative frequencies (RF) of monthly consumption of processed and ultra-processed foods were estimated. Prevalence of hypertension, elevated triglycerides, LDL-C, and reduced level of HDL-C were calculated.

**Results:** Mean age of the participants was 42.05 years. Household socioeconomic status was homogeneous in the community that showed low literacy (22.0%), monthly per capita income and expenditure. RF of processed (28.0%) and ultra-processed (56.0%) food consumptions were high in the sample. The sample had equal number (n = 47) of normotensive and hypertensive individuals (25 men, 22 women in each group). No significant sex differences of characteristics were observed. Mean values of SBP (126.95 mmHg), DBP (83.61 mmHg), TG (148.31 mg/dL) and LDL-C (104.55 mg/dL) were within normal limit. Mean value of HDL-C was low (34.10 mg/dL). Prevalence of Hypertriglyceridemia (53.76%), high LDL-C (23.66%), and low HDL-C (51.61%) were remarkable. Hypertensive individuals had higher mean values of TG, LDL-C, TC, non-HDL-C, and lower HDL-C in comparison with normotensive peers. Hypertension was positively correlated with RF of ultra-processed food consumption.

### Ectocranial and Endocranial Shape in Relation to Dural Folds in Normal and Culturally Deformed Children Aged 1.5 – 2.5 Years

ANNABEL T. DAVIS<sup>1</sup>, JESSICA M. CRONIN<sup>2</sup>, EMILY DAS<sup>1</sup>, GARY D. RICHARDS<sup>3</sup> and REBECCA S. JABBOUR<sup>4</sup>

<sup>1</sup>Cognitive Neuroscience, University of California, Berkeley, <sup>2</sup>Department of Integrative Biology, University of California, Berkeley, <sup>3</sup>Department of Biomedical Sciences, A.A. Dugoni School of Dentistry, University of the Pacific, <sup>4</sup>Department of Biology, Saint Mary's College of California

We previously identified shape changes in plagiocephalic crania. The degree to which these differences deviate from normal conditions and may relate to neural damage relies on knowledge of normal shape variations. Herein we assessed ectocranial/endocranial shape in normal and plagiocephalic infants and the relationship of these shape differences to the major dural fold attachment sites.

We assessed normal (N=27) and plagiocephalic (N=2) crania aged 1.5-2.5 years. Developmental ages derive from crown/root calcification patterns. Crania were scanned on a GE Lightspeed CT-scanner. We established planes on isosurfaces inclusive of 1) a midsagittal plane employing ectocranial landmarks, 2) a midsagittal plane approximating the falx cerebri, and 3) a transverse plane approximating the endocranial anterior/posterior pole maxima. We assessed positioning of the midsagittal ectocranial/endocranial planes, the relative sizes of the right/left and superior/inferior endocranial compartments relative to the above planes, the degree and positioning of vault asymmetries, and the degree of differential fronto-occipital expansion.

In 93% of normals and both plagiocephalics, the falx cerebri deviated from the ectocranial midsagittal plane; others were coincident. In normals (96.3%) and both plagiocephalics, falx deviation was counter-clockwise and greatest posteriorly. Only in plagiocephalics do the two midsagittal planes rotate similarly, documenting a normal falx rotation in plagiocephaly but abnormal external landmark rotation. Further, asymmetric expansion in the temporoparietal region in normal children results in greater contralateral falx deviation posteriorly.

Establishing the range of normal ectocranial shape variation and its relationship to endocranial shape variation could help identify causative factors that result in neurological deficits in plagiocephaly.

### CONSIDERING THE OSTEOLOGICAL PARADOX IN THE CONTEXT OF OYMAAĞAÇ HÖYÜK: A comparison of skeletal lesion prevalence and demographic data in multigenerational and mass grave contexts

MEKENZIE R. DAVIS<sup>1</sup> and KATHRYN E. MARKLEIN<sup>1,2</sup>

<sup>1</sup>Department of Anthropology, University of Louisville, <sup>2</sup>Center for Archaeology and Cultural Heritage, University of Louisville

The osteological paradox poses a challenge for bioarchaeologists when interpreting frailty from paleodemographic and paleopathological data in human skeletal remains. Multigenerational (attritional) and mass (catastrophic) burials within the 2<sup>nd</sup>-4<sup>th</sup> c. CE graves at Oymağaç, northern Turkey, provide an ideal case study for evaluating frailty relative to age-at-death and skeletal/dental conditions. Individuals and partial individuals (N=185) were classified into juvenile (0-4.99/5-9.99/10-15.99 years) and adult (16-25.99/26-35.99/36-45.99/46+ years) age groups, and the latter scored (presence/absence), when observable, for carious lesions, calculus, linear enamel defects (LED), periodontal disease, antemortem fractures, osteoarthritis, and periosteal lesions. Demographic profiles (juveniles and adults) and crude prevalence rates (CPR) in adults were compared between mass and multigenerational burial contexts. Pearson's X<sup>2</sup> results showed significant differences (p<0.05) in overall distribution of all age categories between burial contexts, with higher proportions of older juveniles (5-15.99 years) and middle age adults (26-35 years) observed among mass graves. While adult age distributions were not statistically different, juvenile distributions showed significantly higher percentages of young (0-4.99 years) and middle (5-9.99 years) children in multigenerational (60.9%) and mass (47.6%) graves, respectively.

Paleopathological comparisons revealed significantly higher rates of LED, antemortem fractures, and osteoarthritis among multigenerational/attritional than mass/catastrophic grave contexts. Carious and periosteal lesions occurred at higher rates approaching significance (p<0.10) within mass burial contexts. These results suggest, for this population, that lifetime skeletal and dental lesions were indicative of resilience, not frailty, and highlight the importance of upholding the osteological paradox when considering questions of biological health and frailty in the past.

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# ABSTRACTS

## Investigation of systemic stress in males and females at three Chinese Eastern Zhou sites using the micropolynomial method for assessing linear enamel hypoplasia

CLARE DE JOUX<sup>1</sup>, MELANIE J. MILLER<sup>1</sup>, ALEJANDRA CARES HENRIQUEZ<sup>2</sup>, KATE PECHENKINA<sup>3</sup>, WENQUAN FAN<sup>4</sup>, MARC OXENHAM<sup>5</sup> and SIÂN HALCROW<sup>1</sup>

<sup>1</sup>Anatomy, University of Otago, <sup>2</sup>School of Culture, History and Language, Australian National University, <sup>3</sup>Anthropology, Queens College CUNY, <sup>4</sup>Research Division of Shang and Zhou Dynasties, Henan Provincial Institute of Cultural Relics and Archaeology, China, <sup>5</sup>School of Archaeology and Anthropology, Australian National University

Assessing linear enamel hypoplasia (LEH) is a common bioarchaeological method for quantifying systemic stress within a population. There exists a persisting trend to examine differences in LEH frequency and 'severity' between demographics within a population to reveal overarching differences in systemic stress, especially between the sexes. Previous research on the Chinese Eastern Zhou period (771 – 221 BCE) has indicated a rise in sex-based inequality disadvantaging females during this time based on evidence of dietary differences post-weaning, and number and quality of grave goods. This study assessed LEH in 114 anterior teeth from 39 individuals (13 female, 24 male, 2 indeterminate) from three sites from the Central Plains of China using the new MicroPoly Sharp® program. This method applies a sixth-order polynomial curve to a digitised cross section of a tooth and identifies significant deviations on the tooth surface as potential LEH events. Here, we scored a systemic stress event when two or more teeth had defects occurring during the same time of development. The results suggest no statistically significant differences in LEH frequency between males and females from these sites. Further, there was no difference in the gross numbers of days that these events occurred between the sexes, suggesting most individuals experienced similar levels of stress recorded as LEH. Since sex-based differences in child-rearing and status are known to have existed in this time, this research provides an interesting perspective on the ability for LEH to reflect nuances in systemic stress differences between groups within a population.

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## Genomic and cultural diversity of the Incan Capacocha ceremony in Chile and Argentina

CONSTANZA P. DE LA FUENTE<sup>1,2</sup>, MAANASA RAGHAVAN<sup>1</sup>, CONSTANZA CORTÉS<sup>3</sup>, MARIO

CASTRO<sup>4,5</sup>, RICARDO VERDUGO<sup>2,6</sup> and MAURICIO MORAGA<sup>2,7</sup>

<sup>1</sup>Human Genetics, University of Chicago, <sup>2</sup>Programa de Genética Humana, ICBM, Facultad de Medicina, Universidad de Chile, <sup>3</sup>Instituto de Historia y Ciencias Sociales, Universidad Austral de Chile, <sup>4</sup>Departamento de Morfología, Facultad de Medicina, Universidad del Desarrollo, <sup>5</sup>Museo Natural de Historia Natural, Chile, <sup>6</sup>Departamento de Oncología Btísico-Clnica, Universidad de Chile, <sup>7</sup>Departamento de Antropología, Facultad de Ciencias Sociales, Universidad de Chile

The Inca Empire was established in the 13<sup>th</sup> century CE, spreading from its capital, Cuzco, to southern Colombia and Central Chile. The study of individuals buried on mountain summits along the Andes has been associated with the Inca ritual Capacocha. As part of this ceremony, one or more individuals, mainly children, were buried with Inca-style offerings on these mountain summits. The ritual likely served as a public manifestation of the Inca power, and several questions about the social status and origin of these individuals still remain unclear. Our research aims to assess the genetic diversity of individuals associated with the Capacocha ceremony, in order to understand their origins. Using ancient genomic tools, we analyzed four individuals: three newly-produced genomes from *El Plomo* Mt. (Chile), *Nevado del Quewar* (Argentina), 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 with the individuals from *El Plomo*, *Nevado del Quewar*, and *Aconcagua*. The individual from *El Toro*, however, although geographically closer to the Quechua and Aymara speakers, did not have a close affinity with them, showing instead a proximity with southern groups. Interestingly, the association of this individual with the Capacocha has been questioned before. Our analysis suggests a Central Andean affinity for at least three of the studied individuals, thus contributing to our comprehension of the social dynamics of this ritual.

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## Patterns of sex-biased gene expression in rhesus macaque brains are similar to those observed in human brains

ALEX R. DECASIEN<sup>1,2</sup>, KENNETH L. CHIOU<sup>3,4</sup>, MICHAEL J. MONTAGUE<sup>5</sup>, CHET C. SHERWOOD<sup>6</sup>, MICHAEL L. PLATT<sup>5,7,8</sup>, MELWEEN I. MARTINEZ<sup>9</sup>, SAMUEL E. BAUMAN<sup>9</sup>, OLGA GONZÁLEZ<sup>10</sup>, NOAH SNYDER-MACKLER<sup>11,3,4</sup> and JAMES P. HIGHAM<sup>1,2</sup>

<sup>1</sup>Anthropology, NYU, <sup>2</sup>New York Consortium in Evolutionary Primatology, NYCEP, <sup>3</sup>Nathan Shock Center of Excellence in the Basic Biology of Aging,

University of Washington, <sup>4</sup>Center for Evolution and Medicine, Arizona State University, <sup>5</sup>Department of Neuroscience, University of Pennsylvania, <sup>6</sup>Department of Anthropology, The George Washington University, <sup>7</sup>Department of Psychology, University of Pennsylvania, <sup>8</sup>Department of Marketing, University of Pennsylvania, <sup>9</sup>Caribbean Primate Research Center, University of Puerto Rico, <sup>10</sup>Southwest National Primate Research Center, Texas Biomedical Research Institute, <sup>11</sup>School of Life Sciences, Arizona State University

Humans exhibit sex differences in the prevalence of some psychiatric and neurodevelopmental disorders (e.g., autism), which may be driven by differences in neuroanatomy, cell distribution, and gene expression. However, the evolutionary pressures that may have contributed to these differences remain unknown due to a limited understanding of sex differences in nonhuman primate brains. To address this gap, we quantified sex differences in gene expression across 15 brain regions in a cross-sectional sample of 36 (20F/16M) free-ranging adult rhesus macaques and compared these differences to those observed in humans and other taxa. About 7% of brain-expressed genes were sex-biased. Almost half of these genes were biased in the same direction across all regions, suggestive of consistent regulatory mechanisms. As in humans, we found that: 1) male-biased genes were involved in metabolism ( $p < 0.05$ ) and autism susceptibility ( $p < 0.05$ ); 2) female-biased genes were involved in immune-related pathways ( $p < 0.05$ ); and 3) promoter regions of sex-biased genes tend to contain sex hormone binding sites ( $p < 0.05$ ). Consistent with studies across other taxa and tissues, we found that: 1) sex-biased genes exhibited higher tissue-specificity than non-biased genes ( $p < 0.05$ ); and 2) male-biased genes exhibited higher genetic variance than female-biased genes ( $p < 0.05$ ). These patterns are consistent with reports that sex-biased (especially male-biased) genes exhibit greater evolvability. Together, our findings expand our understanding of sexual dimorphism in the primate brain, and suggest the rhesus macaque is likely to be an appropriate model for sex-biased human neurological disorders.

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## Effects of nasal capsule cartilage in shaping the primate face

VALERIE B. DELEON<sup>1</sup> and TIMOTHY D. SMITH<sup>2</sup>

<sup>1</sup>Anthropology, University of Florida, <sup>2</sup>School of Physical Therapy, Slippery Rock University

The role of the nasal septum as a driver of facial growth has been debated, with emphasis on the inherent growth potential of cartilage. We have previously reported the breakdown of cartilage in

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the posterior nasal cupula in most strepsirrhine primates around birth, earlier than observed in tree shrews and bats. Here, we considered the role of the lateral portions of the cartilage nasal capsule in growth of the face; specifically with regard to formation of intramembranous bone.

We combined image data from microCT and histology to create 3D models of the skull and cartilaginous nasal capsule in a comparative primate sample including strepsirrhines (*Eulemur collaris*), anthropoids (*Saimiri boliviensis*), and tree shrews (*Tupaia belangeri*) as an outgroup. Results illustrate the expectation that the cartilage nasal capsule establishes the initial form of the midface, and intramembranous ossification occurs in the membranes that surround the capsule. Breakdown of the posterior nasal cupula is associated with an inward collapse of the orbitosphenoid, frontal, and palatine contributions to the olfactory recess in *Eulemur*. The effect is more pronounced in *Saimiri*, where even earlier loss of the posterior nasal cupula is associated with medial expansion of the orbits and formation of the apical interorbital septum. The periorbital membrane is apposed to the presphenoid, and there may be no substrate available for rostral expansion of the orbitosphenoid. These results illustrate how different trajectories of nasal capsule development profoundly influence developmental associations of the nascent midface with the basicranium and other facial regions.

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### Craniofacial diversity and the reconstruction of the late Pleistocene and Holocene Native American population history

MIGUEL E. DELGADO

División Antropología, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata, República Argentina, CONICET, Consejo Nacional de Investigaciones Científicas y Técnicas, República Argentina, Ministry of Education Key Laboratory of Contemporary Anthropology Collaborative Innovation Center of Genetics and Development, School of Life Sciences and Human Phenome Institute Fudan University, Shanghai, China

The craniofacial evidence has been pivotal for the investigation of the Native American population history. However, spatially and temporally biased comparisons and the exclusion of key periods have impeded more comprehensive assessments. The aims of this research are to: assess the Native American craniofacial diversity, and its apportionment, across the continent using distinct temporal and spatial scales, and evaluate the role of different evolutionary factors shaping such diversity. Seventeen linear measurements obtained from 950 adult non-deformed crania from distinct New World regions and periods (~12,000-450 BP) were investigated using univariate,

exploratory and quantitative genetic methods. The results show close affinities between early and late Native Americans, complex population histories and diverse amounts of cranial variation across the continent. Non-random evolutionary processes account for a significant portion of the cranial diversification observed in some periods/regions. The early and recent Native American craniofacial diversity supports the entry of one founding population with low cranial diversity, which remained little differentiated until the middle/initial late Holocene (~5000-4000/3500 BP) when an extensive morphological diversification occurred. Such process, which led to the Paleoamerican/Amerindian differentiation, occurred almost synchronically in South American and is best explained as a result of an important mid-Holocene dispersal event from North/Central to South American. The amount of cranial diversity increased progressively –from late Pleistocene to middle Holocene– supporting random processes of local differentiation (gene drift, gene flow), whereas the high diversity observed during the late Holocene could be linked with the differential action of stochastic (gene drift) and non-stochastic factors (natural selection/plasticity).

Fundación de Investigaciones Arqueológicas Nacionales (FIAN Colombia); Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET Argentina).

### Variation in Nonmetric Dental Trait Frequencies and Regional Affiliations of Medieval Hungarians

LARESA L. DERN<sup>1</sup>, ROSE L. PERASH<sup>1</sup>, SÁNDOR ÉVINGER<sup>2</sup>, TAMÁS HAJDU<sup>3</sup>, TAMÁS SZENICZEY<sup>3</sup> and G. RICHARD SCOTT<sup>1</sup>

<sup>1</sup>Anthropology, University of Nevada, Reno,

<sup>2</sup>Anthropology, Hungarian Natural History Museum,

<sup>3</sup>Biological Anthropology, Eötvös Loránd University

Alongside many smaller migration events, the mass migration of two confederations of nomadic steppe tribes significantly impacted the medieval demography of the Carpathian Basin. During the 6<sup>th</sup> century, roughly a century after the collapse of the European Hunnic empire, the Avars migrated to the basin from Inner Asia. Along the way, they were joined by other steppe tribes in Central Asia and Eastern Europe. At the end of the 9<sup>th</sup> century, the Magyars migrated to the basin from the Pontic-Caspian steppe, and by the 11<sup>th</sup> century, they established the Kingdom of Hungary, the foundation for present-day Hungary. Large migration events should result in marked fluctuations in nonmetric dental trait frequencies. Following ASUDAS, dental traits were scored for 335 individuals from 25 sites sampled from bioarchaeological collections at the Hungarian Natural History Museum (Avar = 226, Magyar = 109). A subsample (n=100) of individuals with at least 12 scored traits was analyzed by rASUDAS2, an application that uses a naïve

Bayesian classifier algorithm to compute posterior probabilities of classifying individuals into seven global regions based on up to 32 nonmetric dental traits. The most frequent region of highest posterior probability was Western Eurasia (Avar-56%, Magyar-87%). For individuals with Western Eurasia as their first group, the mean posterior probability was 0.80 while for other regions the mean posterior probability ranged from 0.41-0.66. This suggests many individual dentitions had combinations of nonmetric dental traits that lead to simultaneous classification into multiple regional groups, as expected for a region with many transregional migrations.

### Y-chromosome SNP analysis of Near Oceania Austronesian and non-Austronesian speakers

KATE L. DEROSA and D. ANDREW MERRIWETHER  
Anthropology, Binghamton University

The Pacific Islands were settled via two major waves of migration - first in Near Oceania ~40-60 KYA and second in both Near and Remote Oceania ~3.5 KYA. These migrations are associated with non-Austronesian and Austronesian speakers, respectively. Previous studies of mitochondrial and Y-chromosome variation have demonstrated there are distinct genetic lineages for both major settlements of Near Oceania. Single nucleotide polymorphism (SNP) and microsatellite analysis of Y-chromosomes in these populations have found haplogroups M and O are the dominant lineages for non-Austronesian and Austronesian speaking populations, respectively. This study expanded on these previous works in Near Oceania by focusing on non-Austronesian and Austronesian speakers from the islands of Bougainville (n=37), New Ireland (NI) (n=40) and New Britain (NB) (n=238) with a total of eight SNP markers (M1/YAP M4, M16, M38, M89, M226, and M254). An additional 248 samples were excluded from analysis due to lack of a mutation for any of the eight SNPs included. Of the 315 samples in this study, 14 were positive for the M1/YAP indel, agreeing with expected rates of occurrence for Near Oceania. Preliminary analysis shows haplogroup M1 is the dominant lineage on the islands of NI and Bougainville while haplogroup M2a is the dominant lineage for NB for all populations regardless of language spoken. However, further research is needed to refine haplogroup assignments and to assess genetic variability more accurately among these populations. To better define Y-chromosome lineages, SNP analysis will be expanded to include M9, M74, M130, M214, M175, P87, and P117.

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## Dietary variation by social status and sex in the aftermath of the medieval Black Death in London

SHARON N. DEWITTE<sup>1</sup>, JULIA BEAUMONT<sup>2</sup>, JANET MONTGOMERY<sup>3</sup> and REBECCA REDFERN<sup>4,5</sup>

<sup>1</sup>Department of Anthropology, University of South Carolina, <sup>2</sup>School of Archaeological and Forensic Sciences, University of Bradford, <sup>3</sup>Department of Archaeology, Durham University, <sup>4</sup>Centre for Human Bioarchaeology, Museum of London, <sup>5</sup>School of History, Classics and Archaeology, Newcastle University

Previous bioarchaeological research has revealed evidence of improvements in health following the Black Death in London. These changes occurred in the context of increases in standards of living in England (e.g. higher wages and improved diets) that were a result of the depopulation produced by the epidemic. This study contributes to an effort to determine the underlying mechanisms that might have produced the observed changes in health, specifically addressing the role of diet and possible decreased social inequality thereof in the post-epidemic population of London. This study assesses carbon and nitrogen ratios in a sample of  $n = 98$  human skeletal remains from the St. Mary Graces cemetery in London. This cemetery was in use between 1350 – 1538, and location within the cemetery reflects social status. The results indicate significantly higher  $\delta^{15}\text{N}$  in high status individuals compared to low status individuals, and higher  $\delta^{13}\text{C}$  in high status males compared to high status females. These findings suggest that high status individuals during this time period consumed higher trophic level foods compared to lower status people and that high-status males consumed more marine fish than did females. Contrary to expectations based on the historical literature, these findings suggest the persistence of status-based distinctions in diet in the post-Black Death period; they also suggest that gender, at least among high status individuals, mediated access to resources, and perhaps that improvements in standards of living after the Black Death might not have been equally enjoyed by both sexes.

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## Behavioral Evidence of Wild Bornean Orangutans Navigating to Non-Fruit Foods – Implications for Fallback Foods

ANDREA DIGIORGIO<sup>1,2</sup>, TRIWAHYU SUSANTO<sup>3,4</sup> and CHERYL D. KNOTT<sup>2,4</sup>

<sup>1</sup>Writing Program, Princeton University, <sup>2</sup>Anthropology, Boston University, <sup>3</sup>Biology, Universitas Nasional, <sup>4</sup>Reserach, Gunung Palung Orangutan Project

In 2015, Lambert and Rothman urged primate nutritional ecologists to revise the view of fallback and optimal foods from stable traits inherent in

the food to variable qualities determined by the state of the consumer. Here we provide behavioral evidence to support this revision. In primates, fruit is often the preferred food category because it is typically high-energy, high-carbohydrate, and low in fiber. Orangutans in particular, are said to consume fruit preferentially and when it is available, whereas leaves, bark, and pith are often considered fallback foods. Using movement ecology, we ask if wild Bornean orangutans (*Pongo pygmaeus wurmbii*) navigate only to fruit, or whether navigation to non-fruit foods is supported by our data. We find that orangutans do deviate from a direct fruit-to-fruit path to consume non-fruit foods ( $n = 54$ , range 8% - 84%;  $p = 6.819 \times 10^{-7}$ .) Next, we ask if orangutans consume non-fruit foods when in the proximity of fruit resources. We find that 25.5% of the time that orangutans eat a non-fruit food, there is an available fruit within 50m ( $n=308$ ). Building on previous research finding that orangutans maintain a 10.1:1 NPE:P balance, we use this geospatial data showing that orangutans navigate to and choose non-fruit foods, even when fruit is available, to suggest that orangutans are seeking foods based on their current nutritional state and not only to maximize energy. This supports the claim that 'fallback' is not an inherent characteristic of a food, but rather is in the state-dependent eye of the consumer.

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## Evaluating the aetiology of the geographically isolated Mseleni joint disease: A biocultural multi-method approach

ELIZABETH S. DINKELE<sup>1</sup>, ROBEA BALLO<sup>2</sup>, VICTOR FREDLUND<sup>3</sup> and VICTORIA E. GIBBON<sup>1</sup>

<sup>1</sup>Clinical Anatomy and Biological Anthropology, University of Cape Town, <sup>2</sup>Division of Cell Biology/Nutrition/Physiological Sciences, University of Cape Town, <sup>3</sup>Mseleni Hospital, Kwa-Zulu Natal

Mseleni joint disease (MJD) is a crippling arthropathy of unknown aetiology that is endemic to a rural region in KwaZulu-Natal, South Africa. The geographic confinement of MJD to a remote community of Zulu-language speakers is puzzling as the affected people are neither genetically nor culturally isolated. While environmental, socio-cultural and epigenetic factors are suspected to be aetiological of MJD, these are yet to be confirmed. To identify biocultural causes of MJD, the spatial and demographic distribution were assessed using data from patient surveys, a medical record review and national census publications (HREC 079/2019). Explanatory models of MJD were evaluated by conducting a grounded analysis of survey transcripts. Approximately 96% of MJD patients were local to regions with limited

potable water, with all patients reporting carrying water from off-plot sources (rivers, boreholes and wells) by head loading. Women were almost twice as likely to have MJD than men ( $OR=1.88$ ;  $p=0.03$ ) and several women linked the onset to childbirth and/or performing domestic tasks requiring load-bearing and walking long-distances. Explanatory models of MJD were variant, ranging from the supernatural (witchcraft or evil spirits), natural (physiology, genetics, environmental conditions and sanitation) and/or social (gender-based practices and lifestyle). Further research is underway to contextualise interactions between environmental, socio-cultural and biological risk factors of MJD to facilitate healthcare that meets the needs of the patient and community. This work demonstrates the value gained from integrating biomedical and traditional knowledge to understand disease aetiology, explanatory models and health-seeking behaviours in contemporary populations.

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## A model of human niche construction in a hypervariable environment centered on social memory

KRISTINA DOUGLASS and TANAMBELO RASOLONDRAINY

Anthropology, Penn State University

In this paper we address questions about human adaptations to climate change by analyzing an oral history archive from southwest Madagascar, and integrating its evolutionary logic into the development of a model of human niche construction. Southwest Madagascar is an excellent context in which to study human adaptation to climate change, since the region has long experienced a hypervariable climate and shifting resource distributions. The paleoclimate record of this region indicates that climatic conditions have shifted dramatically over the course of the Holocene, and that human and other biotic communities have experienced multiple extreme droughts over the past two millennia. Archaeological evidence from surface surveys and excavations suggest that short-term occupations of sites and frequent residential mobility have been a central feature of life on the southwest coast for millennia. Today, despite conservation and development initiatives that favor sedentarization of local communities, mobility remains key to the lives of fishing, foraging, herding and farming communities of the region. Our theoretical model highlights the central role of social memory in facilitating community mobility, social networking and shared resource use among groups of foragers, farmers, herders and fishers in the region. Using Niche Construction Theory, we argue that social memory, its maintenance and perpetuation

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contribute to a niche that makes human lifeways possible under the hypervariable conditions of southwest Madagascar. This work demonstrates the importance of preserving and engaging local, Indigenous and descendant (LID) knowledge to promote sustainability and develop robust and inclusive evolutionary theories of human adaptation to climate change.

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### Advisor Influence in the American Journal of Physical Anthropology

RHIAN R. DUNN<sup>1</sup>, NICHOLAS V. PASSALACQUA<sup>2</sup>, JOSEPH T. HEFNER<sup>1</sup> and KATIE ZEJDLIK<sup>2</sup>

<sup>1</sup>Anthropology, Michigan State University,

<sup>2</sup>Anthropology and Sociology, Western Carolina University

Pertaining to their mentorship and research, Drs. Armelagos, Buikstra, and Larsen are commonly considered defining figures in the field of bioarchaeology. However, each figure has a different background and unique ideologies which shape their understanding of human biology, which were likely passed down to their students. To better understand this assertion, this study examined their impact in the American Journal of Physical Anthropology (AJPA) in terms of publication counts by each figure and their students', average citation counts, and research foci.

Students of each figure were identified through the Academic Phylogeny website and AJPA article data (e.g., titles, abstracts) were web scraped in R using the "rvest" package. Article data underwent text analysis in R using the "tidytext" package to obtain word frequency, correlations, and topic predictors (via term frequency-inverse document frequency (tf-idf) scores).

Articles related to the three figures comprise approximately 3% of all AJPA articles. Dr. Armelagos' articles achieved the highest average citation count (53.7), followed by Larsen (29.5), and Buikstra (29.4). When clustered by natural topics, articles could not be accurately classified into their associated lineage, which indicates overlap in article foci. Using tf-idf scores, topic predictors were established for Dr. Armelagos (e.g., "Australopithecus"), Dr. Buikstra (e.g., "heritability") and Dr. Larsen (e.g., "Jomon"). These unique words illustrate different foci that are associated with each figure, highlighting potential research influences. Although these articles cannot be naturally classified by figure, this study aided in understanding how each figure influenced the dissemination and focus of research in the AJPA.

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### Evaluating landmark error and estimates of asymmetry in the hominin proximal femur

LESLEY H. EASON and LIAM M. ZACHARY

Department of Anthropology, University of Arkansas

Three-dimensional geometric morphometric analyses are often used to quantify morphological diversity among hominin fossils. Three-dimensional landmarks are set on anatomically homologous features, which are often considered functionally relevant. In recent years, 3DGM has been used to elucidate differences in postcrania in attempt to reconstruct phylogenies and interpret function from morphology. However, few studies fully examine the extent to which landmarking error affects these interpretations. The current analysis reproduces the most common landmarking techniques for the hominin proximal femur. To assess the effect of error, the degree of intraobserver error of multi-day trials on the same specimen is compared to the degree of differences between right and left femora of the same individual. Ten pairs (n=20) of right and left modern human femora are used for analysis. While trials on the same specimen tend to cluster, it is not always the case. In several instances, differences between trials (i.e., error) exceeds differences between left and right sides of the same individual. Furthermore, femora of different individuals occasionally plot within the degree of error or asymmetry of the same individual. Thus, the degree of error and asymmetry may obviate one's ability to identify femora of the same individual, while error potentially inflates estimates of sample variation. This underscores a lack of appreciation for error in the literature and the potential lack of discriminatory power of 3DGM. These issues may be alleviated by using more advanced techniques that capture more copious amounts of data and rely on computer automation, rather than observer repeatability.

### Our shared genetic mosaic and its implications for privacy

MICHAEL EDGE

Biological Sciences, University of Southern California

Over the last twenty years, large genetic databases have become common, and genetic information from millions of people is retained by recreational genomics services, by researchers, and by law enforcement. Often, even small sets of genetic markers are more informative than is typically appreciated, revealing information both about the person who is the source of the genetic data and about their biological relatives. This extra information often results from the fact that a person's genome is inherited in large pieces, effectively creating a mosaic of genetic tiles that is broadly shared. I will give some examples focusing on

privacy in genetic genealogy databases, where an adversary who uploads ~1000 genomes can, under some circumstances, recover at least one allele at up to 80% of a median person's genome. Further, in the same context, databases that use previous-generation methods for detecting identical-by-descent segments are vulnerable to attacks in which genetic data from every person in the database can be recovered by uploading fake datasets. The special features of genetic privacy problems—including the facts that our genetic information, once revealed, cannot be changed, and that our genetic information is shared across people—call for collective deliberation about the ways in which we will use genetic data.

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### Violence in the Ancient Southwest: Differential Suffering Among Males and Females

EMILY R. EDMONDS and DEBRA L. MARTIN

Department of Anthropology, University of Nevada, Las Vegas

Depopulation of the Mesa Verde region in the late 13<sup>th</sup> century has been largely explained by factors such as drought, resource scarcity, and warfare based on archaeological reconstructions. The burials at Mesa Verde tell a more nuanced story about the period leading up to the mass migrations. This study integrates skeletal material from Pueblo II and III sites on Wetherill Mesa with archaeological contexts. Skeletal trauma data was collected from burials (n=157) using standardized methods. Cranial and post-cranial trauma decreased temporally from 36% to 21%, contradicting theories that violence escalated prior to depopulation. Pueblo III males and females experienced violence differently. Females experienced a temporal increase in cranial trauma (from 40% to 75%) and higher Pueblo III frequencies of cranial trauma (75%) than males (31%). Females also experienced more lethal trauma (40%) than males (13%), who experienced repeated nonlethal trauma. Although not statistically significant, these differences suggest variability in violence-related trauma by sex and time period. Further, 6 individuals at Long House, a Pueblo III cliff dwelling, exhibited perimortem fractures and post-mortem manipulation of bodies in ceremonial kiva spaces. The ritualistic nature of the post-mortem processing and burial locations of these individuals fits the pattern of execution and body annihilation. Previous studies have suggested warfare as a migratory push factor, but this is not supported by the data. Instead, the burial data demonstrates a more complex pattern of violent behaviors, including lethal and nonlethal violence and executions, suggesting Ancestral Puebloans utilized a variety of culturally embedded systems of violence.

# ABSTRACTS

## Use of contact calls by wild woolly monkeys in Amazonian Ecuador

KELSEY M. ELLIS<sup>1,2</sup> and ANTHONY DI FIORE<sup>2,3</sup>

<sup>1</sup>Department of Anthropology, Miami University, Oxford, OH, <sup>2</sup>Department of Anthropology and Primate Molecular Ecology and Evolution Laboratory, University of Texas at Austin, Austin, TX, <sup>3</sup>College of Biological and Environmental Sciences, Universidad San Francisco de Quito, Cumbayá, Ecuador,

Primates characterized by high degrees of fission-fusion dynamics often use vocalizations to coordinate travel, locate and maintain contact with groupmates, recruit new party members, regulate spatial cohesion, and avoid extra-group conspecifics. In this study, we investigated the use of contact vocalizations in wild woolly monkeys (*Lagothrix lagotricha poeppigii*) - a taxon recognized as having fluid and flexible association patterns within and sometimes between groups - at the Tiputini Biodiversity Station in Amazonian Ecuador. During full-day focal follows of recognized individuals, we recorded all instances of vocalizations emitted by our focal animal and used one-zero sampling to record group-wide vocalizations in 5-minute windows throughout the day. In 2,220 hours of focal animal follows, we recorded nearly 10,000 vocalizations. A majority of these vocalizations (92.8%) were classified as short to medium distance contact calls (e.g., chirps and trills). Large adult males called the most out of any age-sex category, but not significantly more than adult or subadult females, while small adult and subadult males called significantly less ( $\chi^2 = 92.66$ ,  $df = 3$ ,  $N = 27347$ ,  $p < 0.001$ ). Given that young males are often found at the periphery of the group, limiting call production and/or participation in vocal exchanges may aid in reducing their exposure to predators or extra-group conspecifics. We also found that larger groups vocalized significantly more often than smaller groups ( $\chi^2 = 240.84$ ,  $df = 3$ ,  $N = 25850$ ,  $p < 0.001$ ), perhaps due to increased subgrouping behavior and the difficulty of coordinating group members at larger group sizes.

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## A Comparison of Fluctuating Asymmetry Across the Human Skeleton

AMANDINE ERIKSEN<sup>1,2</sup> and NOREEN VON CRAMON-TAUBADEL<sup>2</sup>

<sup>1</sup>Department of Basic Medical Sciences, University of Arizona College of Medicine-Phoenix, <sup>2</sup>Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo-SUNY

Fluctuating asymmetry (FA) offers insight into the genetic and environmental factors that disrupt growth and is a widely used measure of early life stress, reproductive fitness, and attractiveness. However, previous studies have made different

*a priori* assumptions about the causes of FA and tend to focus on single skeletal elements, thereby limiting the ability to understand the true source(s) of asymmetry. Here, we make comparisons across body regions, utilizing a sample of 114 individuals (59 males, 55 females) each consisting of a cranium, mandible, sacrum and the right and left os coxa, humerus, radius, femur, and tibia. FA was quantified using landmark configurations on 3D bone models to explore whether magnitudes of FA (1) correlate between bone regions and (2) vary between sexes. Results indicate FA is statistically significant and represents the highest asymmetric component of variation for the entire sample. The most notable difference is observed in males who display higher FA variation among the upper limb bones. However, no correlations are observed between any bone pairing in males. In contrast, females exhibit a significant, albeit relatively weak, correlation between the cranium and tibia ( $r = 0.31$ ,  $p = 0.02$ ). Males and females exhibit similar patterns of variation, with the highest levels observed in upper limb bones and the lowest variation found in the cranium and sacrum. As a whole, these results suggest that the magnitude of FA varies across different parts of the skeleton and therefore illustrates that caution should be exercised when only examining one region of the body.

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## The benefits of selective use of aggression by male hamadryas baboons

KATARINA D. EVANS<sup>1,2</sup>, LARISSA SWEDDELL<sup>1,2,3</sup> and SHAHRINA CHOWDHURY<sup>1,2,4</sup>

<sup>1</sup>Anthropology Program, Graduate Center, City University of New York (CUNY), <sup>2</sup>New York Consortium in Evolutionary Primatology (NYCEP), <sup>3</sup>Anthropology, Queens College, City University of New York (CUNY), <sup>4</sup>Anthropology, Brooklyn College, City University of New York (CUNY)

Understanding the evolution of behavior in multilevel societies, such as that of hamadryas baboons, can offer valuable insights into human evolution. Hamadryas one-male units (OMUs), comprising a "leader" male, females, and sometimes "follower" males, are formed via successive female takeovers, either aggressive or non-aggressive, and male coercion after takeovers is important in maintaining OMUs. Here we use data from Filoha, Ethiopia to examine correlates of aggression during takeovers. We found that a male's presumed number of infants sired increased with his number of non-aggressive takeovers ( $F(1,39) = 14.39$ ,  $p = 0.0005$ ) but not aggressive takeovers. Additionally, we found positive relationships between a male's number of both aggressive ( $F(1,43) = 6.54$ ,  $p = 0.014$ ) and non-aggressive takeovers ( $F(1,43) = 12.95$ ,  $p = 0.0008$ ) and his number of females but not the number of followers in

his OMU (which previous studies have shown is predictive of leader male fitness). We also found negative relationships between a leader male's average intensity of aggression toward other males during takeovers and both his presumed number of infants sired ( $F(1,18) = 6.25$ ,  $p = 0.022$ ) and his total number of followers ( $F(1,18) = 4.81$ ,  $p = 0.042$ ). Lastly, we found that leader male aggression was more intense toward females ( $F(2,20) = 7.97$ ,  $p = 0.003$ ) but not toward other males in interband, compared to intraband, takeovers, reflecting the importance of male-male "respect" for "possession". Our findings suggest that hamadryas leader males selectively use aggression, that those who limit aggression toward other males may have greater success in attracting followers, and that aggressive takeovers may lead to fewer births via female reproductive suppression.

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

## Are linear measurements or areas of birth canal planes more relevant to obstetric studies?

JENNIFER EYRE

Anthropology, Bryn Mawr College

The linear dimensions of the three major birth canal planes are frequently measured in studies concerning obstetrics in hominins and modern humans. However, the skeletal birth canal planes are not regular in shape and simple linear measurements may not accurately capture the two-dimensional area of each plane. In this study I created three-dimensional scans of ecogeographically varied modern human female pelvises ( $N = 128$ ). For each pelvis one innominate and the sacrum was scanned, and the innominate was mirror-imaged in Geomagic to create a full pelvis. Anteroposterior and mediolateral measurements were taken in Geomagic following Tague and Lovejoy (1986). A novel method was utilized to measure the area of each plane. The 3D scan was exported as a 2D image into ImageJ where each plane was outlined based on landmarks and semilandmarks on the pelvis and sacrum. The area enclosed in each outline was then measured. The inlet was outlined in superior view; for the midplane the pelvis was removed superior to the ischial spines laterally, the inferior pubic symphysis anteriorly, and the articulation between the fourth and fifth sacral vertebrae posteriorly; the outlet was outlined in inferior view.

Linear dimensions correlated highly and significantly with measured areas ( $r > 0.8$ ,  $p < 3 \times 10^{-32}$ ). However, a Student's t-test identified significant differences between the linear dimensions and area of the inlet ( $p = 0.00075$ ) and outlet

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( $p=9.3 \times 10^{-14}$ ). I conclude that while the measured areas may be more accurate, they may be less relevant because the perinate may be unable to take advantage of the entire area of each plane.

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### **"When the voices of children are heard": Evaluating the biological effects of socioeconomic status on children in postmedieval London**

ASHLEY EZZO

Anthropology, University of Louisville

Socioeconomic status (SES) is critical to understanding health and disease. Limited access to resources, for example, has been shown to contribute to heightened levels of stress. While the impacts of SES are frequently studied among adults in archaeological samples, this focus negates an especially important and vulnerable sample of populations, children. Previous paleodemographic work has shown higher mortality rates in Postmedieval London among low-SES non-adults without consideration of paleopathological profiles. In this preliminary research, the effects of SES on biological health are considered in non-adults (under 18 years) from two Postmedieval London cemeteries: high-SES St. Bride's Crypt (SBC; N=14) and low-SES St. Bride's Lower (SBL; N=166). Individuals were classified into three developmental age groups (1-5 years/6-10 years/12-17 years) and recorded (presence/absence) for skeletal and dento-alveolar evidence of linear enamel hypoplasia (LEH), carious lesions, antemortem trauma, rickets, scurvy, and cribra orbitalia. Crude prevalence rates (CPR) for all conditions and true prevalence rates (TPR) for LEH, caries, and cribra orbitalia were compared through Fisher's Exact tests between cemeteries and age groups within cemeteries. Results indicated only significant differences ( $p\text{-value}<0.05$ ) in LEH between SBC (TPR: 23.4%; CPR: 50%) and SBL (TPR: 7.74%; CPR: 17%). Although there are individual cases of deliberate antemortem trauma and higher rates of trauma within SBL, there were no significant differences between the two samples. While these individuals represent the frailest children of their communities, they nonetheless demonstrate the complexities of SES and the possible indiscriminate health, environmental, and social conditions affecting all Postmedieval children.

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### **Metanalysis of Postcranial Fractures in Ancient Andean Populations (400 BCE - 1532 CE)**

ANNA FANCHER

Anthropology, Cornell University

This study analyzes previously published data on postcranial fractures from 9 skeletal populations in the prehistoric Andean region, dating to the Early Intermediate Period (ca. 200 BCE - 500

CE), Middle Horizon (ca. 500 -1100 CE), Late Intermediate Period (ca. 1100 - 1450 CE, and Late Horizon (ca. 1450 - 1532 CE). Bioarchaeologists typically consider postcranial fractures indicators of accidental and/or occupational injuries, excepting a few specific fracture types, including parry fractures. Most commonly, bioarchaeologists use postcranial fractures to characterize the risks associated with a specific environment or means of subsistence. This study compares coastal to highland populations (as a proxy for environment) and populations across time periods (as a proxy for changing subsistence and/or sociopolitical complexity) to assess the impact of these factors on postcranial fracture frequency. The difference between rates of all postcranial fractures among coastal (2.9%) and highland (3.0%) populations was not statistically significant ( $p=0.6721$ ). This suggests that these environments did not pose markedly different quotidian hazards to their residents, perhaps due to cultural adaptations. Comparison between the Early Intermediate Period (4.6%), Middle Horizon (1.7%), and Late Intermediate Period/Late Horizon (4.8%) found that the Middle Horizon had significantly lower postcranial fracture rates than the surrounding time periods ( $p<0.00001$  in both cases), suggesting lower participation in risky activities during this period of political centralization. Though several confounding factors, including differential preservation, demography of burial populations, and differing regional chronologies make a comparative approach challenging, these results demonstrate the benefits of a large-scale, diachronic perspective for bioarchaeological data.

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### **Oral processing, folivory, and premolar size in eight cercopithecoid monkeys**

LUKE D. FANNIN<sup>1,2</sup>, DEBBIE GUATELLI-STEINBERG<sup>3</sup>, JAKE ARFT-GUATELLI<sup>4</sup>, NOAH T. DUNHAM<sup>5</sup>, JORDAN E. TRAFF<sup>6</sup>, TAYLOR PALVADORE<sup>6</sup>, ANDREA DONALDSON<sup>7</sup>, PAMELA CUNNEYWORTH<sup>7</sup>, DAVID J. DAEGLING<sup>6</sup> and W SCOTT. MCGRAW<sup>3</sup>

<sup>1</sup>Anthropology, Dartmouth College, <sup>2</sup>Program in Ecology, Evolution, Ecosystems, and Society, Dartmouth College, <sup>3</sup>Anthropology, The Ohio State University, <sup>4</sup>University of California, Berkeley, <sup>5</sup>Conservation and Science, Cleveland Metroparks Zoo, <sup>6</sup>Department of Anthropology, University of Florida, <sup>7</sup>Colobus Conservation Limited

The ecological correlates of premolar size in primates continue to be debated. One explanatory framework – the cyclical loading hypothesis – posits that species who more frequently load their teeth have relatively larger premolars (e.g., P<sup>3</sup>, P<sup>4</sup>, and P<sub>4</sub>) in response to greater cyclical chewing activity. Previous tests of this hypothesis have used (a) time spent feeding or (b) degree of folivory as proxies for cyclical chewing loads; however, recent studies suggest oral processing data – including number of masticatory cycles associated with each ingestive event, better model the

selective pressures acting on tooth size. Here, we test the cyclical loading hypothesis as it pertains to premolars in eight cercopithecoids for whom oral processing profiles are known. Premolar size variation in folivorous and frugivorous cercopithecoids was more strongly and positively correlated with the number of postcanine mastications per ingestive event than either percent leaves consumed or time spent feeding, thus supporting cyclical loading hypotheses. A notable outlier was the papionin *Cercocebus atys*: sooty mangabey premolar dimensions, scaled to both palate area and mandibular length, are the highest in the sample despite this monkey's comparatively low level of postcanine mastication. Premolar area scaled isometrically with mandibular length in all species except *C. atys*, which exhibited positive allometry. We posit this size-shape relationship is attributable to the unique postcanine crushing behavior exhibited by *C. atys* during durophagous feeding. Our study highlights how oral processing profiles can aid in illuminating the different selective forces acting on dental morphology during primate evolution.

Fieldwork in Tai was supported by National Science Foundation (BCS 0840110, 0921770, 0922429) and the Yerkes National Primate Research Center.

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### **Intrauterine hormone effects on tooth morphology in dizygotic opposite-sex twins**

RANDALL FEEZELL<sup>1</sup>, KATHLEEN S. PAUL<sup>1</sup>, TOBY HUGHES<sup>2</sup> and ALAN BROOK<sup>2</sup>

<sup>1</sup>Anthropology, University of Arkansas, <sup>2</sup>Adelaide Dental School, University of Adelaide

Biological anthropologists use dental morphology to study human migration patterns, family relationships, and morphologic trait expression genetics. Studies have identified canine and molar characters as sexually dimorphic. By testing the twin testosterone transfer (TTT) hypothesis, this study examines a potential biological basis of sexual dimorphism in canine and molar morphology. This hypothesis posits that females gestated with male co-twins develop more masculine phenotypes due to androgen exposure in-utero. Studies have shown that hormone levels and Y-chromosome effects lead to significantly larger tooth crowns in human females belonging to opposite-sex dizygotic twin pairs (OSDZ) as compared with females belonging to same-sex monozygotic (MZ) and dizygotic (DZ) twin pairs. Here, we expand the TTT hypothesis to dental morphology in a longitudinal sample of Australian twins (OSDZ females: n=12; MZ/DZ females: n=109). Data for 16 deciduous and 17 permanent crown characters were collected from stone casts following Arizona State Dental Anthropology System standards. Non-parametric mean comparisons and bootstrap resampling revealed significantly elevated character expression in OSDZ females compared with MZ/DZ

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females for six deciduous traits (two canine traits, four molar traits) and four permanent molar traits. Males trend toward increased crown elaboration; these results suggest in-utero effects lead to more masculine dental morphology in female members of opposite-sex twin pairs.

Data collected under NSF 2015 GROW, NSF DDRI Grant 1540313, Wenner-Gren Dissertation Fieldwork Grant (KSP)

### Variation in the sexual dimorphism of nonmetric skeletal traits due to settlement style: A study of hunter-gatherer, rural, and urban populations

MARIA E. FEILER<sup>1,2,3</sup>, ERIN B. WAXENBAUM<sup>3</sup>, SARAH A. SCHRADER<sup>2</sup>, CARLA L. BURRELL<sup>2,4</sup> and MENNO HOOGLAND<sup>2</sup>

<sup>1</sup>Division of Anthropology, American Museum of Natural History, <sup>2</sup>Laboratory for Human Osteoarchaeology, Leiden University, <sup>3</sup>Department of Anthropology, Northwestern University, <sup>4</sup>Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

Human skeletal sexual dimorphism in the cranium and pelvis is inconsistent across populations, resulting in recalibration of nonmetric sex estimation methods for modern samples. Little research has sought the underlying, biological etiology of this inconsistency. Settlement style presents differences in nutrition, disease, and pollution, which could influence the morphology of nonmetric cranial and pelvic traits. Therefore, an analysis of trait expression between differing settlement styles could illuminate patterns of sexual dimorphic variation in humans.

This cross population, comparative study examines sex-balanced archaeological samples of Native Alaskan hunter-gatherers (n=105), post-Medieval rural Dutch (n=118), and post-Medieval urban Dutch (n=91) to investigate the any statistically significant variation between varying settlement lifestyles. Via one-way ANOVAs, Tukey-Kramer post-hoc tests, and Greene's t-tests, the rural Dutch population showed a marked increase in dimorphism compared to the Alaskan hunter-gatherer and Dutch urban populations for the supraorbital margin (p=0.016 versus p=0.014) and the glabella (p=0.0040 versus p=0.048), suggesting that rural lifestyles is correlated with an increased sexual dimorphism in these traits. The greater sciatic notch proved to be the most consistent trait across settlement styles, which could have implications for the evolutionary plasticity of the pelvis.

Despite ancestral and climatic differences between these populations, the variation of these standard nonmetric traits implies that anthropologists need to further explore the relationship between skeletal morphology and an individual's

lived experience. Further investigation will vastly improve forensic and archaeological procedures producing more accurate, population specific, skeletal assessments.

### Does Variation in Quilombos' Diets Influence the Hemogram Profile?

FIONA FELKER<sup>1</sup>, SABRINA GUIMARAES-PAIVA<sup>2</sup>, MARIA DE NAZARÉ KLAUTAU-GUIMARAES<sup>3</sup>, SILVIENE FABIANA DE OLIVEIRA<sup>3</sup> and LORENA MADRIGAL<sup>1</sup>

<sup>1</sup>Anthropology, University of South Florida, <sup>2</sup>Educacion, Instituto Federal de Educação, Ciência e Tecnologia do Tocantins, Araguaína, <sup>3</sup>Instituto de Ciências Biológicas, Universidade de Brasília.

Previous research demonstrates that the genotypes, HbAA, HbAA+HbF, HbAS, and HbAC influences the value of four hemogram profile tests, hematocrit, MCV, MCH, and MCHC, in three *Quilombos* in the Central Brazilian states of Goiás and Tocantins. In addition to genotype, diet is known to influence the outcome of these hemogram profile tests (Billett, 1990; Maner & Moosavi, 2019). The **purpose** of this project is to determine if the variation in diet between these three *Quilombos* has also influenced hemogram profile tests' values. Population 1 is a rural/semi-urban community, Population 2 is an urban community, and Population 3 is a rural/semi-isolated community. Those in the rural/semi-urban community have a relatively more plant-based diet, whereas those in the urban community have a diet with greater meat consumption. We **found** significant variation in the hemogram profile values of hematocrit, MCV, and MCHC, between the three populations. Results of a Kruskal-Wallis test indicate that there were significant differences in the hematocrit values ( $X^2=15.08, df=2, p<0.0005$ ), MCV ( $X^2=20.1169, df=2, p<0.0001$ ), and MCHC ( $X^2=22.6884, df=2, p<0.0001$ ). Population 2's higher hematocrit value of 44.81% compared to Population 1's 42.01% and Population 3's 42.43%, is not surprising, due to the higher consumption of beef in Population 2's diet. We **demonstrate** that dietary differences between *Quilombos* does influence the hemogram profile. The meat consumption associated with Population 2 maybe what is causing the higher hematocrit values. The greater consumption of beef by individuals residing in Population 2 could possibly provide protection against anemia, especially important for individuals who have genotype HbAS.

### Characterization of genetic variants in six individuals from the population of Lagoa Santa, MG, Brazil: contributions to the biocultural understanding of the peopling of America

TATIANA FERREIRA DE ALMEIDA<sup>1,2</sup>, LORENA DA CRUZ AMARAL<sup>2</sup>, ANDRÉ STRAUSS<sup>3</sup> and DANILO VICENSOTTO BERNARDO<sup>2,4</sup>

<sup>1</sup>Laboratório Clínico, Hospital Israelita Albert Einstein, <sup>2</sup>Laboratório de Estudos em Antropologia Biológica, Bioarqueologia e Evolução Humana, Instituto de Ciências Humanas e da Informação, Universidade Federal do Rio Grande, <sup>3</sup>Laboratório de Arqueologia e Antropologia Ambiental e Evolutiva, Universidade de São Paulo, <sup>4</sup>Programa de Pós-Graduação em Antropologia - PPGAnt, Instituto de Ciências Humanas. Universidade Federal de Pelotas

Lagoa Santa is a karst region with unusual archaeological preservation conditions in the American continent. For this reason, the contributions of this region to Bioarchaeology and studies on the settlement of the New World occupy a position of recognized prominence in the debates on this theme. In the last decades, a large number of works based on biological anthropology markers, such as analyzes of biodistances, variation and adaptability and style and quality of life, for example, were produced on the skeletons of Lagoa Santa, keeping the emphasis on the studies carried out on the region. Recently, molecular markers have also started to be used in these studies, initiating the exploration of a new source of information for the investigation of the biocultural interactions of past populations, discussing the origin, dispersion and chronologies of Native Americans. Here, we present a preliminary study based on the genetic data of six individuals from the Lapa do Santo site, with approximate dates of 8500 years BP, in order to characterize their genetic profile in terms of ancestry, kinship and related variants to diseases. Illumina's SNP matrix fastq files were aligned to the human reference build hg38 with BWA-MEM, following the variant call with GATK 4.0 and annotation with VEP (Variant Effect Predictor). Our results did not indicate the occurrence of any variant with a certain clinical interest, but, nonetheless, they present a new approach to population studies with the potential to better understand the biocultural relationships presented by the pristine populations of the region.

### Testing isolation by distance among Brazilian shellmound builders using dental morphology

DANIEL FIDALGO<sup>1,2</sup>, VERONICA WESOLOWSKI<sup>1</sup> and MARK HUBBE<sup>3,4</sup>

<sup>1</sup>Museu de Arqueologia e Etnologia, Universidade de Sao Paulo, <sup>2</sup>CIAS: Research Centre for Anthropology and Health, Universidade de Coimbra, <sup>3</sup>Department of Anthropology, Ohio State

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University, <sup>4</sup>Instituto de Arqueología y Antropología, Universidad Católica del Norte

The Brazilian coast was inhabited by distinct groups of shellmound builders between approximately 8,000 BP and 1,000 BP. In the South coast, populations were sedentary, highly adapted to local environments, and built monumental shellmounds over thousands of years. In the Southeast, shellmound builders occupied not only the Atlantic coast, but also riverine areas within the Atlantic Forest, with possible gene flow between these two environments. Although South and Southeast groups shared many cultural and biological similarities, regional differences challenge the idea of a culturally and biologically homogenous population, and the degree of contact between them has been highly debated by previous archaeological and bio-anthropological studies. To contribute to this discussion, we analyzed the dental morphology of 385 individuals from 14 archaeological sites, using 18 traits from the Arizona State University Dental Anthropological System. Multidimensional scaling of biological distances was used to explore series similarities, and Mantel matrix correlation and partial correlation tests were used to test the hypothesis that regions were biologically isolated from each other. Results show that South shellmound builders were more biologically similar than Southeast series, suggesting that the cultural differences in this region are reflected in biological differentiation during the Holocene. Mantel tests show a significant correlation between biodistances and geography ( $r = 0.3926$ ,  $p = 0.031$ ), even when correcting for chronological differences ( $r = 0.4049$ ,  $p = 0.039$ ). These results support that shellmound builders were low-mobility groups, with gene flow mediated by geographic distances, favoring neighboring populations, while still maintaining limited contact with others from distant geographic areas.

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## A land of confluence: identifying pre-Hispanic migrations in Uruguay through mitogenomes

GONZALO FIGUEIRO and MÓNICA SANS  
Departamento de Antropología Biológica,  
Universidad de la República

The middle and late Holocene archaeological record of Uruguay is similar to the record found in two adjacent territories (southern Brazil and the Paraná River delta in Argentina). However, the extent to which these archaeological similarities have a genetic correlate is only recently beginning to be addressed, through the analysis of mitochondrial DNA data.

We present the results to date on three ancient and 37 present-day mitochondrial genomes from Uruguay, 32 of them unpublished, belonging to Native American founding haplogroups A2, B2, C1, and D1. The ancient samples were selected from archaeological sites in eastern Uruguay, and the modern samples were selected based on their previously known control region sequence: Sequences showing motifs that were either unique (i.e. not shared) or clearly shared with other South American populations were picked for mitogenome sequencing. Similarities and evolutionary relationships to other South American ancient and modern mitochondrial sequences were analyzed through the construction of two successive median-joining networks and an intermediate filtering step of sequences with distant or no relationship with the Uruguayan sequences.

More than one-third of the sequences ( $n=15$ ) showed no affinity with known South American sequences, whether due to sampling or genetic drift. Of the remaining 25 sequences, affinities were found with samples in the southern, western, and northern parts of the continent, with D1j1 and C1d1 sequences showing strong similarities, and A2 and D1g5 sequences showing more deep-rooted relationships. These results taken as a whole point to a complex panorama of population movements throughout the Holocene.

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## The Bioanthropology Study and Research Group of the State University of Pará, GEB/UEPA, Brazil: Education in Biological Anthropology in the Amazon, Achievements and Challenges

LIGIA A. FILGUEIRAS<sup>1,2,3,4</sup>, ROSEANE B.T. OLIVEIRA<sup>3,4</sup>, ARIANA K L S. DA SILVA<sup>2,3,4,5</sup>, HILTON P. SILVA<sup>3,4</sup> and EDSON M L S. RAMOS<sup>3,6</sup>

<sup>1</sup>Natural Sciences, Part State University - UEPA, <sup>2</sup>Education, Part State Education Secretary - SEDUC, <sup>3</sup>Study and Research Bioanthropology Group, GEB/UEPA, <sup>4</sup>Anthropology Department, Part Federal University - UFPA, <sup>5</sup>Social Sciences Department, Part State University - UEPA, <sup>6</sup>Statistics Department, Part Federal University - UFPA

In October of 2018 the I Seminar of the Bioanthropology Study and Research Group of the State University of Pará (GEB/UEPA) was held with the theme "The Biocultural Perspective of Anthropology", including 12 lectures, an exhibition on Human Evolution, scientific poster sessions with national and international participants, film sessions related to the theme, and gathered over 100 participants. In 2019, the II Seminar, entitled "Research in Focus: The Importance of the Consolidation of Bioanthropological Science in the Amazon" was held with 16 lectures, a Forensic Anthropology mini-course and 98 participants. Due to the COVID-19 pandemic in 2020, the III

Seminar, entitled "From Fieldwork to the Virtual World", was held in October completely online, with 34 lectures, and 38 national and international speakers (USA, Europe, Latin America, and Brazil). Even though facing considerable technical difficulties due to limited access to internet in the Amazon, the event provided increased visibility as all lectures were made available on the group's YouTube channel. Despite the attacks on Brazilian science, and particularly on the Social Sciences, by the current government, this is the first research group in the field of Biological Anthropology of this State university, and it is only the second in existence in the North of Brazil. In these three years, this pioneer effort has produced a vast material about Bioanthropology in the region, helped to disseminate and strengthen science education, and promoted research in human evolution, variation and adaptation in the Amazon, and in Brazil.

## Patterns of local paleoenvironmental change and bovid turnover during the emergence of *Paranthropus* and *Homo* in eastern Africa

ELIZABETH N. FILLION<sup>1,2</sup> and TERRY HARRISON<sup>1</sup>

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

The hominin lineages *Paranthropus* and *Homo* emerged in eastern Africa during an important period of global climate change in the Late Pliocene. Teasing apart the complex relationship between global climate and local environmental change and understanding its impact on mammal communities is crucial for uncovering the underlying environmental forces that may have played a role in the divergence of these lineages. We used hierarchical linear models of published stable carbon isotope data derived from paleosol carbonates to determine the extent to which local vegetation change at paleoanthropological sites across eastern Africa conforms to region-wide patterns between 3.5 – 2.5 Ma. We find that most sites follow similar trends of increasing C4 vegetation, suggesting that climate change contributed to shared patterns of local vegetation change across the region. However, exceptions to this pattern in the Turkana Basin suggest that for some sites, factors such as topography, hydrology, or community resilience may have acted to buffer local ecosystems against global climate change. To assess the impact of local vegetation change on mammal communities, we compared changes in the taxonomic diversity of bovids—a group considered to be sensitive ecological indicators—between sites. We find that species turnover is not consistently correlated with vegetation change, indicating that changes in bovid diversity may be driven by broader regional environmental patterns rather than by local conditions. These findings

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have important implications for understanding the environmental factors driving mammal extinction and speciation in the Late Pliocene, including the emergence of *Paranthropus* and *Homo*.

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### Automation: a path to standardisation and quantification of taphonomic data collection

DEVIN A. FINAUGHTY<sup>1</sup>, MAXIMILIAN J. SPIES<sup>2,3</sup>, JUSTIN PEAD<sup>3</sup> and VICTORIA E. GIBBON<sup>2</sup>

<sup>1</sup>School of Anthropology and Conservation, University of Kent, <sup>2</sup>Department of Human Biology, University of Cape Town, <sup>3</sup>Department of Electrical Engineering, University of Cape Town

Forensic taphonomy has long-suffered from the “Five Hindrances” first articulated by Marshall in 1989, and such remain unsolved. At the root of this widely acknowledged failure are narrowly scoped, variably resourced, and biogeographically uncoordinated taphonomic investigations hindered by a lack of standardisation in investigative methodology, producing oft low-resolution data across a limited array of variables implicit in the decomposition ecosystem. We believe a solution to overcoming these challenges lies in automation of taphonomic data collection. To this end, we wish to present our automated taphonomic data collection system. We will share the technical specifications of the current iteration of the device: a modular, scalable, independently-powered platform linking remotely to a central online data handling and systems monitoring interface facilitating real-time monitoring of decomposition. Alongside an 85% reduction in research operating costs, the device has greatly reduced the missing data rate. Manual weight measurements from previous research had, on average, 38.41% missing recordings across four seasonal deployments. The current iteration of the automated device has reduced the missing data rate to just 7.14%. We will also present plans for future improvements to the device and a proposal for the establishment of much called-for large, coordinated multi-biogeographical taphonomic studies based upon deployment of the new technology. We believe this platform can help the discipline achieve the sorely needed standardisation of data collection and increased statistical rigor, quantitative measurement and mathematical description of results demanded by science and the courts – a boon for forensic taphonomy and justice efforts worldwide.

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### Paleodietary Reconstruction through a Modern Food Science Lens – A Big Data Modeling Approach to Calculating $\delta^{15}\text{N}$ Shifts Using Protein Breakdown Sequences

KIMBERLY K. FOECKE and ALISON S. BROOKS  
Anthropology, George Washington University

Paleodietary reconstruction using the nitrogen isotope system is commonly applied to human skeletal remains with the goal of determining trophic position and/or aquatic resource consumption. However, there is limited information about how complex food behaviors affect this system. We focus on assessing the impact of cultural food modification behaviors (e.g. cooking, smoking, preservation) on food item  $\delta^{15}\text{N}$  baselines and how these shifts may be passed into the consumer. A potentially broadly applicable way to address these questions is to use a modeling approach that builds bulk predictions for  $\delta^{15}\text{N}$  shifts in food items based on amino-acid level changes in response to stimuli. The field of food science has been generating experimental and observational data on protein breakdown sequences at the amino acid level for many years. This study has compiled a large database from the food science literature, and combines it with novel experimental  $\delta^{15}\text{N}$  data in order to test whether a big data modeling approach can be a viable tool for assessing the effect of food processing on human  $\delta^{15}\text{N}$  values. We apply this approach to one cultural behavior: cooking. Using a model of amino acid profile changes during protein breakdown in meat cooking, we test whether the molecular model can accurately predict measured bulk  $\delta^{15}\text{N}$  shifts in cooked meat. The results of this study are a first step in a larger effort to use this type of modeling to predict  $\delta^{15}\text{N}$  shifts from food processing through consumption to the final isotopic measurement of human skeletal remains.

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### Deformation-based geometric morphometrics captures the morphology of the modern human hipbone

CINZIA FORNAI<sup>1,2</sup>, ALESSANDRO URCIUOLI<sup>3</sup>, VIKTORIA A. KRENN<sup>1,2</sup>, MARTIN HAEUSLER<sup>1</sup> and NICOLE M. WEBB<sup>1,4</sup>

<sup>1</sup>Institute of Evolutionary Medicine, University of Zurich, <sup>2</sup>Department of Evolutionary Anthropology, University of Vienna, <sup>3</sup>Institut Catal  de Paleontologia Miquel Crusafont, Universitat Aut noma de Barcelona, <sup>4</sup>Department of Palaeoanthropology, Senckenberg Research Institute and Natural History Museum Frankfurt

The human pelvis shows clear sexual variation, where the female birth canal has evolved to accommodate large babies while maintaining bipedal locomotor efficiency. This sexual

dimorphism is pronounced in the hipbone, with females having an elongated pubic ramus, outwardly rotated ischium, and wider greater sciatic notch than males. These traits have been extensively investigated using various morphometric approaches, although the variation of the hipbone as a whole is less studied. Therefore, we assessed modern human hipbone variation by applying a novel, deformation-based morphometric technique using surfaces, thus overcoming drawbacks associated with landmark point collection. The hipbone is particularly suited for testing this method on complex shapes and permits useful methodological comparisons.

3D surface models of modern human hipbones from Central Europe, Africa, and Asia, including 78 males and 71 females, of which 48 are 15 to 18-years-old juveniles, were registered, uniformly scaled and then analyzed using Deformetrica 4 (deformetrica.org). Deformation fields reflecting orientation and amplitude of deviations from the mean were analyzed via Principal Component Analysis.

Our results successfully captured the expected distribution of the hipbone's sexually diagnostic characteristics along PC1 (ischio-pubic relative length, shape of the greater sciatic notch, relative acetabulum size) and PC3 (relative ilium height). The analysis further allowed identification of an ontogenetic trend, where, differently from males, female adult hipbones differentiated from juveniles along PC2 for ilium orientation. This demonstrates the successful application of a time-efficient, deformation-based morphometric method, which offers the operative advantage of a landmark-free approach while highlighting important shape patterning.

The analyses were performed using High Performance Computing resources from Barcelona Supercomputing Center (BCV-2020-1-0008). This research was funded by the Swiss National Science Foundation grant No 31003A\_176319.

### Microstructure and Fracture Strength in Primate Tooth Enamel

FREDERICK R. FOSTER

Anthropology, Rutgers, the State University of New Jersey

Changes in relative enamel thickness constitute major patterns in hominin and primate evolution. Recent work has drawn attention to the role of thick enamel as a stress shielding adaptation in teeth, using predictive equations that relate the force required to propagate cracks within enamel to the thickness and geometry of molar cusps. These equations use simplifying assumptions, that enamel has a homogenous internal structure and is isotropic in its mechanical properties. However, enamel is composed of a hierarchically organized microstructure with mechanical properties that vary throughout the cusp, both of which

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have been linked to tooth resilience and enhanced fracture strength. Here, I characterize the mechanical properties and microstructure in primate molar enamel and integrate these features with our broader understanding of enamel thickness as a stress shielding adaptation. Nanoindentation is used to determine how the stiffness and hardness of enamel changes throughout the cusp. Microindentation and tensile testing are used to assess the relative toughness of different types of enamel within the cusp. Scanning electron microscopy is used to image the microstructural features that are important for enhancing fracture strength throughout the thickness of enamel. The sample includes nine individuals from *Macaca mulatta*, allowing for the characterization of within-species variation in microstructure and properties. The results highlight the important contributions that microstructural adaptations make to the toughness of teeth within the context of changing relative enamel thickness. The findings have implications for how we interpret changing relative enamel thickness within the hominin lineage and primate dietary ecology more broadly.

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### Patterns of same-sex relationships in women across the globe: what do we know?

STEPHANIE A. FOX

Department of Anthropology, University of New Mexico

The formation of social bonds between unrelated individuals is considered a hallmark of human behavior and research in humans as well as several other social animals has indicated the importance of social ties for health, survival and fitness. While kin selection theory predicts that individuals will form stronger social bonds with kin, individuals may also invest in social relationships with non-kin when these ties confer fitness gains. Here, I summarize our current understanding of women's same-sex relationships, highlight limitations and suggest research priorities.

Previous research on women's cooperation and social networks is skewed toward the cooperative childcare observed within kin-networks, while relationships among non-kin are painted as rare, less cooperative and ephemeral. However, these data come from few populations, making generalizations about women's social ties premature. For example, where cross cultural data are available, women are reported to regularly form social relationships with non-kin, even when kin are accessible. Additionally, while ethnographic reports suggest that ties can be helpful for subsistence work in addition to childcare, we have no systematic studies examining the

full extent of women's bonds across different domains of life. Further, we lack documentation on the stability of relationships, whether relationships with kin and non-kin have unique functions, and how relationships change across life history stages. Finally, where women's friendships are mentioned in ethnographic literature, these relationships are often reported as peripheral to the community's social activities, leaving it unclear whether women's social lives have historically been under documented due to their occurrence outside the public sphere.

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### Secular trend in body weight of Rhesus macaques (*Macaca mulatta*) at Cayo Santiago

GEORGE N. FRANCIS and QIAN WANG

Biomedical Sciences, Texas A&M College of Dentistry

Secular trend in body weight is an indicator of environmental adaptation and changes in nutrition and health over time. In this study, we examined body weight of *Macaca mulatta* from Cayo Santiago to investigate body weight change in the past 80 years. Rhesus macaques were introduced from India to the Caribbean island in 1938, and the colony history was characterized by fluctuations in resource provisioning, population dynamics, and medical care, in addition to acclimation. We collated body weight data of 921 females and 1202 males born between 1938 and 2009, collected by researchers between 1956 and 2014. All subjects were categorized by sex, partitioned into five period cohorts based on colony conditions at the time of their birth (1938-55, 1956-68, 1969-74, 1975-83, 1984-2009), and body weights for each cohort were calculated at different age-intervals (yearly from 0-1 to 5-6, then 6-10 and 11-15). Results revealed that overall, males and females alike, in early age-intervals (0-4 years), the 1938-55 cohort had the lightest body weight, while in the young adulthood age-intervals (6-10 years) the 1969-74 cohort had the heaviest body weight. This latter cohort experienced low population densities, unlike subsequent generations (1975-83), and a protein increase in provisioning relative to previous generations (1956-68). However, the most recent cohort (1984-2009) displayed the lowest mean body weights across almost all age-intervals, despite them receiving a tetanus vaccine (hence longer expectancy), annual population culling and regular provisioning. Further investigation is warranted to differentiate the effects of different environmental factors on the Cayo Santiago colony.

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### Estimation of sex from the patella in European Americans

ERIC FRAUENHOFER

Anthropology, SUNY Buffalo State

Sex is an important aspect of the biological profile used to identify unknown human skeletal remains. Although sex is commonly estimated from the skull or pelvis, forensic anthropologists must routinely assess sex from other skeletal elements. It is therefore useful to develop methods for estimating sex from bones other than those of the skull or pelvis in case of the absence of these elements. One of the most commonly used metric sex estimation methods is discriminant function analysis (DFA), which has been applied to many bones, including the patella. A limitation of DFA, however, is that it is population specific. Therefore, the purpose of this research was to derive discriminant functions from patellar measurements for estimating the sex of European Americans, which, to the author's best knowledge, has not yet been reported. The sample consisted of 200 European American individuals (100 females and 100 males) from the Hamann-Todd Osteological Collection. Seven measurements were taken of each individual's left patella. SPSS was used for discriminant function analysis. The overall accuracy of sex classification ranged from 81.0% to 84.0% and 81.0% to 84.0% for the direct and stepwise methods, respectively, indicating the patella is useful for estimating the sex of European Americans. However, the patella should only be used to estimate sex when more accurate bones, such as those of the skull or pelvis, are unavailable. This study will impact the forensic anthropology field by establishing an accurate method for estimating the sex of European Americans from patellar measurements.

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### A validation study of the Albanese metric sex estimation method for the proximal femur on a modern North American population

KATELYN I. FREDERICK

Anthropology, Texas State University

When estimating the sex of a skeletonized individual, the pubic bone of the os coxae is considered the best source of information due to its sexually dimorphic traits. However, as the pubic bone can be easily damaged during excavation in both bioarchaeological and forensic anthropological contexts, the development of non-pelvic sex estimation methods has become crucial.

Albanese (2008) introduced an alternative method of sex estimation that implements measurements between three newly defined landmarks on the proximal femur. These landmarks create a triangle which reflects both the angle of

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the femoral neck and the concomitant adaptations from the female pelvis. The original study generated logistic regression equations for sex estimation from these three measurements that are not population specific and have achieved a 95-97% allocation accuracy.

In this validation study, Albanese's method was applied to samples from the Texas State University Donated Skeletal Collection ( $n = 100$ ) and the William M. Bass Donated Skeletal Collection ( $n = 50$ ) and achieved an allocation accuracy of 89% and 92%, respectively. I conducted an intra-observer error assessment ( $n = 20$ ) and obtained an error margin of less than 1%. Considering these results, the Albanese (2008) method of sex estimation is an exceptionally reliable method thus far and would benefit strongly from other studies to further validate or negate it as a universally applicable approach.

### Collaborating with Local Communities in Developing Conservation Bioarchaeology Projects: The Historic Belen Bioarchaeology Project

J. CRISTINA FREIBERGER<sup>1</sup>, DEBRA L. MARTIN<sup>1</sup>, PAMELA K. STONE<sup>2</sup> and CLAIRA RALSTON<sup>1</sup>

<sup>1</sup>Anthropology, University of Nevada, Las Vegas, <sup>2</sup>Anthropology, Hampshire College

Community-based bioarchaeology projects are far fewer than archaeological projects. Planning for these projects and negotiating state permits along with community participation takes coordination, collaboration and attention to detail. This presentation provides an overview of the steps involved in establishing a successful community-based bioarchaeology project. In New Mexico, the Historic Belen Archaeology Project was conceived through outreach by a local archivist. A 19<sup>th</sup> century church and cemetery on private land was a target for vandalism and property damage, in addition to continuously having human remains exposed on the surface. We visited with the landowners, local political and social leaders who collectively decided to have the burials excavated, analyzed and reinterred in the current Catholic cemetery. Additionally, the landowners desired that the land be developed into a permanent heritage site, as the historic church played an important role in the town's unique social heritage. Over the past three field seasons, the excavation and recovery project included the integration of volunteers from varied groups within the town, from school children, church members, firefighters, boy scouts and local teachers. A small grant provided the opportunity for local middle school girls to participate in immersive learning at the site as part of STEM outreach. As human remains were excavated, they were shown to visitors and volunteers accompanied with bioarchaeological interpretations. On-going activities provided pathways for community engagement

and continuing education about bioarchaeological methods and usefulness. The project aims to encourage the largely BIPOC local school children to consider a career in bioarchaeology.

*American Association of University Women (AAUW)-Community Action Grant "Archaeology Girls! Excavating Belen, New Mexico's History."*

### PMI Problems: a first insight into quantifying the effects of scavenging by the Cape grey mongoose (*Galerella pulverulenta*) in South Africa.

GABRIELLE M. FRENCH<sup>1</sup>, MAXIMILIAN J. SPIES<sup>2</sup>, VICTORIA E. GIBBON<sup>2</sup> and DEVIN A. FINAUGHTY<sup>1</sup>

<sup>1</sup>School of Anthropology and Conservation, University of Kent, <sup>2</sup>Division of Clinical Anatomy and Biological Anthropology, Department of Human Biology, University of Cape Town

This research provides the first phase in identifying significant markers of scavenging by the Cape grey mongoose (*Galerella pulverulenta*) (CGM) – a key element in accounting for potential acceleration of decomposition when estimating the post-mortem interval (PMI). Currently, forensic death investigations in South Africa do not account for the scavenging activity of this species. Conducted in a forensically significant location, carcass feeding sites and manoeuvres were examined. CGM carrion feeding behaviours have not yet been distinguished, this paper being the first to outline and define these characteristics. A Kruskal-Wallis test determined certain feeding behaviours were more common at specific decomposition stages. Scratching behaviours were more common in the early, 'fresh' stages, whereas twisting flesh was seen almost exclusively in the lattermost stages. This suggests that the desiccated tissue in later stages is more difficult to tear away, leading to a need for higher tension manoeuvres. Scratching is used to create an opening in the flesh, which has been observed anecdotally in previous studies. This study used a single carcass, whereas previous research used multiple. It is likely that the CGM will spend more time trying to access the tougher areas on the carcass when there are less resources in the area, suggesting a likelihood that this would be seen in death investigations where a single body has been found. This study is the first to establish a methodology for quantifying the effects of scavenging and advances knowledge of the impact of scavenging on PMI estimation, providing local and global significance.

### Social Differentiation and Identity in the Kingdom of Lindsey

MEGAN HANNA. FRY<sup>1</sup>, GEORGE D. KAMENOV<sup>2</sup> and JOHN KRIGBAUM<sup>1</sup>

<sup>1</sup>Department of Anthropology, University of Florida, <sup>2</sup>Department of Geological Sciences, University of Florida

Isotopic evidence of diet and mobility is well documented in Early Medieval Britain; however, the Anglo-Saxon Kingdom of Lindsey has been largely overlooked. Historical records written after Lindsey was absorbed by Merca indicate it was an independent kingdom until AD 620, but during its short tenure the region underwent many sociopolitical changes which directly affected the daily lives of Lindsey's inhabitants, leaving traces in the skeleton. Six sites within the boundaries of Lindsey were surveyed for skeletal markers of malnutrition and demographic factors, which were paired with radiogenic (<sup>87</sup>Sr/<sup>86</sup>Sr, <sup>208</sup>Pb/<sup>204</sup>Pb) and light isotope data ( $\delta^{18}\text{O}_{\text{ap}}$ ,  $\delta^{13}\text{C}_{\text{en}}$ ,  $\delta^{15}\text{N}_{\text{co}}$ ,  $\delta^{13}\text{C}_{\text{co}}$ , and  $\delta^{13}\text{C}_{\text{ap}}$ ). Significant trends have been identified between isotopic signatures of  $\delta^{13}\text{C}_{\text{co}}$  and sex ( $p=0.02465$ ) as well as status ( $p=0.03415$ ). One individual from Fonaby, had low  $\delta^{13}\text{C}_{\text{co}}$  (-23.3‰) which varied greatly from the overall mean of -20.5‰ for  $n=31$ . Further, rates of malnutrition (linear enamel hypoplasia and cribra orbitalia) were much higher in females than males in Lindsey. To assess these trends, we contrast these new data from Lindsey to published data, which permits spatial and temporal comparisons between Anglo-Saxon Kingdoms allowing for broader discussions of inter-settlement relationships, mobility, and independent identity. Rates of nutritional insult occurred at similar rates in Lindsey (13.75%) compared to Mercia (13.4%) but much higher rates than East Anglia (5%). These analyses demonstrate that although isotopic evidence indicates similarity in dietary patterns overall, nuanced variation can be identified, especially when considered with demography and mobility.

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### Microbiome diversity in Kinda baboons and their water resources

AMANDA J. FUCHS<sup>1</sup> and JASON M. KAMILAR<sup>1,2</sup>

<sup>1</sup>Department of Anthropology, University of Massachusetts, Amherst, <sup>2</sup>Organismic and Evolutionary Biology Graduate Program, University of Massachusetts, Amherst

Primate gut microbiomes are known to be influenced by environmental factors, such as diet and social interactions. Although we are gaining a greater understanding on how these factors affect the gut microbiome, little is known about how water influences primate gut microbiomes. This is critical to consider for primates that inhabit relatively dry environments with seasonal rainfall because water is known to be one of the richest natural habitats for bacteria. It has been suggested, however, that primates avoid fecally contaminated water and that the microbial composition of water could impact primate gut microbiomes, but no studies have directly measured water microbiomes. Therefore, we examined

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how diet and water impact Kinda baboon (*Papio kindae*) gut microbiomes in Kasanka National Park, Zambia. We collected 33 fecal samples from eight adult female baboons and 18 samples from water sources used by the baboons. We successfully extracted microbial DNA from all samples and sequenced the 16S rRNA gene on an Illumina MiSeq using a Nano reagent kit. Fecal samples contained relatively high amounts of bacteria from the *Firmicutes*, *Bacteroidetes*, and *Spirochaetes* phyla. Water samples were relatively high in *Proteobacteria* and *Bacteroidetes* taxa. Many of these phyla are typically found in gut microbiomes, including the gut microbiomes of other baboon and primate species. Future work will focus on how water microbiota influences the gut microbiome of Kinda baboons across the year and from water sources with varying *E. coli* and *Giardia* abundances.

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### Changes in Decompositional Processes in a Desert Environment

KAITLYN J. FULP<sup>1</sup>, MEGHAN M. GAST<sup>2</sup>, JACOB A. HARRIS<sup>3</sup> and KATELYN L. BOLHOFNER<sup>2</sup>

<sup>1</sup>Sociology, Anthropology, and Social Work, Texas Tech University, <sup>2</sup>School of Mathematics and Natural Sciences, Arizona State University, <sup>3</sup>Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University

Reconstructing the taphonomic history of a skeletal assemblage is a critical component of research in a broad range of fields including archaeology, bioarchaeology, paleoanthropology, and forensic science. Numerous post-depositional forces can act upon a skeleton and affect both the physical appearance and the dispersion of skeletal elements. The taphonomic process begins with the decomposition of soft tissue, the rate of which is largely dependent on the depositional environment. In extreme climates, the ways in which organisms decay and the disposition of their final state can deviate from the "standard progression". These differences are not fully understood. The Sonoran Desert in Arizona possesses an extreme climate characterized by large diurnal temperature changes, low humidity levels, and intense ultraviolet (UV) exposure. We present a pilot study examining the effects of this extreme climate on the process of decomposition.

Two adult domestic pig carcasses were clothed and placed in a region of native Sonoran Desert in July, when daytime temperatures can exceed 120 degrees Fahrenheit and relative humidity can drop below 10%. To examine the effects of differential UV exposure, one carcass was placed in direct sunlight and the other in the shade of a Palo Verde tree. For 25 days, the rate of decomposition was monitored using time-lapse photography taken at

30-minute intervals in addition to temperature and humidity readings taken at 10-minute intervals. The results of this study suggest that differences in UV light exposure alters both internal and external processes of decomposition, as well as the timeline of taphonomic change.

### Recent Local Adaptation in Worldwide Human Populations

ALYSSA FUNK<sup>1,2</sup> and EMILIA HUERTA-SÁNCHEZ<sup>2,3</sup>

<sup>1</sup>Molecular and Cellular Biology, Brown University, <sup>2</sup>Center for Computational and Molecular Biology, Brown University, <sup>3</sup>Ecology and Evolutionary Biology, Brown University

Since expanding out of Africa, humans have been exposed to a diverse array of environments with different climates, food sources, and diseases. In response, genetic variants have evolved that are specific to certain populations, which may represent local adaptation to different environments. We use whole genome sequences from the 1000 Genomes Project to examine variants rare in African populations but common in other populations to identify "local variants". We annotate the genomic location of local variants and determine allele-specific effects on gene expression, and we test for positive selection acting on these variants. We find that the majority of local variants are in non-coding regions, with the highest percentage in introns, which suggests that alterations in gene expression may be a potential route for local adaptation. When examining local variants that are unique to a single population, we find that Peruvians, Japanese, and Finnish have significantly more variants, suggesting that demographic factors like bottlenecks and isolation contribute to population-specific variants.

### Assessing the similarities between photogrammetric and microCT scanning of 3D models of hominin molars

MARGARET J. FURTNER<sup>1</sup> and JULIET K. BROPHY<sup>1,2</sup>

<sup>1</sup>Department of Geography & Anthropology, Louisiana State University, <sup>2</sup>Evolutionary Studies Institute, University of the Witwatersrand

Photogrammetry is an under-utilized, yet cost- and time-effective scanning methodology that does not expose fossils to doses of radiation that affect ESR dating. This study expands upon previous work and examines the viability of close-range photogrammetry as an alternative scanning methodology on isolated teeth using samples of fossil (*Homo naledi*), archaeological, and contemporary human molars. The photogrammetric scans included 96 digital images per tooth and the resulting models were compared to their corresponding CT mesh models using point-to-point surface deviation analysis. The surface difference between the CT models before and after processing were subsequently assessed in order to determine if the surface deviation between the

differently-acquired models were within acceptable levels. Paired t-tests comparing the surface deviation between each set of mesh pairs show no significant difference in the level of deviation within the archaeological and contemporary molar samples. A threshold range of acceptable surface difference was devised and applied to the *H. naledi* sample, which did not have pre-processed CT meshes available. A total of 73% of the *H. naledi* teeth provided photogrammetric meshes that fell into this range of acceptable difference. The meshes that fell outside the established range had higher surface deviation on their non-occlusal surfaces compared to their occlusal surfaces. This result is likely due to the lack of staining and the glossy texture of said molars. The results therefore suggest that, provided sufficient texture and color contrast data, close range-photogrammetry can provide an accessible alternative to microCT scanning for generating 3D models of isolated teeth.

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### Preliminary Relationships of Cross-Sectional Geometry in Human Clavicles with Sex and Age

NICOLE M. FYE<sup>1</sup>, ANGELA L. HARDEN<sup>1</sup> and AMANDA M. AGNEW<sup>1,2</sup>

<sup>1</sup>Skeletal Biology Research Lab, Injury Biomechanics Research Center, The Ohio State University, <sup>2</sup>Department of Anthropology, The Ohio State University

Relationships between cross-sectional geometry and sex and age have been studied extensively in numerous long bones, but research in the clavicle is limited. Functional adaptation to varied loading is expected to create differences in clavicular cross-sectional geometry between individuals. Therefore, the objective of this study was to determine whether sex and age differences exist in clavicular cross-sectional geometry. Histological sections were obtained from the left clavicles of 32 post-mortem human subjects (females=16, males=16; 23–98 years) and were age-matched across decades. Midshaft clavicular sections were prepared following standard hard tissue histology procedures. All slides were imaged at 40x magnification and the following cross-sectional geometric variables were quantified using ImageJ software: cortical area, total area, relative cortical area, endosteal area, area moments of inertia, and section modulus. All variables demonstrated statistically significant differences between sexes ( $p < 0.004$ ), except for relative cortical area ( $p = 0.19$ ; Kruskal-Wallis tests). These results suggest that males have larger clavicles with greater resistance to bending and torsion than females, but not a greater proportion of cortical bone. Males and females demonstrated similar trends of increases

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with age, although statistically insignificant (linear regression,  $p > 0.09$ ), for every variable except endosteal area in males (decrease,  $p = 0.02$ ) and total area (no change,  $p > 0.36$ ). This suggests that clavicles may infill with age, with associated changes in cross-sectional geometry. These preliminary findings imply that the clavicle may adapt differently than other long bones due to its unique functional position. Therefore, it is important to continue exploring intra-skeletal variation and inter-skeletal variation in long bone geometry.

### Phylogenetic analysis of the UCP1 gene in primates reveals clade-specific structural variation

CHRISTIAN M. GAGNON and CHRISTOPHER A. SCHMITT

Anthropology, Boston University

The UCP1 gene plays an important role in non-shivering thermogenesis by providing the mechanism for heat generation in brown adipose tissue (BAT). This unique mammalian trait is viewed as a critical adaptation which contributed to their adaptive radiation, particularly into colder climates. Most primates are considered tropical species, yet BAT and UCP1 function are conserved, with few investigations into variation in this important gene region. In this study, we examine the phylogenetic history of the UCP1 gene in primates using publicly available genomes from 28 primate species, using the tree shrew (*Tupaia belangeri*) as an outgroup. Strepsirrhines and haplorhines show major structural variants not found in tree shrews, including large clade-specific intronic insertion and duplication elements. The tarsier showed a significantly higher number of unique intronic insertions including the expansion of a 241 b.p. CpG island following the first exon. We identify two separate codon deletions, in amino acid positions 104 in tarsiers, and 111 in lemurs, respectively. Maximum-likelihood analyses using a clade model suggest that strepsirrhines and haplorhines have experienced a functional divergence in UCP1 (strepsirrhines:  $2\delta\text{LnL} = 19.468$ ,  $P\text{-value} = 0.00001$ ; haplorhines:  $2\delta\text{LnL} = 17.446$ ,  $P\text{-value} = 0.00003$ ). Overall, these results suggest that UCP1 has been subject to differential selection across major primate lineages, most likely reflecting the need to adapt to differing thermoregulatory needs, particularly for some smaller-bodied taxa such as the tarsiformes and some members of the order strepsirrhini.

### Growth rate changes during the Middle Ages (ca. 500–1500 AD) in Central Europe

PATRIK GALETA and ANNA PANKOWSKI

Department of Anthropology, University of West Bohemia

The previous research on growth and fertility rates in the region of Central Europe detected a major shift during the transition from foraging to farming

(ca. 5,500 BC). The knowledge about the growth and fertility changes in the following periods is, however, limited. In this paper, we reconstructed growth rate changes during the Middle Ages in Central Europe (ca. 500–1500 AD). We collected age-at-death data for 9,500 individuals of 44 medieval Central European skeletal samples and estimated their growth rates. The growth rate estimations were done using regression equations with D5+/D20+ age-at-death index (the number of deceased older than 5 years to those older than 20 years) as predictor. The growth rate of each skeletal sample were estimated using a unique set of 1000 simulated skeletal samples with the same number of adults as in the corresponding real sample to take into account the stochastic variation due to different sample sizes. The results suggest that growth rate gradually decreased during the period from ca 2% to almost zero with a maximum observed around 900 AD. The growth rate peak correspond to the formation of Great Moravia, which was the first politically relevant power of the Slavs in Central Europe and which experienced significant cultural and political development including the recognition of Christianity as an official ideology.

This research was supported by the project GA19-17810S.

### Adaptive Utilization of Digital Forums for Bioanthropological Outreach

ABIGAIL S. GANCZ and MAKENNA B. LENOVER

Anthropology, Penn State

Pedagogy and outreach are as important as research to the longevity and goals of anthropology. Specifically, engaging young children is critical as it provides extracurricular scientific content and promotes diversity within the field. Typical bioanthropological outreach often involves visits to schools, guest lectures, or one time programming. In the age of Covid-19, sustainable and long term outreach avenues are critical, and this requires a shift in pedagogical approach. Anthropological outreach can be made sustainable through accessible, child-focused publications. However, there is a systemic underrepresentation of anthropological content in such formats, suggesting a need for a shift in pedagogical training and approach. Through review of the *Frontiers for Young Minds* journal, we found that representation of biological anthropology topics was low. By drafting our own outreach article, we created a guide of effective pedagogical strategies for engaging in this form of crisis-resilient outreach. When writing, it is critical to remember the age group of the readership and to select topics of interest to the audience. For example, even though we are biological anthropologists studying development and health, we focused our paper on broader and interesting information about our study topic, the skull. CONC: Sustainable outreach

and pedagogy are essential during these remote times, and publishing complimentary outreach journals to your research articles is a long-lasting way to make your research accessible

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### Different patterns of integration of the hyoid, mandible and tongue size in Hominoidea – Implications for reconstructing the tongue size in fossil hominins

XIUYAN GAO<sup>1</sup> and SANDRA A. MARTELLI<sup>2</sup>

<sup>1</sup>Institute of Archaeology, University College London, <sup>2</sup>UCL Centre for Integrative Anatomy (CIA), Department of Cell and Developmental Biology, Division of Life Sciences, University College London

Information extracted from the hominoid hyo-mandibular morphology could predict tongue-size of the fossil hominin vocal tract. We assume that hyoid, mandible and tongue morphology reflect phylogeny, body size and breathing, feeding and vocalising functions, then investigate whether representative hominoid taxa share patterns of relationships of these structures during postnatal ontogeny and the resulting adult morphology.

We used One-way ANOVA and multivariate correlations to analyse inter- and intraspecific variation of volumetric tongue, hyoid and mandible size of cross-sectional ontogenetic samples (neonates-adult) of *Homo sapiens* (N=56) and *Pan troglodytes* (N=41) and a partial ontogenetic sample (infant-adult) of *Hylobatidae* (N=11).

*Homo* and *Pan* ontogenetic growth patterns differ as follows: the human tongue, hyoid and mandible volumes increase steadily, with a growth spurt at subadult stage. *Pan* volumes increase rapidly from late juvenile and overtake *Homo* from subadult stage onward. The gibbon sample is too small for secure observations but tends to follow the human pattern.

Human and gibbon adult hyoid, mandible and tongue volumes correlate strongly ( $p < 0.01$ , all comparisons) whereas *Pan* volumes are non-significant (exception: hyoid-mandible correlation,  $p < 0.01$ ). All human volumes are significantly correlated with bodymass, while all ape volumes, with the exception of mandibular volume in *Pan*, are non-significantly correlated.

Tongue, hyoid and mandible-size correlation patterns seem not to follow *Hominoidea* phylogeny, with humans and *Hylobatidae* having tighter relationships than *Pan*. However, bodymass correlations with hyoid, mandible and tongue are strong in humans and might be so in close-related fossil hominins too – further research on functional adaptations on these sizes is needed.

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### Using a multi-level systems approach to address structural violence in COVID-19 and other health inequities

ANGELA R. GARCIA

Center for Evolution and Medicine, Arizona State University, Department of Anthropology, Emory College

The contemporaneity of the COVID-19 pandemic alongside months of civil unrest that erupted in response to the murders of George Floyd, Breonna Taylor, and so many others, focused attention on the abject racism and legacy of unequal treatment of Blacks in the U.S., and highlights a complex relationship between structural violence and health inequity. For example, Black Americans experience the highest COVID-19 mortality rates nationwide—more than twice that of Whites. Genetic anthropology is uniquely situated to address inequities in diseases including COVID-19. However, to progress in this space, we need to advance research on gene–environment interactions and multiple determinants of health.

This talk focuses on using a "systems approach" to address COVID-19, which recognizes and integrates the interconnectedness between determinants and outcomes at various levels: from heritable, genetic components, to how genes are influenced by processes at individual, ecological, and structural levels.

Structural inequities (discrimination, crowded housing, non-remote jobs) influence individuals directly (e.g. likelihood of infection, access to medical care) and indirectly (e.g. disruption of endocrine-immune functions and metabolic processes that cause co-morbidities). Localized factors interact with genomic features (e.g. genetic variation and expression) to create a complex network of risk. Most genome-wide association studies (GWAS) fail to consider how local-level variation influences gene expression, and rarely focus on differences in disease etiology, potentially driven by structural violence. Using systems-based analytical tools, genetic anthropologists can leverage existing GWAS data, alongside diagnostics and multi-leveled data, to investigate unique disease pathways, and aid in the development of interventions for COVID-19.

### The influence of migration and urbanization on the metabolic health of mobile Amazonian people residing in Yurimaguas Peru— a pilot study

J. CHADWICK GERHOLD<sup>1</sup> and MJ MOSHER<sup>1,2</sup>

<sup>1</sup>Laboratory of Biological Anthropology, University of Kansas, <sup>2</sup>Department of Anthropology, Western Washington University

Non-insulin dependent diabetes mellitus (NIDDM) is a global metabolic disease assumed to be rare among Amazonian peoples due to their mixed subsistence pattern integrating hunter gathering with subsistence farming. Migration from rural

to urban communities may place them at greater risk for developing metabolic diseases due to changes in diet and lifestyle. Here we examine the effects of human migration on metabolic markers of NIDDM among those who migrated to the Amazonian port town of Yurimaguas, Peru, and those born there. We collected demographic/health questioners, anthropometric measurements, blood lipids panels (HDL, LDL, total cholesterol, and blood triglycerides), systolic and diastolic blood pressure, and A1c levels from 168 individuals (113 females, 55 males) residing in and around Yurimaguas. Log-linear models were used to fit multidimensional categorical data using iterative proportional fitting. Linear regression models were used to fit categorical and continuous variables. Individuals born and raised in Yurimaguas had lower A1c levels, lower blood glucose, lower waist-to-hip ratios, and lower incidence of NIDDM than individuals who migrated to the city. No significant difference was noted between these two groups in their incidence hypertension, elevated triglycerides levels, LDL/HDL ratios, or total cholesterol. These findings suggest as Amazonians migrate into more urbanized settings, A1c levels and central obesity are important biomarkers for the onset of NIDDM. We conclude with factors such as socioeconomic status, endocrine disrupting toxins, diet, and lifestyle changes that may play a pivotal role in the onset NIDDM amongst Amazonian migrants as they adapt to their new urban surroundings.

Funded by: Diabetes Institute of the University of Kansas Medical Center Pilot Funding for Research into Diabetes.

### The nutritional chemistry of bamboo lemur (*Haplemur griseus*) foods and niche separation among sympatric lemurs in Madagascar rainforests

CHLOË N. GHERARDI<sup>1</sup>, SARAH NAUGHTON<sup>2</sup>, MOLLY C. FITZPATRICK<sup>3</sup>, VOLOLONIRINA RAHALINARIVO<sup>4</sup>, JEAN-FREDDY RANAIVOARISOA<sup>4</sup>, JEANNOT RANDRIANASY<sup>4</sup>, JEAN-LUC RAHARISON<sup>5</sup>, BRUNO RAMORASATA<sup>5</sup>, JESSICA M. ROTHMAN<sup>6,7</sup> and MITCHELL T. IRWIN<sup>3,5</sup>

<sup>1</sup>Biological Sciences, Northern Illinois University,

<sup>2</sup>Institute for the Study of Environment,

Sustainability and Energy, Northern Illinois University, <sup>3</sup>Anthropology, Northern Illinois University, <sup>4</sup>Mention Anthropobiologie et

Développement Durable, University of Antananarivo,

<sup>5</sup>ONG, SADABE, <sup>6</sup>Anthropology, Hunter College,

<sup>7</sup>Graduate Center, CUNY

Bamboo lemurs show an unusual evolutionary innovation, foraging on one of the primate order's most specialized diets: bamboo. This is rare among vertebrates, and requires large amounts of the enzyme rhodanese, the amino acids cysteine and methionine (obtained mainly from dietary protein), and readily available energy to detoxify cyanide. Many studies have documented bamboo lemurs' diet, but only one has analyzed the nutritional components of *Haplemur griseus* foods,

with limited methods. We present the nutritional content of 10 dry season foods consumed by *H. griseus* at Tsinjoarivo, Madagascar, measuring crude protein, available protein, simple sugars, fat, and fiber. Kruskal-Wallis comparisons with two sympatric lemurs (*Propithecus diadema* and *Eulemur fulvus*) showed significant differences in all variables except for lignin. Foods of *H. griseus* had high available protein (11.8% vs 5.2% for both other species), consistent with the detoxification limitation hypothesis and a higher protein need. *H. griseus* foods were the highest in neutral detergent fiber (70.5%), but lowest in lignin (10.9%); much of the diet consists of partly digestible fiber. Future studies should calculate total energy and examine daily intakes alongside food composition. Further research would be needed to answer more specific questions, such as whether foods are targeted for sulfur-containing amino acids, or other compounds linked to detoxification. Ongoing efforts to understand divergent primate feeding strategies and macronutrient profiles will help in understanding nutritional requirements, food choices and limits to survival, and will aid in managing wild and captive primate habitats in the face of climate and habitat change.

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### Sexual orientation-based disparities in food security among American adults

JAMES K. GIBB<sup>1</sup>, MOSTAFA SHOKOOHI<sup>2</sup>, TRAVIS SALWAY<sup>3,4,5</sup> and LORI E. ROSS<sup>2</sup>

<sup>1</sup>Health and Society, University of Toronto, <sup>2</sup>Dalla Lana School of Public Health, University of Toronto, <sup>3</sup>Faculty of Health Sciences, Simon Fraser University, <sup>4</sup>British Columbia Centre for Disease Control, <sup>5</sup>Centre for Gender and Sexual Health Equity

Access to sufficient, safe, culturally-appropriate and nutritious food is essential for maintaining both physical and mental health. Despite a growing body of evidence suggesting that sexual minority (SM) people experience significant disparities in socioeconomic and material resource security, there remains a paucity of empirical studies examining food insecurity among SM people relative to their heterosexual peers. This study examined the extent of food insecurity among sexual minority (SM) people. We combined five cycles of US National Health and Nutrition Examination Survey, 2005-2016 (Total N = 19,447) to examine sexual orientation-based differences in adult food security among Lesbian/Gay (n = 341), Bisexual (n = 582), Same-Sex Experienced (n=651), and Heterosexual (n = 17,873) adults. Multivariable multinomial logistic regression analysis was used to examine the association of sexual orientation and food insecurity adjusted for multiple socioeconomic, demographic and behavioural factors. Associations were examined separately for males and females. Sexual orientation-based

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disparities in adult food insecurity were observed across all SM groups relative to heterosexual individuals. Estimates of severe food insecurity was nearly double among bisexuals (13.1%), same-sex experienced (12.0%) and lesbians/gays (11.7%) compared to heterosexuals (6.6%). Regression analysis showed that bisexuals, same-sex experienced, and lesbians/gays were more likely to experience moderate-to-severe food insecurity in the entire sample, as well as separately among males and females. Our analysis suggests that SM people experience increased rates of food insecurity relative to heterosexuals, and that broader structural, socioeconomic and biocultural factors intersect with sexual orientation to differentially influence resource security.

### The impacts of the COVID-19 pandemic on maternity care preferences for future pregnancies among women living in the United States

THERESA E. GILDNER<sup>1,2</sup> and ZANETA M. THAYER<sup>2,3</sup>

<sup>1</sup>Anthropology, Washington University in St. Louis, <sup>2</sup>Anthropology, Dartmouth College, <sup>3</sup>Ecology, Evolution, Environment & Society Program, Dartmouth College

The COVID-19 pandemic has impacted maternity care decisions, including plans to change providers or delivery location due to pandemic-related restrictions and fears. A relatively unexplored question, however, is how the pandemic may shape future maternity care preferences post-pandemic. Here, we use data collected from an online survey of 498 women living in the United States to evaluate how and why the pandemic has affected women's future care preferences. We hypothesize that while the majority of women will express a continued interest in hospital birth and OB/GYN care due to perceived safety of medicalized birth, a subset of women will express a new interest in out-of-hospital or "community" care in future pregnancies. However, factors such as local provider and facility availability, insurance coverage, and out-of-pocket cost could limit access to future preferred care options. A total of 29 participants (5.82% of the sample) reported a novel preference for community care during future pregnancies. Several participants described how the pandemic led them to learn more about community care options. Common reasons given for now favoring community care included a preference for a natural birth model, a desire for more person-centered care, and a belief that community births are safer. However, a relatively high percentage (29.2%) of participants with novel preference for community care indicated that they expected limitations in their ability to access these services. These findings highlight

how the pandemic has potentially influenced care preferences, with implications for how providers and policy makers should anticipate and respond to future care needs.

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### Investigating signatures of selection and morphological diversity in the extant great ape face

ALFIE GLEESON<sup>1,2</sup>, AIDA ANDRÉS<sup>2</sup> and AIDA GOMEZ-ROBLES<sup>1</sup>

<sup>1</sup>Anthropology, University College London, <sup>2</sup>Genetics, Evolution and Environment, University College London

Facial morphology is a diverse phenotype in humans that is crucial for signalling individual identity. Evolutionary processes that generate facial diversity are not fully understood. It's thought that neutral processes generate the majority of this diversity, although it's been suggested that selective pressures contribute to some extent. Different facial regions could be constrained by different processes, particularly if signalling identity via the face imposes a strong selective pressure. By combining genomic and morphological techniques we aim to explore whether signatures of selection are evidenced in genes associated with facial morphology, and if this is reflected in anatomical diversity of the skull.

Signatures of selection were investigated by combining two datasets obtained from published population genomic studies; 1) collated set of genomic regions identified as associated with diversity in human facial morphology via GWAS (Genome-Wide Association Studies), and 2) great ape genomes with a calculated statistic, NCD (Non-central deviation), which identifies genomic signatures of balancing selection. Preliminary results showed some genes contain nominal signatures of balancing selection across species, suggesting that some aspects of face diversity may be actively maintained by selection.

Morphological diversity of the great ape skull was measured using geometric morphometrics incorporating dense 3D configurations of landmarks. Diversity was variable by region, e.g. gorillas and orangutans showed high levels of intraspecific diversity in upper craniofacial regions, but low variation in mid-face regions when compared to humans and chimpanzees.

Comparing these interdisciplinary datasets across great apes provides a powerful tool for better understanding the evolution of the face.

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### Sex-specific adaptive effects of an ancient deletion polymorphism of the human growth hormone receptor

OMER GOKCUMEN

Biology, 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.

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### An Alternative to the Mandibulometer: Testing the Replicability of a New Method

LESLIE GOLDMANN, ANASTASIA TEMKINA and JONATHAN D. BETHARD

Anthropology, University of South Florida

Mandibular measurements are an essential part of bioanthropological investigations of the skeleton. However, traditional mandibulometers are costly instruments not accessible to every biological anthropologist or laboratory. Recently, Garvin and Severa (2019) developed an alternative method for measuring human mandibles with freely available computer software. This approach requires a digital camera, scale, and the software package *ImageJ* to reconstruct mandibular length, ramus height, and mandibular angle from photographs.

The purpose of this study was to examine if the new alternative method equals data collection protocols requiring the mandibulometer. Human mandibles (n = 35) from the Human Osteology Laboratory at the University of South Florida were

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photographed and measured in *ImageJ* following the protocol of Garvin and Severa (2019). Data were also recorded with the mandibulometer for comparative purposes. Reconstructed mandibular measurements were analyzed in R. Results demonstrated that inter-observer agreement is higher when using a traditional mandibulometer than when using the digital method. Intra-observer error using the digital method was low, meaning the observers followed the method consistently. Mandibular height and angle assessed using the digital method agree with the traditional measurement, while ramus height measured from a photograph deviates from its mandibulometer counterpart. All technical error of measurement (TEM) values are less than 3 mm regardless of observer or method. TEM values were higher for ramus height measurements. Our results demonstrate that the alternate digital method could be a viable alternative to the traditional mandibulometer in bioanthropological research; however, slight improvements to its instructions are suggested.

### Supporting Diversity, Equity, and Inclusion During Civil Unrest and a Global Pandemic

FELICIA GOMEZ, JESSICA SILVA-FISHER, DAVID M. ALVARADO, AMANDA SMITH, AMBER GRIFFITH, GABRIEL MBALAVIELE and JOSEPH PANGELINAN

Medicine, Washington University School of Medicine

We find ourselves in a moment in history that is unlike any other. The global pandemic has reshaped how we live, work, and play. We are also in a new chapter of our national struggle with the social construction of race and the inequality that persists because of this flawed idea. Those of us who work to improve diversity in academia are in a challenged situation, but we are rising to meet this challenge. In 2016, the Trainee Inclusion and Cultural Awareness Task Force at Washington University School of Medicine asked trainees who are underrepresented in medicine what, if any, institutional barriers are impacting their ability to achieve their career goals. The task force identified a deficit in quality mentorship as the most salient barrier. To address this need we are creating a platform, geared toward underrepresented trainees, that consists of online and in-person opportunities to identify mentors, colleagues, and sponsors; it will be the first of its kind in our department. We will build a community that provides support and guidance to propel trainees toward their career goals. The pandemic has derailed our progress. This is especially difficult because we are in a watershed moment in history when communities like the one we are building are needed the most. Nonetheless, we are creating solutions and moving forward. We will discuss how the pandemic has uniquely

impacted underrepresented trainees, what we have learned throughout our platform development, and our efforts to continue community building while confined to virtual spaces.

### Parasitic load in grey-bellied owl monkeys (*Aotus lemurinus*) living within city limits of Manizales, Colombia

PAMELA GONZALEZ VANEGAS<sup>1,2</sup>, MAJA ŠEŠELJ<sup>1</sup> and WILLIAM A. CAÁN-FRANCO<sup>3</sup>

<sup>1</sup>Anthropology, Bryn Mawr College, <sup>2</sup>Biology, Bryn Mawr College, <sup>3</sup>Departamento de Salud Animal, Universidad de Caldas

Anthropogenic activities including habitat fragmentation, urbanization, and pollution not only have direct adverse impacts on biodiversity, but also contribute to parasite transmission to and from wildlife. Given our close evolutionary relationship, primates are vulnerable to many of the same parasitic infections as humans. While there is a relative paucity of research into parasites affecting platyrrhines in general, there is even less research into parasites affecting the species of the genus *Aotus*, despite their wide geographic distribution across Central and South America. This is the first report of parasites affecting wild grey-bellied owl monkeys (*Aotus lemurinus*) in Manizales, Colombia. The monkeys live in a fragmented semi-arid, premontane forest trail encircling approximately two hectares of hilly terrain on the edge of a densely populated neighborhood. Out of 16 fecal samples, six (37.5%) were positive for at least one parasite; three of these showed evidence of multiple infections. The five identified parasite genera include protozoa *Cryptosporidium* (n=3) and *Eimeria* (n=1), and nematodes *Trypanoxyuris* (n=2), *Ancylostoma* (n=1), and *Physaloptera* (n=1). Of these, *Cryptosporidium*, *Physaloptera*, and *Ancylostoma* could have potentially been introduced into the owl monkey population from infected humans and/or household animals. Interestingly, only *Trypanoxyuris* has been previously reported in wild *Aotus azarai* in Argentina and free-ranging *Aotus nigriceps* in Peru; *Cryptosporidium* was detected in captive *Aotus nigriceps* in Brazil. Further research is needed to elucidate the relative contributions of natural versus anthropogenic factors impacting parasite loads and transmission in the Colombian owl monkeys.

### The role of Christian traditions in bioarchaeological practice: how public, professional, and ethical attitudes impact the archaeological disturbance of human remains

ELLIE GOODERHAM and HUGO FV. CARDOSO

Department of Archaeology and Centre for Forensic Research, Simon Fraser University

Practices within bioarchaeology have been largely shaped by Western and Christian ideologies. However little research has been conducted to understand how religious social frameworks shaped and continue to regulate the archaeological disturbance of human remains. This paper examines Catholic and Protestant perspectives on death and burial to understand how they have influenced the study of human remains in bioarchaeology. This analysis was conducted to bridge the knowledge gap between the work bioarchaeologists do and the underlying social context. For this, an extensive review of professional codes of conduct, professionally and nationally regulated ethics, and national law was undertaken to understand how each of these shape practices within bioarchaeology. These practices were then meta-analyzed to understand how and where Catholic and Protestant ideologies have influenced them. Results showed that while there is a trend in science towards secularization, often deeply entrenched religious perspectives remain. We conclude that differences in bioarchaeology are often due to how public attitudes shape professional practice. The social context of bioarchaeology is largely shaped by each country's history of religion and colonization.

MITACS Research Training Award

### Snapshots of Representation in Bioanthropology Textbooks

ELLISON J. GOODRICH<sup>1</sup> and MELISSA S. SEABOCH<sup>1,2</sup>

<sup>1</sup>Anthropology, University of Utah, <sup>2</sup>Anthropology, Salt Lake Community College

Representation matters and diversity in research teams fosters better science. A 2014 survey showed that 86.9% of AAPA members identified as "white". The percentage is higher in AAPA compared to AAA and to other STEM fields. The goal of this project was to assess representation in textbook images. We predicted that male researchers would be represented more frequently than female researchers, and that "white" researchers would be represented more frequently than people of color (POC) researchers. We also predicted that representation of both women and POC researchers would increase from the first to the current editions. For images in first and current editions of six introductory bioanthropology textbooks, we recorded role (researcher or subject), sex, and "ancestry" ("white" or POC). We compared representation in current textbooks with binomial tests and representation over time with Z-tests (alpha=0.01). Of 199 researchers depicted in the current textbooks, more males (N=144, 72.4%) were represented than females (binomial test p<0.001) and fewer POC researchers (N=32, 16.1%) were depicted (binomial test p<0.001) supporting our hypotheses. Representation of female researchers increased from the first to the current editions

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by 20.9% ( $Z=-4.3267$ ,  $p<0.00001$ ), but POC representation did not significantly change ( $Z=-1.383$ ,  $p=0.16758$ ). When POC were depicted ( $N=161$  photos), they were more frequently as subjects (80.1%,  $N=129$ ) than as researchers (binomial test  $p<0.001$ ). These results illustrate the underrepresentation of women and POC in bioanthropology textbooks. To increase the diversity of bioanthropologists, students must see themselves represented in their bioanthropology classes, including in the textbook.

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### Paraspinal muscle activation during bipedal walking in orthograde primates and its implications for the evolution of trunk balance

RYOSUKE GOTO<sup>1</sup>, NEYSA GRIDER-POTTER<sup>2</sup>, YUKI KINOSHITA<sup>3</sup>, KENJI OKA<sup>4</sup>, TETSUYA SHITARA<sup>5</sup> and YOSHIHIKO NAKANO<sup>5</sup>

<sup>1</sup>Faculty of Health Sciences, Gunma Paz University, <sup>2</sup>Department of Clinical Anatomy and Osteopathic Practices and Principals, Rocky Vista University, <sup>3</sup>Primate Research Institute, Kyoto University, <sup>4</sup>Faculty of Rehabilitation, saka Kawasaki Rehabilitation University, <sup>5</sup>Graduate School of Human Sciences, Osaka University

To maintain balance during bipedal walking, the human spine must attenuate the antero-posterior acceleration of upper body. Previous research has shown that humans stabilize the trunk via a 'top-down' activation of paraspinal muscles, in which cranial muscle fascicles activated earlier than caudal fascicles. We expect that similar mechanisms exist in other primates that use orthograde bipedal walking under natural conditions. Here we hypothesize that 'top-down' activation of paraspinal muscles facilitates balance during hominoid bipedalism using humans ( $n=5$ ), a gibbon ( $n=1$ ), and Japanese macaque ( $n=1$ ). We simultaneously recorded activations of paraspinal muscles at multiple vertebral levels (C7, T1, T4, T8, T12, and L4 during bipedal walking using electromyography. Cross-correlation coefficients were computed between the activation signals at each vertebral level and L4 to understand shifts in activation patterns among species

Our preliminary results showed the 'top-down' activations in the gibbon and human thoracolumbar region, but not in the macaque. Both the gibbon and human paraspinal muscles activate incrementally along the spine (e.g. T4 fascicles activate before T8 and so on). Although the macaque shows a similar pattern at T4 and T8, the T12 fascicles activate after those at L4. These results may imply that the torso-balancing mechanism

necessary for human bipedalism evolved within the hominoid clade. Future research will focus on how activation patterns influence locomotor kinematics.

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### Interpreting kinship, relatedness, and biological health in historic Oymaağaç, Turkey via *os acetabuli* and *os naviculare*: An analysis and critique of the use of bony ossicles in bioarchaeology

MADELYN K. GREEN<sup>1</sup> and KATHRYN E. MARKLEIN<sup>2,3</sup>

<sup>1</sup>Department of Anthropology, The Ohio State University, <sup>2</sup>Department of Anthropology, University of Louisville, <sup>3</sup>Center for Archaeology and Cultural Heritage, University of Louisville

In modern populations, some accessory bones ("*os*" bones) have been shown to exhibit high heritability. Despite implications for kinship analysis, bony ossicles oftentimes go undetected and under-examined in bioarchaeology. *Os acetabuli* and *os naviculare* were recovered from Oymaağaç, Turkey, in both Hellenistic-Roman (1st c. BCE-4th c. CE) and Roman-Byzantine (5th c.-9th c. CE) periods. Mass and multigenerational burial circumstances, presence or absence of grave goods, and temporal periods were investigated for differences in ossicle prevalence. Any occurrences of the two ossicle types were noted; while *os acetabuli* was only observed in one individual, multiple occurrences of *os naviculare* allowed for statistical analysis based on burial circumstances ( $n=222$ ), grave good presence ( $n=238$ ), and time period ( $n=238$ ). Total prevalence rates (TPR) for right, left, and total *os naviculare* were compared using parametric Pearson's  $\chi^2$  tests. Comparisons showed overall higher TPR of *os naviculare* in mass burial circumstances (18.6%), within Hellenistic-Roman contexts (6.60%), and among burials with associated grave goods (7.93%). Significant differences ( $p\text{-value} \leq 0.05$ ) were only observed between mass and multigenerational burial contexts: 17.4% and 4.21% (right), 20% and 3.57% (left), and 18.6% and 3.91% (total), respectively. The differences of *os naviculare* between mass and multigenerational burial contexts illustrate how bony ossicles, as proxies for kinship and relatedness, can contribute to interpretations of biological health and mortality risk factors. Overall, there is a need for more critical methods of excavation and analysis to identify accessory ossicles, as they can bolster inferences of past lifeways, especially regarding relatedness and health.

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### Residential Mobility, Pastoralism, and Community in Ancient Kush

LESLEY A. GREGORICKA<sup>1</sup> and BRENDA J. BAKER<sup>2</sup>  
<sup>1</sup>Department of Sociology, Anthropology, & Social Work, University of South Alabama, <sup>2</sup>School of Human Evolution & Social Change, Arizona State University

The Kingdom of Kush in what is now northern Sudan and southern Egypt is often depicted as a secondary state relative to ancient Egypt. More recent investigations have set aside Egyptocentric and colonialist perspectives of state development focused on control of land and agricultural surplus. Instead, Kushites from ancient Nubia are examined through the lens of African-based models of mobile pastoralism in which power and authority were achieved through control of herds and alliance-building. From Kerma period cemetery sites around al-Qinifab, Sudan, located between the fourth and fifth cataracts of the Nile River, we analyzed the strontium isotope ratios of 27 individuals dating from the Early through Late Kerma/New Kingdom phases (ca. 2500-1100 BCE) to investigate diachronic shifts in mobility patterns linked to pastoralism and state development.

Individuals from the Early and Middle Kerma phases demonstrated considerable  $^{87}\text{Sr}/^{86}\text{Sr}$  ratio variability (mean =  $0.7085 \pm 0.0012$ ), while later Classic ( $0.7075 \pm 0.0005$ ) and Late Kerma/New Kingdom ( $0.7075 \pm 0.0004$ ) ratios largely fell within locally bioavailable strontium ranges produced by modern fauna ( $0.7062\text{-}0.7084$ ). These changes indicate a potential transformation in social organization as early communities engaged in a more mobile lifestyle than later groups, perhaps reflecting a greater degree of pastoralism followed by increased linkage to the Kerma core area and declining mobility with state coalescence. Females and males from all periods exhibited non-local ratios in equal numbers. Because  $^{87}\text{Sr}/^{86}\text{Sr}$  ratios from enamel reflect childhood geographic residence, this observation suggests that mobility involved the entire community and not just transhumant adults.

*Funding was provided by the Qatar-Sudan Archaeological Project, the Center for Bioarchaeological Research at ASU, and the University of South Alabama Faculty Development Council Grant.*

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### The influence of locomotor mode on nuchal muscle activity in *Macaca fuscata* and *Hylobates lar*

NEYSA GRIDER-POTTER<sup>1</sup>, RYOSUKE GOTO<sup>2</sup>, TETSUYA SHITARA<sup>3</sup> and YOSHIHIKO NAKANO<sup>3</sup>

<sup>1</sup>Department of Clinical Anatomy and Osteopathic Practices and Principals, Rocky Vista University, <sup>2</sup>Department of Physical Therapy, Gunma Paz University, <sup>3</sup>Department of Human Sciences, Osaka University

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Nuchal muscles maintain head stability during locomotion in order facilitate visual and vestibular feedback necessary to navigate the environment. However, extrinsic nuchal muscles also move the forelimb when the head and neck are stable. How do nuchal muscles function during locomotion to both maintain head stability and move the forelimb? We hypothesize that 1) locomotor modes relying on forelimb activity will require greater muscular effort on the part of the extrinsic nuchal muscles and 2) intrinsic nuchal muscle activity will correspond to extrinsic activity in order to maintain both head stability and provide an anchor for the forelimb muscles. To test these hypotheses, we collected fine wire electromyographic data during locomotor experiments using *Macaca fuscata* and *Hylobates lar*. Data were collected from two extrinsic nuchal muscles (trapezius and sternocleidomastoid) and two intrinsic muscles (splenius capitis and rectus capitis posterior minor). For each species, muscle activity was compared between forelimb-assisted locomotion (terrestrial quadrupedalism,  $n_m=131$ , and brachiation,  $n_h=55$ ) and hindlimb-dominant locomotion (bipedalism,  $n_m=71$  and  $n_h=143$ ) using linear mixed models.

Locomotor mode significantly influences muscle activity across all muscles in both species. As expected, extrinsic muscle activity is greater during forelimb-assisted gait cycles ( $p<0.001$ ). Further, in both *Macaca* and *Hylobates* sternocleidomastoid activity correlates positively with that of splenius capitis indicating that increases in extrinsic muscle activity necessitates a corresponding increase in intrinsic muscle activity ( $r^2_m=0.91$ ,  $r^2_h=0.51$ ). This pattern has implications for understanding the mechanics of locomotor head stability and how locomotion may influence the evolution of primate musculoskeletal morphology.

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### Trade-offs in the pelvic floor constrain human pelvic evolution: A finite element approach

NICOLE D.S. GRUNSTRA<sup>1,2,3</sup>, KRISHNA KUMAR<sup>4</sup>, PHILIPP MITTEROECKER<sup>2</sup> and EKATERINA STANSFIELD<sup>2</sup>

<sup>1</sup>KLI, Konrad Lorenz Institute for Evolution and Cognition Research, <sup>2</sup>Department of Evolutionary Biology, University of Vienna, <sup>3</sup>Mammal Collection, Natural History Museum Vienna, <sup>4</sup>Department of Civil, Architectural and Environmental Engineering, Cockrell School of Engineering, University of Texas at Austin

Humans are characterized by a tight fetopelvic fit, with the relatively small birth canal a "compromise" between multiple antagonistic selection pressures. Obstetric selection is assumed to favor

a more spacious birth canal in women, whereas the source for opposing selection favoring a small birth canal remains hotly debated. One explanation is that a more expansive birth canal results in the soft tissue of the pelvic floor being suspended across a larger area, which is disadvantageous for supporting the weight of the inner organs and fetus and for maintaining continence. To test this "pelvic floor hypothesis", we varied a three-dimensional finite element model of the human pelvic floor in size (expressed as the square root of the surface area) and thickness and studied the effects on pelvic floor deflection (downward deformation). Our results showed that deflection increased disproportionately with pelvic floor size and that it was mitigated by increasing thickness. Nonetheless, even when thickness was varied proportionately to pelvic floor size, deflection increased disproportionately fast for models at, or larger than, the mean modern human female size. Thus, larger pelvic floors deflect relatively more than smaller pelvic floors, which supports the pelvic floor hypothesis. Increased pelvic floor thickness considerably reduced deflection, but as a side effect it also increases the intra-abdominal pressure necessary for successful childbirth. Our results thus highlight functional trade-offs not only in the size of the birth canal but also in the thickness and stiffness of the pelvic floor.

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### Relationships between sex, body mass and tooth wear in Cayo Santiago rhesus monkeys (*Macaca mulatta*)

DEBBIE GUATELLI-STEINBERG<sup>1</sup>, ELIZABETH MALDONADO<sup>2</sup>, TERRY B. KENSLER<sup>2</sup>, LUCI A.P. KOHN<sup>3</sup>, MARTIN Q. ZHAO<sup>4</sup> and QIAN WANG<sup>5</sup>

<sup>1</sup>Department of Anthropology, The Ohio State University, <sup>2</sup>Caribbean Primate Research Center, University of Puerto Rico Medical Sciences Campus, <sup>3</sup>Department of Biological Sciences, Southern Illinois University, <sup>4</sup>Department of Computer Science, Mercer University, <sup>5</sup>Department of Biomedical Sciences, Texas A&M University College of Dentistry

Understanding factors affecting tooth wear in primates is of interest because as teeth wear, their chewing efficiency can change—in some species positively and in others negatively. It is well known that teeth wear with age, but relationships between sex and tooth wear and between body size and tooth wear are less well understood. Here we analyze molar wear scores from a cross-sectional sample of 212 Cayo Santiago rhesus monkey (*Macaca mulatta*) adults examined in 1985. Because males are generally larger than females—potentially processing more food over their lifetimes—we hypothesized that with age included in an ordinal logistic regression model, males would exhibit significantly greater wear than females. We further hypothesized that

males of larger body mass would exhibit greater wear than males of smaller body mass. Finally, because many of the females were pregnant or lactating at the time of dental examination, we hypothesized that there would be no relationship between body mass and wear in females. We found that with age included in ordinal logistic regression models, males had significantly more worn molars than females, larger males had more worn molars than smaller males, and that for females, molar wear was not significantly related to body mass. These results suggest that over the life course, animals with larger body sizes (males vs. females and larger vs. smaller males) may accumulate more wear than those with smaller body sizes. Future analyses to be conducted on the Cayo Santiago monkeys' skeletal remains will further evaluate this possibility.

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### Envisioning an anti-racist anthropological genetics: Using our power as scholar-teachers for transformative change within our institutions

ELAINE E. GUEVARA

Evolutionary Anthropology, Duke University

The civil rights movement of 2020 has called for academics to dismantle white supremacy within and beyond our institutions. Many anthropological geneticists have long been vocal in condemning the central roles of both anthropology and genetics in essentializing white supremacy. We must continue and prioritize these efforts within our classrooms and the public sphere. However, this work is insufficient without seriously working for inclusivity and diversity within our field. Doing so will require examining how we perpetuate inequity in our profession. I urge us to see this challenging moment as an opportunity to begin conversations about how to make transformative change within our institutions. I offer a few specific challenges, starting with counteracting the harmful, persistent myth of the meritocracy in science by acknowledging that access to doing the undeniably hard work of science itself is a privilege available to very few. I advocate abandoning assimilationist approaches to diversity initiatives and teaching, which can re-enact rather than redress injustice, as well as dampen the positive impact of diversity on science. I suggest rethinking classroom practices like presenting a procession of Western geniuses as the engine of scientific advancement, which promote incomplete and exclusionary understandings of how knowledge builds. Additionally, I make the case that true inclusivity will require envisioning a more humane work environment where those with a broader range of life responsibilities and priorities can truly thrive. Ultimately, effecting meaningful

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change will require resisting quick fixes and instead a commitment to critical reflection, challenging conversations, collaborative action, and courage.

### What accentuated striae in tooth enamel reveal about physiological stress differences in two Ohio populations of disparate socioeconomic status

KAITA N. GURIAN<sup>1</sup>, SARAH HOLT<sup>1</sup>, LEIGH OLDERSHAW<sup>1</sup>, MARK HUBBE<sup>1,2</sup> and DEBBIE GUATELLI-STEINBERG<sup>1</sup>

<sup>1</sup>Anthropology, The Ohio State University, <sup>2</sup>Instituto de Arqueología y Antropología, Universidad Católica del Norte, Chile

Accentuated Striae (AS) are enamel disruptions visible as thick dark lines in histological slides of enamel, paralleling normal growth lines known as brown striae of Retzius. They have been used as indicators of stress in archaeological, forensic, and primate studies in biological anthropology. Previous studies have suggested a link between specific stressors, the formation of AS, and future mental and physical health risks. This research investigates whether there is a relationship between the manifestation of AS and (1) socioeconomic status (SES) differences between two Ohio populations, and (2) several biological attributes of the sample.

Deciduous teeth were collected from 48 individuals representing two populations with known disparities in overall stress level (Population A: high-income population from affluent neighborhoods in Central Ohio; Population B: low-income population from primarily rural Appalachian Ohio). Histological slides of enamel were created, and the presence of AS was observed in each tooth using a Nikon polarizing transmitted light microscope with Cannon digital camera. AS prevalence was compared between samples and contrasted with several demographic and biological health variables (gestation length, birth mode, sex of the infant, gestational diabetes).

AS were only observed among the low-income population (31%) and this prevalence is significantly higher than that observed among the high-income population (0%) (chi-square test;  $p=0.007$ ). There are no associations between AS and any other variable ( $p>0.05$  for all comparisons). This result supports the link between AS and non-specific population stress, reinforcing the validity of this indicator for studies reconstructing population health in the past.

### Which came first: the pelvis or the EGG? Energetics of Gestation and Growth versus Obstetrical Dilemma

MARTIN HAEUSLER<sup>1</sup>, NICOLE D.S. GRUNSTRA<sup>2,3,4</sup>, CINZIA FORNAI<sup>1,5</sup>, VIKTORIA A. KRENN<sup>1,5</sup>, ROBERT D. MARTIN<sup>1,6</sup> and NICOLE M. WEBB<sup>1,7</sup>

<sup>1</sup>Institut of Evolutionary Medicine, University of Zurich, Switzerland, <sup>2</sup>Konrad Lorenz Institute for Evolution and Cognition Research, Klosterneuburg, Austria, <sup>3</sup>Department of Evolutionary Biology, University of Vienna, Vienna, Austria, <sup>4</sup>Mammal Collection, Natural History Museum Vienna, Vienna, Austria, <sup>5</sup>Department of Evolutionary Anthropology, University of Vienna, Austria, <sup>6</sup>Negaunee Integrative Research Center, The Field Museum, Chicago, USA, <sup>7</sup>Palaeoanthropology Department, Senckenberg Research Institute and Natural History Museum Frankfurt, Germany

The "Energetics of Gestation and Growth" (EGG) hypothesis posits that labour is initiated when the energetic demands of the fetus surpass the mother's sustained metabolic capacity. Thus, human neonates are neurologically and physically more immature than non-human primates, i.e., "secondarily altricial", because gestation length is capped by supposedly exponentially increasing energetic demands of the developing fetus. This contrasts with the assumption of the "Obstetrical Dilemma" hypothesis that maternal pelvic dimensions constrain neonatal size and thus gestation length. Our analysis of nearly continuous data of fetal growth showed a decline in energy requirements for the offspring between gestation week 36 and shortly after birth. Thereafter, the same growth rate is resumed as prior to gestation week 36, before it again slows down and exceeds the mother's alleged metabolic ceiling only about 6 months after birth. These findings contradict previous extrapolations implying an energetic demand that exponentially increases prenatally, thus challenging the EGG hypothesis. Moreover, the metabolic ceiling of the expectant mother is assumed to be around 2.1x basal metabolic rate (BMR), corresponding to only 628 kcal above the energy requirements of non-pregnant, non-lactating women. However, this proposed metabolic threshold has yet to be directly tested. Further, data derived from endurance athletes suggest that the maximum sustained metabolic scope plateaus around 2.5x BMR, making it increasingly unlikely that pregnant women approach this level by the end of pregnancy and that it is crossed by the fetus before birth. These findings warrant reservations regarding an energetic basis as the sole determinant to human birth timing.

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### Ancient perspectives on pandemics, prenatal health, and pregnancy loss

SIÁN E. HALCROW<sup>1</sup> and GWEN ROBBINS SCHUG<sup>2,3</sup>

<sup>1</sup>Department of Anatomy, University of Otago, <sup>2</sup>Department of Anthropology, Appalachian State University, <sup>3</sup>Department of Anthropology, The University of North Carolina

There have been recent calls for research on the effects of COVID-19 on prenatal stressors, birth outcomes, developmental patterns, and assessment of the effects of the pandemic on later health. The psychosocial effects for the mother in the COVID environment are becoming apparent and there is clinical evidence for placental injury and neurological damage in children. The current global COVID-19 pandemic presents an opportunity for bioarchaeologists to contribute long-term perspectives and interpretive models towards understanding and responding to the current-day global crisis in health. The investigation of the maternal-infant nexus is a nascent field in bioarchaeology, which is particularly informative for understanding past population health, healthcare, and disparities imposed by structural inequalities based on factors such as ethnic identity, caste, class, and/or socioeconomic status. We present case studies from South and Southeast Asia that highlight a bioarchaeological approach for assessing the burden of epidemics on the maternal-fetal pair. We find that during epidemics that the greatest burden of mortality and morbidity is found in the remains of women and babies, including substantial evidence for prenatal stress in the form of nutritional insufficiencies and growth disruption. We demonstrate that the experience of pregnancy loss and stress during these epidemics are shaped by structural inequalities, comorbidities and biocultural frailty, and changes in human-animal interactions, paleodemography, migration and the environment.

### Utilizing local corporate partnerships to aid in conservation at a small chimpanzee (*Pan troglodytes verus*) conservation site in Sierra Leone

ANDREW R. HALLORAN<sup>1</sup> and CHRISTINA T. CLOUTIER BARBOUR<sup>2</sup>

<sup>1</sup>Chimpanzee Behavior & Care, Save the Chimps, <sup>2</sup>Primates, Lion Country Safari

The Tonkolili Chimpanzee Project is a small community-based conservation project focused on 15 km<sup>2</sup> in central Sierra Leone. The chief aim of the project is to mitigate conflict between the local humans and the wild chimpanzee populations in the region, which may manifest as chimpanzee crop raiding, habitat destruction and degradation, and poaching events. Mitigation strategies have been targeted, and have included policies such as agricultural intensification of land deemed to be undesirable chimpanzee habitat. Historically, the project has subsisted off small grants and

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private donations, but we have recently engaged local companies in Sierra Leone to assist with our initiatives. The engagement has resulted in more initiatives as well as greater in-situ visibility. In the past year, we have partnered with a Sierra Leonean subsidiary of an international brewery to plant over 50 hectares of sorghum, which the brewery will, in turn, purchase from the local communities once harvested. Somewhat more controversially, the project has engaged with a local biofuel company in order to provide agricultural equipment that can be used to transform desertified seasonal floodplains into agricultural fields. We contend that small community-based conservation efforts are crucial to the preservation of wild chimpanzees across Africa, but especially for the critically endangered western subspecies, where suitable habitat has declined by over 80% in just the past few decades. Without large swaths of protected forests, conservation of this particular population requires a targeted, community-based approach. In the absence of large grants, novel approaches to project sustainability are necessary.

### Examining the relationships of intact and fragmentary osteons in human ribs at multiple locations

ANGELA L. HARDEN<sup>1</sup>, VICTORIA M. DOMINGUEZ<sup>2,3,4</sup> and AMANDA M. AGNEW<sup>1,5</sup>

<sup>1</sup>Injury Biomechanics Research Center, The Ohio State University, <sup>2</sup>Department of Anthropology, Lehman College, City University of New York, <sup>3</sup>Department of Anthropology, The Graduate Center, City University of New York, <sup>4</sup>New York Consortium of Evolutionary Primatology, <sup>5</sup>Department of Anthropology, The Ohio State University

Osteon population density (OPD) is a common variable utilized in histological age-at-death methods. OPD is determined by combining the total number of intact (It.On) and fragmentary (Fg.On) osteons over a given surface area. However, research analyzing the constituent variables on their own is lacking. It has been suggested that pooling these data may obscure relevant information. The aim of this research is to evaluate the differences in It.On and Fg.On at multiple locations to provide additional data on rib histomorphometry both along the length of the rib and between sexes. Sixth level human ribs were ethically obtained from ten post-mortem human subjects (females=5, males=5) at three specific sampling locations (posterior [25%], midshaft [50%], and anterior [75%]). Nine sections from each rib were analyzed (three seriated sections at each location), for a total sample of 90 sections. The number of It.On and Fg.On were counted and cortical area (Ct.Ar) was calculated, which was used to calculate It.OPD and Fg.OPD. Analysis of Variance (ANOVA) was performed to examine the relationships between section location (posterior, midshaft, or anterior) within the entire sample, females only, males only, and between

sexes. Overall, trends in It.OPD and Fg.OPD were similar, with comparable means at the anterior and midshaft locations and decreasing posteriorly. However, when comparing sexes, significant differences were found at all locations. These observed differences in both It.OPD and Fg.OPD suggest that further investigation into the roles of these individual variables and their individual contributions to OPD in age-at-death estimation methods is warranted.

### Incongruence between self-reported health and chronic disease risk amongst rural Nicaraguan women experiencing an epidemiological transition

DREW HARDIN<sup>1</sup>, BARBARA A. PIPERATA<sup>1</sup>, JASON DE CARO<sup>2</sup>, NATASHA HOEHN<sup>3</sup>, GARIEL E. BROWN<sup>3</sup>, KAMMI K. SCHMEER<sup>4</sup> and WARREN WILSON<sup>3</sup>

<sup>1</sup>Department of Anthropology, The Ohio State University, <sup>2</sup>Department of Anthropology, University of Alabama, <sup>3</sup>Department of Anthropology and Archeology, University of Calgary, <sup>4</sup>Department of Sociology, The Ohio State University

Self-rated health (SRH), a subjective measure of health status, is used in national health surveys, including in low- and middle-income countries experiencing epidemiological transitions, as a proxy for overall health. However, the extent to which SRH reflects risk of emerging chronic disease in such settings remains unclear. We test the relationship between SRH and objective measures of risk for cardiometabolic diseases among 200 rural Nicaraguan women, where the rate of these diseases is on the rise. SRH was measured with a Likert scale (bad to excellent). Measures of chronic disease risk included BMI, waist-to-height ratio, blood pressure, and blood glucose. Using international cut-offs, women were categorized as within the normal range (0) or above it (1). These data were combined to create a chronic disease risk index (CDRI) (range 0-4). For SRH, responses were 7.5% bad, 61% regular, 24.5% good, 4% very good, 3% excellent. For CDRI, 4.5% scored a 0, 39.5% scored a 1, 35.5% scored a 2, 17% scored a 3, 3.5% scored a 4. Using an OLS regression that included potential correlates of SRH and chronic disease risk, we found no association between SRH and CDRI ( $\beta=0.057$ ,  $p=0.48$ ). Of the additional correlates considered, only mental health status (SRQ-20), was significantly associated with SRH ( $\beta=.27$ ,  $p=0.001$ ). Results indicate that SRH was a poor predictor of cardiometabolic disease risk in this setting and raise questions as to the use of SRH as proxy for overall health in contexts experiencing epidemiological transitions.

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### Genetically Determined Strength of Natural Killer Cells is 1 Enhanced by Adaptive HLA class I Admixture in East Asians

GENELLE F. HARRISON

Division of Personalized Medicine, University of Colorado, Anschutz Medical Campus

Human natural killer (NK) cells are essential for controlling infection, cancer and fetal development. NK cell functions are modulated by interactions between polymorphic inhibitory killer cell immunoglobulin-like receptors (KIR) and polymorphic HLA-A, -B and -C ligands expressed on tissue cells. All HLA-C alleles encode a KIR ligand and contribute to reproduction and immunity. In contrast, only some HLA-A and -B alleles encode KIR ligands and they focus on immunity. By high-resolution analysis of KIR and HLA-A, -B and -C genes, we show that the Chinese Southern Han are significantly enriched for interactions between inhibitory KIR and HLA-A and -B. This enrichment has had substantial input through population admixture with neighboring populations, who contributed HLA class I haplotypes expressing the KIR ligands B\*46:01 and B\*58:01, which subsequently rose to high frequency by natural selection. Consequently, over 80% of Southern Han HLA haplotypes encode more than one KIR ligand. Complementing the high number of KIR ligands, the Chinese Southern Han KIR locus combines a high frequency of genes expressing potent inhibitory KIR, with a low frequency of those expressing activating KIR. The Southern Han centromeric KIR region encodes strong conserved, inhibitory HLA-C specific receptors, and the telomeric region provides a high number and diversity of inhibitory HLA-A and -B specific receptors. In all these characteristics, the Southern Han represent other East Asians, whose NK cell repertoires are thus enhanced in quantity, diversity and effector strength, likely through natural selection for resistance to endemic viral infections.

*1) Science, Technology and Innovation Commission of Shenzhen; 2) the National Natural Science Foundation of China; 3) the National Institutes of Health of the USA*

### Collecting Bodies Down La Plata: Bioarchaeology of three sites along the La Plata River in southern Colorado occupied during the Basketmaker III and Pueblo I transition

RYAN P. HARROD

Anthropology, University of Alaska Anchorage

From 1913 to 1927, human skeletal remains were recovered from three sites in La Plata River drainage at Site 19, Site 22, and Site 23. The remains were excavated by Earl Morris and Harry Shapiro and some of them were sent to the American Museum of Natural History in New York. In prior analyses of these collections of human skeletal remains, I focused on comparing them to other larger, more notable sites in the

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region like Chaco Canyon or Aztec Ruins. This approach was problematic because it revealed relatively little about the people living at La Plata. Additionally, there is question of how representative is this collection of the region and time period. The intent of this research was to conducting a thorough review of the literature to better understand the motivation behind the collection of the skeletal remains, and highlight some of the pitfalls of period-specific methodological and theoretical approaches. I also created what Frank Saul called osteobiographies for each set of remains to reconstruct demography and determine who was missing and why. Analysis of the collection reveals that 49 of the 57 individuals could be identified, of these the majority were adults with relatively few non-adults despite the mention of more in the original field reports. Only about half of the remains included both cranial and postcranial elements, so many of the osteobiographies were incomplete. The missing non-adults and isolated crania and postcranial remains, highlight the importance of understanding the collection limitations of prior comparative research.

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### A new ontogenetic framework for analyzing fossil hominin tracks

KEVIN G. HATALA<sup>1</sup>, PETER L. FALKINGHAM<sup>2</sup> and STEPHEN M. GATESY<sup>3</sup>

<sup>1</sup>Department of Biology, Chatham University, <sup>2</sup>School of Biological and Environmental Sciences, Liverpool John Moores University, <sup>3</sup>Department of Ecology and Evolutionary Biology, Brown University

Skeletal fossils have been the predominant focus of most studies that investigate the evolution of human locomotion. Experiments have demonstrated how cortical and trabecular bone adapt to mechanical stresses, and these results have equipped paleoanthropologists with toolkits for detecting functional signals from hominin skeletal fossils. Fossil tracks offer perhaps more direct evidence of hominin locomotion, with the potential to substantially augment information gleaned from skeletal analyses. However, their mechanistic origins are complex, and a nascent understanding of these data has hindered their utility and prominence in paleoanthropology. Here we present results that open the black box of the mechanics of human track formation, and allow us to directly observe and understand how anatomical and functional signals are recorded in track morphology. By integrating biplanar X-ray experiments, 3-D animation, and particle simulation, we developed techniques to accurately simulate the surface and sub-surface substrate deformations that occur during track formation. Through this lens we can observe and quantify foot-substrate mechanics throughout "track ontogeny". This window reveals that tracks do

not reflect plantar pressure distributions due to substantial fore-aft and medial-lateral particle dispersions. The "plantar anatomy" evidenced in the floor of a track does not mirror the foot anatomy that created it, and is instead largely influenced by foot motion and substrate flow, even in relatively shallow, foot-like tracks. Using fossil examples, we demonstrate why the framework of track ontogeny is essential for interpreting hominin tracks, and how this unique toolkit can be used to accurately infer anatomical and functional signals.

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### An extinction-oriented perspective on genealogical networks

JOHN HAWKS

Department of Anthropology, University of Wisconsin-Madison

Genomic data has transformed the way we look at the relationships of living and past humans. However, the nature of ancient genome samples tends to skew analytical approaches toward those that build from the higher-quality data found in samples of living people. Beginning in the 1980s, many researchers have relied upon coalescent approaches, which considers gene genealogies in a backward-time perspective, tracing a decreasing number of ancestors of present-day lineages back to the common ancestor of a sample. This perspective tends to miss what happens to extinct gene lineages, which do not survive into living samples. Here, I develop methods of visualizing gene networks across generations, focusing on extinction and decline of genealogical lineages. I apply this approach to consider the dynamics of Neandertal gene lineages prior to their extinction. The examination of extinction processes in genealogies provides a different perspective than survival-centric traditional approaches. Visualization of extinct gene lineages found within three high-coverage Neandertal genomes (Chagyrskaya 8, Vindija 33.19, and Denisova 5) suggests greater spatial or temporal heterogeneity than surviving lineages. Visualization of Neandertal haplotypes in these genomes that are inferred to reflect gene flow from ancient Africans shows that these do not deviate significantly from other gene lineages in extinction probability, but the extinct subset of these lineages does deviate from the heterogeneity among other extinct lineages.

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### Evidence of a behavioral tradeoff between parenting effort and mating effort in a polygynandrous primate

CAITLIN R. HAWLEY<sup>1,2</sup> and JOAN B. SILK<sup>1,2</sup>

<sup>1</sup>Anthropology, Arizona State University, <sup>2</sup>Institute of Human Origins, Arizona State University

In many primate species, males are expected to face trade-offs between mating and parenting effort due to constraints on males' time and energy. Most evidence to date on male reproductive trade-offs has focused on mechanisms that underline trade-offs but have not looked purely at behavior. Baboons (*Papio spp*) are an ideal taxa to examine behavioral trade-offs because males mate with multiple females but also form primary associations. Primary associations function as a form of parenting effort, where males maintain bonds to mothers of dependent offspring and protect mothers and offspring from harassment. Using 4 years of data on wild olive baboons (*Papio anubis*), we ask whether males face a trade-off between forming additional primary associations and approaching fully swollen females. We used zero-inflated negative binomial mixed-effects models to demonstrate that males with more primary associates approach fully swollen females less, controlling for rank and number of fully swollen females available. We also found that males with more primary associates played a less active role in establishing proximity to their female partners than males with fewer primary associates. Our results suggest that maintaining bonds with primary associates (a form of parenting effort) inhibits males in their behavior towards sexually receptive females and towards additional primary associates. We argue that constraints on time or energy force males to make reproductive decisions in a polygynandrous mating system.

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### Ethics of engaging in genetic research with underrepresented populations: progress and pitfalls

NICOLA L. HAWLEY

Chronic Disease Epidemiology, Yale School of Public Health, Anthropology, Yale University

Despite a numeric increase in the number of minority participants engaging in genetic research globally, the percentage of indigenous people represented in genome-wide association studies worldwide decreased from 0.06% to 0.05% between 2009 and 2016. Many such communities have expressed concern that they do not sufficiently benefit from genetic research, that a focus on genetics diverts attention and resources away from non-genetic, social, and economic causes of health disparities, including racism, and that genetic research could actually reinforce racism by implying that indigenous people have specific genetic susceptibilities to disease and are therefore inherently unhealthy. Another troubling issue is that many diverse ancestry populations are located in low- and middle-income countries (LMICs) or low resource settings. It is difficult to discuss genetic research in the usual context of reciprocity when the benefits of the genetic

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research are, for the time being, unlikely to benefit participants and their communities. Finally, there are concerns that potential commercial value from genetic research is not explicitly identified in discussions with local leadership or formally agreed to in pre-revenue agreements. This raises fears that genetic researchers are bioprospecting, whether actively or passively.

This presentation will speak to my experience with a decade long collaboration on genetic research in Samoa. I will describe some of the progress toward establishing equitable partnerships and building community capacity in Samoa, but also the pitfalls, challenges, and considerations associated with working in a community and publishing genetic research on a community that is not my own.

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### **Asymmetry and discordance in carabelli's trait and the hypocone: Do monozygotic and dizygotic twins point to common underlying epigenetic factors?**

SAVANNAH HAY<sup>1</sup> and G. RICHARD SCOTT<sup>2</sup>

<sup>1</sup>Anthropology, University of Kansas, <sup>2</sup>Anthropology, University of Nevada, Reno

Family and twin studies show a strong genetic component underlying the development of nonmetric tooth crown traits. If these traits are controlled by genes alone, then (1) left and right antimeres should exhibit identical trait expressions, and (2) MZ twins, with identical genotypes, should display identical phenotypes. However, antimeres exhibit some asymmetry in trait expression and MZ twins exhibit some discordant trait expression. Antimere asymmetry and MZ twin discordance suggest factors at work beyond genes that moderate crown trait expression, possibly common epigenetic mechanisms.

This study looks beyond the "genetically controlled" paradigm of nonmetric crown tooth traits by examining the asymmetry and discordance in Carabelli's cusp and hypocone of 288 Australian monozygotic (MZ) and dizygotic (DZ) twin pairs. The asymmetry between antimeres is almost identical for MZ and DZ twins. Scores for discordance were similar for MZ twins but consistently lower for DZ twins. Measures of asymmetry in both twin types and discordance in MZ twins are almost identical, suggesting both are likely caused by epigenetic factors operating at the same magnitude. However, these factors may work independently on asymmetry and discordance as they do not covary in twins. As an ancillary test, birth weight data were compared to asymmetry and discordance scores in both twin types. Neither absolute birth weights nor birth weight differences between twins were associated with levels of asymmetry or discordance.

Birth weight, a reflection of developmental perturbations and prenatal stress during pregnancy, was not reflected in the development of Carabelli's trait or the hypocone.

### **Mixed-economic strategies in an arid subsistence context: Sub-Saharan hunter-gatherers facing climate change**

ASHLEY HAZEL

Earth System Science, Stanford University

Climate change is already affecting subsistence-living communities. Arid-living people are among the earliest and most severely impacted by increasing environmental unpredictability, drought intensification, and food insecurity. Livelihood diversification will likely be crucial to navigate increasing unpredictability. Also, support networks will have amplified value during scarcity. Herein, we describe livelihood options, food availability, and social ties among Ju/'hoansi San hunter-gatherers in the Nyae Nyae Conservancy, eastern Namibia to ask the following questions:

- 1) What subsistence strategies are available to rural Ju/'hoansi?
- 2) Are monetary/market strategies preferred to subsistence?
- 3) Are households that engage most intensely in hunting-gathering more or less food secure?
- 4) Are people with more and stronger network ties able to access more livelihood strategies?

In this preliminary study, we collected household census, economic and subsistence surveys, and name-generator network data among 37 household heads (women=20; men=17) in four villages. We found that while several subsistence practices are present, very few households access all. Also, although paid labor is increasingly common, people report that government subsidies (pension) are most critical because they are frequent (monthly) and dependable. Furthermore, although the most diversified households were the most food secure, 100% of interviewees report being able to eat daily because of gathered food. Finally, the majority of social ties are among family, but people with broader networks beyond the close family reported more diverse resource bases and greater food security. These findings offer insights into how economically vulnerable communities might manage increasing environmental insecurity wrought by climate change.

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### **Conservation Impact and Implications of Orangutan Rehabilitation Youtube Videos**

ERIN G. HEANING<sup>1</sup>, IMANI R. MULRAIN<sup>2</sup>, CATHRYN A. FREUND<sup>3</sup>, ANDREA L. DIGIORGIO<sup>4</sup> and JESSE B. MCCANN<sup>5</sup>

<sup>1</sup>Psychology, Princeton University, <sup>2</sup>Chemistry, Princeton University, <sup>3</sup>Biology, Wake Forest University, <sup>4</sup>Writing Program, Princeton University, <sup>5</sup>Technology Support, Independent

All three species of orangutan, endemic to Malaysia and Indonesia, are critically endangered due to large-scale deforestation, hunting and poaching, and wildlife trade. Orangutan rescue and rehabilitation centers are a central conservation tool to combat this species decline. These centers connect with funders and supporters through social media, but this is a double-edged sword: it can be an effective tool for education and fundraising, but can also have counter-productive impacts on public understanding of wildlife conservation. Previous research shows that increasing human-animal interaction in media may increase video popularity, but animals shown in anthropogenic contexts are also viewed as less endangered and as appealing pets. Here we explore how the characteristics of social media posts (YouTube videos) from orangutan rescue organizations relate to viewers' reactions to the posts. Specifically, using YouTube analytics and sentiment analysis of video comments, we ask how viewer responses to 23 videos, including a total of 7012 comments, correlate with 1) the amount of human-orangutan interaction depicted and 2) the ages of the orangutans featured. We found no clear relationships between the amount of human-orangutan interaction in the videos and viewer responses, and that videos that only showed adult orangutans elicited a significantly higher proportion of comments with positive conservation impact than did videos with infants only ( $p = 0.02$ ) or multiple age groups ( $p = 0.005$ ). This study is a pilot for a larger ongoing project, the results of which will be used to develop a set of social media guidelines for primate rescue centers.

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### **Evolutionary pressures diversifying *Paranthropus* teeth**

NOMAETHU HLAZO<sup>1,2</sup>, LAUREN DR. SCHROEDER<sup>2,3</sup> and REBECCA R PROF. ACKERMANN<sup>1,2</sup>

<sup>1</sup>Department of Archaeology, University of Cape Town, <sup>2</sup>Human Evolution Research Institute, University of Cape Town, <sup>3</sup>Department of Anthropology, University of Toronto Mississauga

Robust "hyper megadont" morphology across the genus *Paranthropus* has traditionally been interpreted as resulting from shared dietary adaptations. However, recent studies of the

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cranium and mandible suggest that divergent, species-specific adaptations do occur. Moreover, our previous research suggests that non-adaptive processes play much more of a role than previously appreciated in shaping the highly variable *Paranthropus* morphology. This study expands on previous work by first investigating inter and intra-specific variation in the teeth of *Paranthropus* using Elliptical Fourier Analysis. Following this, a hypothesis testing framework developed from Landé's neutral theory of evolution is used to test whether this variation is a result of selection versus genetic drift. This study includes fossil samples of *Paranthropus* (*P. robustus*, *P. boisei*, *P. aethiopicus*, *Paranthropus* sp.; n=21), and comparative samples of *Australopithecus africanus* (n=7), *A. sediba* (n=1), *Australopithecus* sp. (n=3), *A. prometheus* (n=1), and early *Homo* (n=1). Extant taxa (*Homo sapiens* (n=50), *Pan troglodytes* (n=50) and *Gorilla gorilla* (n=50)) serve as models of within species variation for the fossil samples. Results are roughly consistent with previous analyses on the face, and indicate that both selection and drift play roles in shaping *Paranthropus* dental morphology. Moreover, dental morphology is variable in ways that do not consistently map with current taxonomic affiliations. The Gondolin molar appears to be adaptively different from the rest of the *P. robustus* sample, in addition to being distinct in both size and shape, possibly lending credence to suggestions that this represents a second *Paranthropus* species in South Africa.

Funded by the University of Cape Town, the National Research Foundation, the Centre of Excellence in Palaeosciences (CoE-Pal), and the Australian Research Council Future Fellowship hosted by LaTrobe University, Australia.

## Exploring the impact of anemia on bone collagen and carbonate stable isotope ratios among soldiers in Napoleon's Grand Army

SAMMANTHA HOLDER<sup>1</sup>, LAURIE J. REITSEMA<sup>1</sup>, TOSHA L. DUPRAS<sup>2</sup> and RIMANTAS JANKAUSKAS<sup>3</sup>

<sup>1</sup>Anthropology, University of Georgia,

<sup>2</sup>Anthropology, University of Central Florida,

<sup>3</sup>Anatomy, Histology, and Anthropology, Vilnius University

Anemia can have variable impacts on stable isotope ratios in human tissues depending on etiology, with some studies finding significantly higher isotope ratios in individuals diagnosed with anemia and other studies finding no difference. The purpose of this research is to explore the relationship between anemia and stable carbon and nitrogen isotope ratios in bone collagen and stable carbon and oxygen isotope ratios in bone carbonate among Napoleonic soldiers. Anemia was differentially diagnosed through the presence of orbital, humeral, or femoral cribra. A total of 11 individuals diagnosed with anemia were compared to 78 individuals without

skeletal indicators of anemia. All 89 individuals were excavated from the mass gravesite of šiaurės miestelis associated with Napoleon's Grand Army, located in Vilnius, Lithuania. Mean  $\delta^{13}\text{C}_{\text{coll}}$  are  $-18.9\text{‰} \pm 1.2\text{‰}$ ,  $\delta^{15}\text{N}$  are  $10.6\text{‰} \pm 1.1\text{‰}$ ,  $\delta^{13}\text{C}_{\text{carb}}$  are  $-12.9\text{‰} \pm 1.0\text{‰}$ , and  $\delta^{18}\text{O}$  are  $-5.8\text{‰} \pm 1.2\text{‰}$  for individuals with anemia. Mean  $\delta^{13}\text{C}_{\text{coll}}$  are  $-19.4\text{‰} \pm 0.7\text{‰}$ ,  $\delta^{15}\text{N}$  are  $10.9\text{‰} \pm 1.0\text{‰}$ ,  $\delta^{13}\text{C}_{\text{carb}}$  are  $-13.3\text{‰} \pm 1.0\text{‰}$ , and  $\delta^{18}\text{O}$  are  $-6.1\text{‰} \pm 1.3\text{‰}$  for individuals without skeletal indicators of anemia. There are no statistically significant differences between groups for  $\delta^{13}\text{C}_{\text{coll}}$  ( $W=325.5$ ,  $p=0.197$ ),  $\delta^{15}\text{N}$  ( $W=506.5$ ,  $p=0.337$ ),  $\delta^{13}\text{C}_{\text{carb}}$  ( $W=299$ ,  $p=0.106$ ), or  $\delta^{18}\text{O}$  ( $W=297$ ,  $p=0.646$ ). These results indicate that anemia did not significantly impact bone stable isotope ratios in this sample. This research contributes to the growing body of literature that examines the complex relationship between disease etiology and processes, diet, and stable isotope ratios in tissues with long turnover times (i.e., the skeleton).

This research was supported by the University of Georgia's Innovative and Interdisciplinary Research Grant, Dean's Award, and Melissa Hague Field Study Award, and Sigma Xi's Grants-in-Aid-of-Research.

## NR3C1 methylation changes are associated with early childhood height growth trajectories

ELIZABETH A. HOLDSWORTH

Department of Anthropology, University at Albany, State University of New York

The hypothalamic-pituitary-adrenal (HPA) axis may be a pathway to allocate energy across life history traits in response to the environment. The life history domain of linear growth responds to the social-emotional environment, indicating that the HPA-axis may be the pathway by which the social-emotional environment stimulates allocation of energetic resources away from growth. If the HPA-axis is involved in allocating energetic resources across life history traits, then postnatal epigenetic programming of HPA-axis reactivity (changes in NR3C1 methylation, which is similarly sensitive to the social-emotional environment) should predict reduced height growth rates in childhood, a previously unexplored hypothesis.

This hypothesis was tested using the Avon Longitudinal Study of Parents and Children, which is rare in its repeated clinical measures of childhood growth and repeated methylation measures. Individual growth trajectories were derived from a piecewise mixed effects growth linear model of clinically-measured height in children from birth to 5 years of age. Change in NR3C1 methylation principal components score from birth to 7 years of age was included as a variable in multiple linear regression models for each growth spline. The lowest tertile of NR3C1 methylation change significantly predicted lower rates of height growth from 51-157 weeks of age

( $\beta=-0.007$ ,  $p=0.038$ ) and 157 weeks-5 years of age ( $\beta=-0.004$ ,  $p=0.048$ ), controlling for maternal leg length. These results indicate that NR3C1 methylation can influence linear growth in early childhood, with possible downstream effects on other life history traits. This suggests that the social-emotional environment influences growth through epigenetic programming of the HPA-axis.

This research was supported by a National Science Foundation Doctoral Dissertation Improvement Grant (NSF BCS-1729258) and the University at Albany.

## Change in Cuisine: A First Look at the Shift in Childhood and Adult Diet at Saint-Jean de Todon

JANE HOLMSTROM<sup>1</sup>, TOSHA DUPRAS<sup>1</sup>, YANN ARDAGNA<sup>2</sup> and LAURENT VIDAL<sup>3</sup>

<sup>1</sup>Anthropology, University of Central Florida, <sup>2</sup>Faculté des Sciences Médicales et Paramédicales, Aix-Marseille Université, <sup>3</sup>Centre de Recherches Archéologiques, Institut National de Recherches Archéologiques Préventives

The Medieval Christian cemetery (9<sup>th</sup> to 13<sup>th</sup>AD) site of Saint-Jean de Todon, located on a plateau in southern France near Laudun l'Ardoise, held the remains of 226 high status adult males, females, and non-adults. Stable carbon and nitrogen isotope analyses were employed on bone and tooth collagen from a sample of 50 individuals to investigate preservation and diet. All samples were found to be well preserved. The childhood values for nitrogen and carbon from tooth dentin (n=46) range from 9.1‰ to 12.7‰ for  $\delta^{15}\text{N}$ , and -19.9‰ to -17.4‰ for  $\delta^{13}\text{C}$ . The adult values for bone collagen for nitrogen and carbon (n=50) range from 8.5‰ to 11.7‰ for  $\delta^{15}\text{N}$ , and -21.6‰ to -17.9‰ for  $\delta^{13}\text{C}$ . Although these individuals held a higher status, carbon and nitrogen isotope data indicate a differentiated diet, possibly suggesting a hierarchy within the elite group. Especially notable is that the female diet was likely restricted in access to certain foods (female childhood values,  $\delta^{15}\text{N}=9.5\text{‰}$  to 11.7‰,  $\delta^{13}\text{C}=-19.4\text{‰}$  to -18.1‰; female adult values,  $\delta^{15}\text{N}=9.5\text{‰}$  to 10.8‰,  $\delta^{13}\text{C}=-20.7\text{‰}$  to -19.3‰), when compared with the male diet (male childhood values,  $\delta^{15}\text{N}=9.1\text{‰}$  to 12.2‰,  $\delta^{13}\text{C}=-19.9\text{‰}$  to -17.4‰; male adult values,  $\delta^{15}\text{N}=9.5\text{‰}$  to 11.7‰,  $\delta^{13}\text{C}=-21.6\text{‰}$  to -17.9‰). Although the study is limited to a randomized selection of the cemetery population, it illustrates a differentiated diet during breastfeeding as well as a dietary shift from more C<sub>4</sub> foods in childhood to mainly C<sub>3</sub> foods during adulthood.

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### Chimpanzee and human foot strike forces and the evolution of heel strike walking in hominins

NICHOLAS B. HOLOWKA<sup>1</sup>, VINCENT BHANDAL<sup>2</sup>, OTTO LAM<sup>2</sup>, MATTHEW C. O'NEILL<sup>3</sup>, NATHAN E. THOMPSON<sup>4</sup> and BRIGITTE DEMES<sup>2</sup>

<sup>1</sup>Department of Anthropology, University at Buffalo, <sup>2</sup>Department of Anatomical Sciences, Stony Brook University Medical Center, <sup>3</sup>Department of Anatomy, Midwestern University, <sup>4</sup>Department of Anatomy, New York Institute of Technology

When humans walk, their feet contact the ground heel first, resulting in high, rapid impact forces that have been implicated in long-term joint damage. It has long been argued that chimpanzees and other African apes also walk with a heel strike, implying that heel striking is plesiomorphic in hominins. Recent studies suggest that the human heel strike is kinematically distinct, but no study has investigated how differences in foot strike kinematics affect impact forces in humans and chimpanzees.

We measured ground reaction forces and hind limb kinematics in three male chimpanzees walking bipedally ( $n = 108$  steps) and quadrupedally ( $n = 54$  steps), and quantified the magnitude and rate of impact forces at foot strike, as well as foot contact and joint angles. Chimpanzees used a wide range of foot contact angles in both quadrupedal and bipedal walking, variably contacting the ground with the heel ('heel strikes') or more distal parts of the foot ('midfoot strikes'). Midfoot strikes were associated with significantly lower rates of loading at impact than heel strikes. Additionally, we compared these data to steps from a human sample (6 subjects, 38 steps), and found that chimpanzees have similar impact forces to humans when walking bipedally with a heel strike.

These results indicate that chimpanzees are distinct from humans in having more variable impact forces and foot strike postures. Further, our findings suggest that the human 'heel strike' is a uniquely derived aspect of hominin walking, selected for despite its associated high impact forces.

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### Characterizing evolutionarily divergent patterns of gene expression during osteogenesis using a comparative primate skeletal cell culture model

GENEVIEVE HOUSMAN<sup>1</sup> and YOAV GILAD<sup>1,2</sup>

<sup>1</sup>Section of Genetic Medicine, University of Chicago, <sup>2</sup>Department of Human Genetics, University of Chicago

Comparative skeletal anatomy is integral in anthropological research, but the underlying molecular mechanisms that drive the development and evolution of complex skeletal traits

are not well characterized. Evaluating gene expression in primate skeletal tissues is particularly challenging because samples are difficult to obtain, often have preservation issues, and contain heterogeneous populations of cells. As a more accessible way of evaluating gene expression in the skeleton, we established a comparative primate skeletal cell culture model and characterized gene expression patterns in this system. We optimized protocols to differentiate six human and six chimpanzee induced pluripotent stem cell lines (iPSCs) into mesenchymal stem cells (MSCs) and subsequently into osteogenic cells. Single-cell RNA-seq data were collected from over 100,000 cells that represent samples and replicates at each stage of differentiation. Technical replicates collected from each species and stage of differentiation show strong correlations of average gene expression patterns ( $r > 0.95$ ), validating the reproducibility of our differentiations. Data recovery was also similar across species. While most genes display conserved patterns of expression across species, hundreds of genes are differentially expressed (DE) between humans and chimpanzees within and across stages of differentiation. Significantly higher levels of gene expression variation in osteogenic cells as compared to iPSCs and MSCs hinted at increased cellular heterogeneity. Thus, more detailed classifications of cells across osteogenesis were identified, revealing additional species-specific DE genes. Altogether, the gene expression patterns identified during primate skeletal cell development hint at possible evolutionarily divergent mechanisms that may contribute to skeletal trait differences between species.

### Starting from scratch in a patrilineal society: how women make friends after marriage in rural Bangladesh

DANIEL J. HRUSCHKA

School of Human Evolution and Social Change, Arizona State University

Humans rely on social ties with both kin and non-kin for a wide range of support. In patrilineal societies that practice village exogamy, women can become disconnected from their established networks when they move to their husband's household. Starting from scratch in a new village creates a crucial challenge as women seek to cultivate new supportive relationships. In this paper, we track how women in four Bengali communities in rural Bangladesh grow new networks of support after migrating ( $n=573$ ). Furthermore, we compare this with neighboring Santal ( $n=92$ ) and Mandi ( $n=70$ ) communities where matrilineal residence is more common. Although facing a common challenge, we find women follow diverse trajectories in building social networks in their

new villages. Moreover, women migrating to new villages ultimately achieve networks of comparable sizes and composition with those remaining in their home village.

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### Gene expression in placental tissue compared with gene expression in venous blood from mothers and newborns in the Democratic Republic of Congo

CHU J. HSIAO<sup>1,2,3</sup>, ANNA C. WALTERS<sup>4</sup>, EDWARD B. QUINN<sup>1,2</sup>, FELICIEN MAISHA<sup>1</sup> and CONNIE J. MULLIGAN<sup>1,2</sup>

<sup>1</sup>Anthropology, University of Florida, <sup>2</sup>Genetics Institute, University of Florida, <sup>3</sup>MD-PhD Program, University of Florida, <sup>4</sup>Digital Worlds Institute, University of Florida

The placenta is one of the earliest pathways through which a new fetus interacts with the world. This organ plays an instrumental role in fetal development, serving respiratory, circulatory, excretory, and endocrine functions. We investigate the role that the placenta may play in mediating the impact of maternal psychosocial stress on newborn health outcomes (i.e. birthweight). Using a biocultural approach, we integrate culturally-derived measures of maternal stress with transcriptomic signatures in the placenta to investigate impacts on newborn birthweight in a set of mother-placenta-baby triads recruited from the eastern Democratic Republic of Congo ( $n=100$ ). Blood samples from mothers and newborns and tissue samples from placentas were stabilized in RNAlater. Total RNA was extracted using a modified TRIzol and RNeasy protocol (placenta) and RiboPure kits (blood). RNA quantity and quality were assessed using Qubit and TapeStation, respectively. Samples were hybridized on the Human ClariomD microarray, which queries over 540,000 transcripts. The RNA Integrity Numbers (RIN) differed significantly by tissue origin (median RIN 8.4 for moms, 9.0 for babies, 7.3 for placentas). Samples passed QC metrics with a minimum positive versus negative area under curve threshold of 0.88. Genes in the placenta involved in newborn birthweight and placental genes responsive to maternal stress were identified by comparing to gene expression patterns in maternal and infant venous blood. By contrasting gene expression among three different biological sources (mom, baby, placenta), we provide a more

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comprehensive understanding of the placenta's influence on newborn birthweight, which expands anthropological understanding of early-life human adaptations.

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## The biological diversity of early Americans as seen through cranial morphology: comparisons between Lagoa Santa, Brazil, and Quintana Roo, Mexico

MARK HUBBE<sup>1,2</sup>, ALEJANDRO TERRAZAS MATA<sup>3</sup>, BRIANNE HERRERA<sup>1</sup> and NOREEN VON CRAMON-TAUBADEL<sup>4</sup>

<sup>1</sup>Department of Anthropology, Ohio State University, <sup>2</sup>Instituto de Arqueología y

Antropología, Universidad Católica del Norte,

<sup>3</sup>Instituto de Investigaciones Antropológicas, Universidad Nacional Autónoma de México,

<sup>4</sup>Department of Anthropology, State University of New York – Buffalo

In the past decades, several studies have defended a wide range of scenarios to explain the initial settlement of the Americas, which tend to oversimplify the diversity observed across the continent and associate the process with a variable number of discrete population dispersion events. While these scenarios have contributed immensely to the understanding of the origins of Native American populations, they disregard the importance of local population dynamics in the continent and their role in shaping the biological variance in the American continents across space and time. In this study, we use geometric morphometric techniques to analyze the morphology of early remains from Quintana Roo, Mexico, and from Lagoa Santa, Brazil, in the context of other modern human worldwide reference series. Morphological data for 13 3D craniofacial landmarks were analyzed through exploratory visual multivariate analyses, multivariate classification based on Mahalanobis distances, and within-group variance estimates. The results show very different patterns of morphological affinities between the Quintana Roo and the Lagoa Santa samples. While Quintana Roo shows high morphological diversity and individual classifications with different reference series, Lagoa Santa has smaller within group variance and a more homogeneous classification pattern for its individuals. This reinforces previous results that the initial populations of North America had a high level of morphological diversity, which was reduced as populations dispersed into the southern continent. As such, they reinforce the importance of incorporating regional and continental realities in the reconstruction of past population dynamics in the American continents.

## Identifying candidates for adaptive introgression in admixed individuals from the Americas

EMILIA HUERTA-SANCHEZ, KELSEY WITT, FERNANDO VILLANEA and ALYSSA FUNK

Ecology and Evolutionary Biology, Brown University

It has been shown that archaic introgression has facilitated adaptations in European and Asian populations, but much less is known about the role of archaic variation in facilitating adaptation to environments in the Americas. Using the 1000 Genomes Project's admixed populations from the Americas, and methods to scan genomes for adaptive introgression, we identify several candidate genes in these populations. Since these admixed individuals exhibit Native American, European and African ancestry, we identify whether the adaptively introgressed haplotypes are on European, African or Native American tracts. We find that several candidate genes for adaptive introgression are on Native American tracts, and that the archaic alleles at these loci exhibit larger frequencies in admixed Americans than in East Asians, suggesting perhaps adaptations to new environments in the Americas. We also leverage DNA from published ancient American genomes (from Scheib *et al.* 2018 *Science*), and confirm the presence of some putative adaptively introgressed haplotypes in these ancient individuals at the candidate loci.

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## What does it mean to practice decolonial biological anthropological research?: A case study from Cape Town, South Africa

ROBYN A. HUMPHREYS<sup>1,2</sup>, WENDY BLACK<sup>2,3</sup>, JUNE BAM HUTCHISON<sup>4</sup> and REBECCA ROGERS ACKERMANN<sup>1,2</sup>

<sup>1</sup>Archaeology, University of Cape Town, <sup>2</sup>Human Evolution Research Institute, University of Cape Town, <sup>3</sup>Archaeology, Iziko Museums of South Africa, <sup>4</sup>Centre for African Studies, University of Cape Town

There is an urgent global need to reconsider biological anthropology through a decolonized lens. Here we use a case study from Cape Town to explore what it means to have a decolonial practice in bioanthropology research. This is done by reflecting on the experience of attempting to connect with the descendent communities of those buried at Prestwich Place Burial Ground who have now found rest in the Prestwich Place Ossuary. This significant colonial-era burial ground was discovered in 2003 with >2500 human remains. The exhumation process and the subsequent development of a hotel on the burial ground was deeply contested. Neither descendent communities nor archaeologists/biological anthropologists saw the full potential of this discovery realized in terms of making meaning

of the history of slavery and colonial dispossession of indigenous Khoen and San. The Ossuary remains a static memorial, with a coffee shop. In attempts to do research with the human remains from the site, one of us (Humphreys) reconnected with descendent communities, including through a facilitated workshop on human remains. These interactions necessitated deep reflection into the meaning of ethical practice on human remains, given the racist history of biological anthropology in South Africa and the slow process of repatriation. This involved confronting the history of biological anthropology practice and how it has marginalized communities. New priorities are required as we forge relationships with descendent communities that center their needs, and look beyond the scientific value of the human remains, shifting priorities from getting consent to centering healing and justice.

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## Interspecific variation in extant primate and fossil hominin calcaneal articular facet curvature

ALEXANDRA C. IDSO<sup>1,2</sup>, CHRISTOPHE SOLIGO<sup>3</sup> and WILLIAM CH. PARR<sup>4</sup>

<sup>1</sup>Department of Anthropology, CUNY Graduate Center, <sup>2</sup>New York Consortium in Evolutionary Primatology (NYCEP), <sup>3</sup>Department of Anthropology, University College London (UCL), <sup>4</sup>Surgical and Orthopaedic Research Laboratory (SORL), University of New South Wales (UNSW)

Calcaneal joint surfaces are of particular interest in understanding adaptations to hominin bipedalism. The calcaneus plays a crucial role in transmitting weight-bearing forces during locomotion, heel strike patterns, inversion-eversion of the foot, pronation-supination of the forefoot, midfoot stability, and the formation of the longitudinal arch. Technological innovations, such as 3D laser surface scanning, have made the accurate quantitative statistical analysis of characteristics such as articular facet curvature possible. This study uses three-dimensional models of 63 extant primate species calcanei (N=323) and a range of fossil hominin calcanei including OH8, U.W. 88-99, and U.W. 101-1322 to test a novel approach of quantifying articular facet curvature as a means of distinguishing between forms of primate locomotion. This novel approach uses 25 radii of curvature measurements across all articular surfaces of the calcaneus. The data were analyzed using phylogenetic regressions against body mass and principal component analysis. The results show curvature-reflected locomotor categories by distinguishing modern human bipeds from other locomotor specializations in some facet metrics, thereby confirming the method's potential to interpret joint movement and infer

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locomotor classification in fossil species. Overall, the OH8 and U.W. 101-1322 fossils' articular facet curvature most closely resembles bipedal modern humans. However, the results also indicate locomotor diversity in the hominin fossil record. U.W. 88-99 exhibits a morphology similar to that of African apes with a flexible medial side of the foot that would allow for hyper-pronation of the foot beneficial for vertical climbing, and a posterior talar facet reflective of bipedalism.

### Survival Knowledge in a Two-year Old Orangutan Infant (*Pongo pygmaeus morio*) in the Wild

ELLEN J. INGMANSON<sup>1</sup> and DINDA PRAYUNITA<sup>2</sup>

<sup>1</sup>Anthropology, Bridgewater State University,

<sup>2</sup>Research, Kutai Orangutan Project

Orangutans are among the most endangered primates. With long interbirth intervals of 6-8 years, the likelihood is high that mothers will leave an orphaned immature offspring at death. Crucial to aiding their survival is understanding when young orangutans learn survival skills. The Kutai Orangutan Project in Borneo has collected data on mothers and offspring in relation to the long birth intervals since January 2010. In April 2018, staff reported sighting a known adult female orangutan with a male infant estimated to be 2-3 years old. In May they found an emaciated adult female orangutan, tentatively identified as the same female, dead on the ground below a nest near a large fig tree. Indications of scavenging on the body were present. Approximately 3 days after her death, a lone male infant was found nearby. His survival was unlikely, so arrangements were made to move him to an orangutan rehabilitation facility for care and eventual release to free forest life. During the 3 days prior to this move, both authors and additional project staff observed him. Due to his young age, it was expected his independence skills would be limited and might compromise his health. Instead this infant was observed making nests in trees, feeding on figs and herbs, and using complex climbing techniques. Observers characterized his demeanor as "determined," not despondent. Importantly, he *knew* what to eat and where to sleep. These opportunistic observations contribute important understanding about the development of infant orangutan knowledge and survival skills.

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### Reconstructing ancient migrations from modern genomes across Latin America and the Pacific

ALEXANDER G. IOANNIDIS<sup>1,2</sup>, JAVIER BLANCO-PORTILLO<sup>2</sup>, KARLA SANDOVAL<sup>2</sup>, ERIKA HAGELBERG<sup>3</sup>, JUAN FRANCISCO MIQUEL-POBLETE<sup>4</sup>, VICTOR MORENO-MAYAR<sup>5</sup>, JUAN

ESTEBAN RODRIGUEZ-RODRIGUEZ<sup>2</sup>, CONSUELO D. QUINTO-CORTES<sup>2</sup>, RICARDO A. VERDUGO<sup>5</sup>, MAURICIO MORAGA<sup>6</sup>, ALEXANDER J. MENTZER<sup>7</sup>, CARLOS D. BUSTAMANTE<sup>1</sup> and ANDRES MORENO-ESTRADA<sup>2</sup>

<sup>1</sup>Biomedical Data Science, Stanford University,

<sup>2</sup>National Laboratory of Genomics for Biodiversity (LANGEBO), Cinvestav, Mexico, <sup>3</sup>Department of Biology, University of Oslo, <sup>4</sup>Facultad de

Medicina, Pontificia Universidad Católica de Chile, <sup>5</sup>Computational Genomics, National Institute

of Genomic Medicine, <sup>6</sup>Facultad de Medicina, University of Chile, <sup>7</sup>Wellcome Centre for Human

Genetics, University of Oxford

The possibility of voyaging contact between prehistoric Polynesians and Native Americans has long intrigued researchers. Proponents have pointed to New World crops, such as the sweet potato and bottle gourd, found in the Polynesian archaeological record, but nowhere else outside the pre-Columbian Americas, while critics have argued that these botanical dispersals need not have been human mediated. The Norwegian explorer Thor Heyerdahl controversially suggested that prehistoric South Americans played an important role in the settlement of east Polynesia and particularly Easter Island (Rapa Nui). Several limited molecular genetic studies have reached opposing conclusions, and the possibility continues to be hotly contested as new genomic evidence accumulates. Here we analyzed genome-wide variation in individuals from islands spanning Polynesia for signs of Native American admixture, analyzing 807 individuals from 17 island populations and 15 Pacific coast Native American groups. We found conclusive evidence for prehistoric contact of Polynesians with Native Americans (ca. 1200 CE) contemporaneous with the settlement of remote Oceania. Our analyses suggest strongly that a single contact event occurred in eastern Polynesia, prior to the settlement of Easter Island (Rapa Nui), between Polynesians and a Native American group most closely related to the indigenous inhabitants of present-day Colombia. Our results are consistent with either Native Americans drifting west, or Polynesians sailing east to the Americas and returning before Europeans made contact centuries later. Our genetic data cannot pinpoint these dynamics but the current archaeological and anthropological evidence favors the latter given the prominent voyaging culture of Polynesians.

### *Uranopithecus macedoniensis*: 3D geometric morphometrics analysis of mandibular fragments (Late Miocene, Greece)

MELANIA IOANNIDOU<sup>1</sup>, GEORGE KOUFOS<sup>2</sup>, LOUIS DE BONIS<sup>3</sup> and KATERINA HARVATI<sup>1</sup>

<sup>1</sup>Paleoanthropology, Institute for Archaeological Sciences Senckenberg Center for Human Evolution and Paleoenvironment, University of Tübingen, <sup>2</sup>Laboratory of Geology & Paleontology,

School of Geology, Aristotle University of Thessaloniki, <sup>3</sup>Laboratoire de Paléontologie, Evolution, Paléoécosystèmes, Paléoprimatologie (PALEVOPRIM), Université des Poitiers

Material belonging to the Late Miocene hominoid *Uranopithecus macedoniensis* has been poorly analyzed using advanced techniques. This study aims to explore mandibular shape variation among *Uranopithecus macedoniensis* and a comparative sample of extant great apes, using three-dimensional (3D) geometric morphometrics. Additional aims include the examination of homogeneity within *Uranopithecus* and the exploration of sexual dimorphism in its mandibles and in comparison to the extant great apes. Apart from the four *Uranopithecus* mandibular bodies (two female and two male), the comparative sample consists of digitized mandibles from adult extant great apes (*Gorilla*, *Pan*, and *Pongo*). The analysis includes the registration of 3D landmarks on the mandibular body and the hemimandible. Multivariate statistical analyses were conducted, including ordination, Procrustes distances pairs, and correlation analyses. Our results showed that the mandibular shapes of the male and female specimens of *Uranopithecus* are quite similar, although they differ in size. *Uranopithecus* also showed some similarities in mandibular shape to the larger great apes, *Gorilla*, and *Pongo*. Additionally, *Uranopithecus* displays a similar – and possibly even greater – degree of sexual dimorphism to that of *Pongo*. Lastly, the results of our correlation analyses indicated that some PCs were significantly correlated with size, while the degree of correlation varied from moderate to substantial. This study suggests that the mandibular morphological similarities of *Uranopithecus* to the larger great apes may reflect similarities in size. Despite the presence of sexual dimorphism in size, the shape of the mandibular body is homogenous between male and female *O. macedoniensis*.

This work was supported by the Senckenberg Gesellschaft für Naturforschung, the Leventis Foundation, and the Deutsche Forschungsgemeinschaft (DFG INST 37/706-1).

### Human infrastructure affects the occupancy of lemurs living in a fragmented landscape in southeastern Madagascar

ZACHARY S. JACOBSON<sup>1</sup>, PAMELA NARVÁEZ-TORRES<sup>1</sup>, DEVIN M. CHEN<sup>2</sup>, OLIVIA TIAFINJAKA<sup>3</sup>, EDWARD E. LOUIS JR.<sup>4</sup> and STEIG E. JOHNSON<sup>1</sup>

<sup>1</sup>Department of Anthropology and Archaeology, University of Calgary, <sup>2</sup>Department of Wildlife, Fisheries, and Aquaculture, Mississippi State University, <sup>3</sup>Faculté des Sciences, de Technologies et de l'environnement, Université de Mahajanga, <sup>4</sup>Conservation Genetics Department, Omaha's Henry Doorly Zoo and Aquarium

Habitat fragmentation and habitat disturbance are critical threats to tropical forests globally, contributing to species extinction and ecosystem

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collapse. These anthropogenic processes are especially prevalent in Madagascar, where nearly all lemur species are threatened with extinction due to extensive forest loss. To investigate the effects of habitat fragmentation and disturbance, we integrated camera traps with remotely sensed satellite imagery to quantify the occupancy of two lemur species, the greater dwarf lemur (*Cheirogaleus major*) and the red-fronted lemur (*Eulemur ruffifrons*). We hypothesized that increased distance to forest edge, increased distance to roads, and a higher Normalized Difference Vegetation Index (NDVI)—a measure of vegetation quality—would be positively associated with occupancy for both lemur species. From May-August 2019, we used arboreal and ground camera traps to sample 30 sites within fragmented forests in Kianjavato, southeastern Madagascar. Following data collection, we quantified distance to forest edge, distance to roads, and NDVI values for each camera site using Google Earth and Sentinel-2 datasets. We found that distance to roads was an important covariate for *C. major* occupancy (occupancy=0.26, detection=0.46), with increased distance to roads correlating with increased occupancy. However, distance to edge and NDVI did not improve model performance for *C. major*. No covariates were important for predicting *E. ruffifrons* occupancy (occupancy=0.57, detection=0.41). Our results indicate that roads, which are associated with increased human presence and hunting pressure, are an important determinant of *C. major* occupancy. These findings highlight the differential ability of lemur species to persist in fragmented human-modified habitats.

Research was supported by Alberta Innovates, the Natural Sciences and Engineering Research Council of Canada, Global Wildlife Conservation, American Society of Primatologists, Primate Conservation Inc., and the Animal Behavior Society.

### Skeletal completeness of the catarrhine fossil record and the importance of dense character sampling in phylogenetic reconstruction

RUTGER J. W. JANSMA

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

Fossils provide critical information for resolving patterns of morphological change and speciation through time that cannot be precisely reconstructed from living species alone. However, the quality of the fossil record affects our understanding of these macroevolutionary patterns. This study quantifies the catarrhine fossil record using 65 species to explore how taphonomic factors impact our phylogenetic inferences. For each species, I calculated a skeletal completeness metric (SCM: % skeletal elements available) and a character completeness metric (CCM: %

scoreable characters from a cladistic dataset) and plotted these metrics against time, geography, and body size. The results show strong positive correlations between SCM and CCM, suggesting that the two metrics record the same signal. Average catarrhine completeness for both metrics improves through time from the late Oligocene to the late Miocene, but this slope is steeper for CCM than for SCM. Unexpectedly, neither geography nor body size correlates significantly with fossil completeness, indicating that the preservation in this sample is fairly uniform in these aspects. Application of a hypothetical fossilization filter to *Gorilla* using four different CCM profiles (*Oreopithecus*, *Nacholapithecus*, *Dendropithecus*, and *Gigantopithecus*) in a new phylogenetic dataset consistently recovers the hominoid molecular tree topology, suggesting that the affinities of highly incomplete taxa can be accurately resolved when character sampling is sufficiently dense. This study highlights the importance of assessing taphonomic controls on fossil record quality through geological time. Furthermore, it suggests that differences between phylogenetic analyses may stem from surmountable differences in either taxonomic or character sampling rather than missing data.

Support for this project was received from the Leakey Foundation and the University of Minnesota Department of Anthropology.

### Race/ism in U.S. forensic anthropology: A literature review

KENT M. JOHNSON<sup>1,2</sup>, RENEE HEBERT<sup>1</sup> and COLLEEN PASTORE<sup>1</sup>

<sup>1</sup>Sociology/Anthropology Department, SUNY Cortland, <sup>2</sup>Center for Bioarchaeological Research, Arizona State University

Research in critical race studies highlights the role of scientific research in supporting a biologically essentialist worldview in which human biological variation patterns along racial lines. In recent decades, there has been a shift away from the use of “race” in U.S. forensic anthropology in favor of “ancestry” (or ancestral geographic origin). However, some scholars question whether this shift in terminology has resulted in meaningful change in practice, or if analysis of ancestry in forensic contexts remains embedded within a racialized framework. This study uses a quantitative and qualitative literature review to investigate the prevalence of a racialized framework within the forensic anthropology literature.

We surveyed articles published between 2001 and 2020 in ten journals that publish forensic anthropological research. We performed keyword searches to identify relevant articles. We used quantitative and qualitative content analysis to analyze the terms, data types, samples, analytical methods, and analytical frameworks for describing and classifying human biological variation within forensic contexts. Results indicate

a statistically significant decrease in the use of “race” and increase in the use of “ancestry” during the study period. Some current scholars employ an evolutionary population approach, more diverse samples, and careful use of terminology. However, the continued use of racialized classification categories (e.g., “White” and “Black”) suggests there has been minimal change in practice. Overall, there is an overreliance on racialized samples and analytical methods that maximize differences between predefined samples (e.g., discriminant function analysis). Ultimately, the study of human biological variation remains undertheorized in U.S. forensic anthropology.

### Incorporating DNA-centered activities in an introductory biological anthropology laboratory curriculum is linked with greater student understanding of evolution and variation

SUSAN L. JOHNSTON<sup>1</sup>, MAUREEN KNABB<sup>2</sup>, JOSH AULD<sup>3</sup> and LORETTA RIESER-DANNER<sup>3</sup>

<sup>1</sup>Anthropology & Sociology, West Chester University, <sup>2</sup>Biology, West Chester University, <sup>3</sup>Psychology, West Chester University

College students demonstrate persistent misconceptions about evolution even after completion of life science courses. It has been suggested that in order for students to fully comprehend evolution, they need to understand that it is fundamentally about genetic change. Typical lab curricula in introductory biological anthropology focus largely on phenotypic phenomena, e.g., morphology and function; hands-on opportunities for students to link phenotypic with genetic variation are not standard. From 2013-2016, faculty at West Chester University (WCU) developed an inquiry-based laboratory curriculum for introductory biological anthropology. As reported previously, students taking this curriculum demonstrated greater improvement in their understanding of evolution, as assessed via an evolution concepts survey, over the period of instruction compared with students enrolled in introductory biological anthropology courses with standard lab curricula at other institutions. A unique facet of the WCU curriculum was the incorporation of exercises engaging students directly with genetic evidence of evolution linked to phenotypic variation at several points in the semester (e.g., comparison of DNA sequences between multiple primate species in order to test a morphology-based hypothesis about phylogeny; DNA fingerprinting to help “identify” a fossil species). Notably, the particular evolution concept survey items that more WCU students answered correctly at the end of the course than students at the comparison institutions ( $p < .05$  to  $p < .001$ ) were addressed by these DNA-based lab activities; the labs that students subjectively rated as most effective in

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helping them learn about evolution and human variation incorporated DNA. We present these data and provide examples of the relevant lab activities.

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### 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 substantial delay from the time of investment to consumption. Delayed payoffs entail both opportunity costs and risk. 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, presenting a paradox: How is it that *Homo sapiens* emerged as a globally dominant species when our capacity to manage these two crucial features of adaptation is apparently faulty? Using novel models that combine fitness maximization and economic preferences, I show that both the observed inconsistencies in time and risk preferences have been mis-interpreted and that this evolutionary approach helps resolve the paradox. With a simple Bayesian learning model I show that present bias arises in people with otherwise time-consistent preferences in the presence of uncertainty. With a hierarchical evolutionary model of preferences, I show 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. For instance, using an expanded Ramsey equation, I show that social discount rates should be far lower than they are typically set and that more aggressive mitigation policies are optimal.

### Genetic adaptations to potato starch digestion in the Peruvian Andes

KELSEY C. JORGENSEN<sup>1</sup>, OBED A. GARCIA<sup>2</sup>, MELISA KIYAMU<sup>3</sup>, MARIA RIVERA-CHIRA<sup>3</sup>, FABIOLA LEON-VELARDE<sup>3</sup>, TOM D. BRUTSAERT<sup>4</sup> and ABIGAIL W. BIGHAM<sup>5</sup>

<sup>1</sup>Department of Anthropology, Wayne State University, <sup>2</sup>Department of Biomedical Data Science, Stanford University, <sup>3</sup>Facultad de Ciencias y Filosofía, Universidad Peruana Cayetano Heredia, <sup>4</sup>Department of Exercise Science, Syracuse University, <sup>5</sup>Department of Anthropology, University of California, Los Angeles

With few local food sources available, potatoes are a highly significant crop in the Andes and were cultivated as early as 8,000 years ago. Ancient populations that primarily relied upon high-starch foods to survive may have developed genetic adaptations to digest starch more efficiently, and these adaptations may still be present in modern-day descendant populations. Here, we analyzed genomic data from two candidate genes associated with starch-digestion, *AMY1* and *MGAM*, in Peruvian populations. Peruvian populations were derived from both highland Quechua individuals (n=580) and 1000 Genomes Peruvians from Lima (n=40). Control populations from the 1000 Genomes project included: Han Chinese (CHS, n=63), Mende in Sierra Leone (MSL, n=87), and Gambian Mandinkas (GWD, n=60). Although these control populations consume starch, potatoes were more recently introduced to their diets (>500 years), with MSL/GWD populations among the lowest consumers of potatoes worldwide. Therefore, we hypothesized that these populations will not have developed the same starch-digestive genetic adaptations present in highland Peruvians. We calculated LSBL and Tajima's *D* to identify selection, as well as an odds ratio measure as a proxy for starch digestion. Our results indicate that *MGAM*, (rs10246939, OR=15.29, p<0.01), shows the strongest signature of selection in Peruvian populations, which may have aided with starch digestion in this population. Given that potatoes are one of the most important domesticated crops in the world, these results indicate there is global variation in human ability to digest this high-starch food, adding further support to diet being a driver of human evolutionary change.

### Poor Memory and Depression in Older Adults: Results from the Study on global AGEing and adult health (SAGE)

TYRA R. JUDGE<sup>1</sup>, ALICIA M. DELOUIZE<sup>1</sup>, PAUL KOWAL<sup>1,2,3</sup>, NIRMALA NAIDOO<sup>2</sup>, SOMNATH CHATTERJI<sup>2</sup> and J. JOSH SNODGRASS<sup>1</sup>

<sup>1</sup>Anthropology, University of Oregon, <sup>2</sup>World Health Organization, (Switzerland), <sup>3</sup>University of New Castle Research Centre for Generational Health and Ageing, (Australia)

Worldwide, over 20% of older adults suffer from a mental health disorder. The most common mental health disorders are dementia and depression, affecting 5% and 7% of the world's older adult population, respectively. It is sometimes difficult to distinguish between the two conditions, which leads to a misdiagnosis of early-stage dementia as depression. In our research, using Wave 1 data from the World Health Organization's Study on global AGEing and adult health (SAGE), we found that poor memory predicted the presence of depression in every country except India. Poor self-rated memory predicted depression in China, Ghana, Mexico, and Russia (ORs = .42 to

.62, p's <.001) and backward digit span or verbal recall predicted depression in China, Ghana, and South Africa (ORs = .43 to .49, p's <.01). Our results demonstrate a close association between poor memory and depression in middle-income countries. Here, we examine this and discuss its implications for the potential misdiagnosis of early-stage dementia globally.

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### Examination of magnitudes of integration in the catarrhine axial skeleton

HYUNWOO JUNG and NOREEN VON CRAMON-TAUBADEL

Anthropology, University at Buffalo (SUNY)

This study examines the magnitude of integration in the axial skeleton in catarrhines. It is hypothesized that hominoids will show relatively lower magnitudes of integration than cercopithecoids, and that the evolution of 'novel' axial skeletal morphology in hominoids may have been facilitated by the reduced constraint of lower magnitudes of integration.

For this, 3D scans of the cranium, mandible, vertebrae (13 elements), and sacrum of 30 *Cercopithecus*, 32 *Chlorocebus*, 39 *Macaca fascicularis*, 45 *Hylobates lar*, 31 *Pan troglodytes*, and 86 *Homo sapiens* were used. Variation attributable to sex, species, identity of the last thoracic or lumbar vertebrae, and/or the number of sacral vertebrae was controlled by mean-standardization within genera. Magnitudes of integration were calculated using the integration coefficient of variation (ICV) from inter-landmark distances. A resampling method was applied for generating distributions of ICV for each axial skeletal element. Comparison of ICV scores of axial skeletal element (i.e., combination of cranium, mandible, vertebrae, and sacrum) between taxa were conducted using Mann-Whitney U tests with Bonferroni adjustment.

The results support the hypothesis as hominoids showed significantly lower magnitudes of integration than cercopithecoids (p<0.0033 for all comparisons). Mean ICV scores in the axial skeleton were 1.899 in *Chlorocebus*, 1.844 in *Macaca*, 1.7442 in *Cercopithecus*, 1.5298 in *Hylobates*, 1.4703 in *Pan*, and 1.4233 in *Homo*. These results indicate that hominoids have lower levels of integration than cercopithecoids, which likely led to reduced constraints on the evolution of axial skeletal morphology in the clade.

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## Prevalence of periodontitis and odontogenic abscesses in *Pan paniscus*

SAI KALLURI<sup>1</sup>, EMMANUEL GILISSEN<sup>2,3</sup> and QIAN WANG<sup>1</sup>

<sup>1</sup>Department of Biomedical Sciences, Texas A&M University College of Dentistry, <sup>2</sup>Department of Biology, Royal Museum for Central Africa, Tervuren, Belgium, <sup>3</sup>Faculté des Sciences de la Motricité, Université Libre de Bruxelles

Periodontitis and odontogenic abscesses are common dental ailments that affect the ability to obtain sufficient nutrition. They thus are important indicators of oral health and quality of life. In this study, oral health status was evaluated in *Pan paniscus* (bonobo). In CT images of 140 bonobo skulls housed in the Royal Museum for Central Africa, Belgium, odontogenic abscesses and periodontitis (Diagnosis criteria: loss of alveolar bone which includes loss of interdental bone and exposure of root furcation in multi-rooted teeth) were investigated. Male and female specimens, as well as specimens of unknown sex, were categorized as juvenile/subadult, young adult, and adult depending on the dentition stage and root canal apices closure. Results indicated that 7 specimens (5%) had signs of odontogenic abscesses (3 males, 2 females, 2 unknown; 6 adults, and one young adult). In addition, there was a high prevalence of signs of periodontitis. In adults, the prevalence of periodontitis was 85.7% in adults (males 75.0%, females 86.4%), and 53.3% in young adults (males 40.0%, females 55.6%). In juveniles/subadults, 46.2% of males and 50.0% of females were showing signs of incipient periodontitis. Signs of other oral pathology or anomaly were rare. These findings suggest that bonobos generally had good dentition and oral health, while periodontitis was common (biased to females) and increased with age. The knowledge of oral health in bonobos, which along with chimpanzees are the closest extant relatives of humans, can thus provide valuable insights into the epidemiology of the disease from an evolutionary perspective.

## Maternal rank and infant development of Kinda baboons at Kasanka National Park, Zambia

JASON M. KAMILAR<sup>1,2</sup>, ANNA H. WEYHER<sup>1</sup>, MEGAN PETERSDORF<sup>3</sup>, KENNETH L. CHIOU<sup>4</sup> and INDIA SCHNEIDER-CREASE<sup>4</sup>

<sup>1</sup>Department of Anthropology, University of Massachusetts Amherst, <sup>2</sup>Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst, <sup>3</sup>Department of Anthropology, New York University, <sup>4</sup>Center for Evolution and Medicine, Arizona State University

In philopatric primate species, high ranking females have been associated with better access to resource quantity and quality. These rank-related benefits to the mother have consequences for their offspring in the form of increased

survivorship, earlier age of menarche, and the timing of other developmental milestones. Here, we investigated whether female rank was associated with infant development, defined by infant locomotor behavior, in a group of habituated Kinda baboons at Kasanka National Park, Zambia. Kinda baboons are known to have female philopatry, though differ from other savanna baboons by exhibiting greater within-group social partitioning and lower levels of inter-individual aggression. We collected behavioral data from 28 infants and 19 mothers across three years. Our quantification of infant locomotor development was defined by an ordinal variable with three ranks of increasing independence, clinging ventrally, clinging dorsally, and moving independently. We used a generalized linear mixed model with female rank as a fixed effect, infant age as a covariate, and infant ID as a random effect. We found that female rank was positively associated with infant development while accounting for infant age. These results imply that female rank is associated with benefits to the mother as well as the infant and have important implications for understanding Kinda baboon behavior in the context of better known baboon species.

## Developmental tradeoffs: fruit availability and age influence mother and offspring activity in Bornean Orangutans (*Pongo pygmaeus wurmbii*)

ERIN E. KANE<sup>1</sup>, TRI WAHYU SUSANTO<sup>2</sup> and CHERYL D. KNOTT<sup>1,3</sup>

<sup>1</sup>Anthropology, Boston University, <sup>2</sup>Biology, National University of Indonesia, <sup>3</sup>Biology, Boston University

Bornean orangutans' extended life history may be an adaptation to their forest habitat, characterized by dramatically fluctuating fruit availability. We hypothesize that juveniles rest and are carried more when fruit availability is low, spending less time in developmentally important behavior including play and independent travel to conserve energy. We test this using generalized linear mixed models and data derived from 976 follows of infant and juvenile orangutans collected during periods of varying fruit availability. Age ( $p < 0.001$ ), but not fruit availability ( $p > 0.05$ ) significantly affected offspring's time being carried ( $\beta = -8.1$ ) and resting ( $\beta = -2.6$ ,  $p < 0.001$ ). Younger individuals spent more time clinging and resting regardless of fruit availability. Fruit availability and offspring age interact to affect the proportion of time juveniles play ( $\beta = 1.5$ ,  $p < 0.001$ ) and travel ( $\beta = -0.8$ ,  $p < 0.001$ ). Fruit availability impacts younger juveniles' play behavior more dramatically than older juveniles: younger juveniles play more when fruit availability is high than when it is low, while older juveniles exhibit little variation in time spent playing depending on fruit availability. Juveniles aged 6-8 travel more when fruit availability is medium and high, juveniles aged 2-5 travel slightly less when fruit availability is high, and juveniles under 2 rarely

travel independently. We also examined relationships between fruit availability, offspring age, and maternal travel distance using 2065 mother-offspring follows, demonstrating that females travel shorter distances with offspring under four, and when fruit availability is low. Thus, orangutans shift activity in response to fruit availability and throughout development, buffering young orangutans against energy depletion but suppressing developmentally important activities.

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## Energetic Demands and Sexual Dimorphism in Inuit Nasal Morphology

ALEXA P. KELLY and SCOTT D. MADDUX

Center for Anatomical Sciences, University of North Texas Health Science Center

As the nasal complex is primarily responsible for heating, humidifying and filtering inspired air prior to entry into the lungs, geographically-patterned variation in nasal morphology has long been attributed to climatic adaptation. However, previous studies have also demonstrated sexual dimorphism in overall nasal size, with larger nasal passages in males hypothesized to reflect greater volumetric demands for oxygen intake due to higher metabolic requirements. Yet, to date, no study has attempted to assess adult nasal variation in conjunction with associated body mass/basal metabolic rate data. Here, we employ data collected from both the nasal and post-cranial skeletons of 43 (22 female/21 male) modern humans from the geographically/climatically circumscribed site of Point Hope, Alaska. Twenty-seven 3D-coordinate landmarks were collected from CT scans of the nasal skeleton, while associated postcranial data for each individual were obtained from the Goldman Dataset (Auerbach & Ruff 2004) and used to calculate body mass and basal metabolic rate (BMR) using climate-specific formulae. Following theoretical expectations, multivariate regression results indicate that nasal passage size is significantly correlated with both body mass ( $r = 0.444$ ,  $p = 0.003$ ) and BMR ( $r = 0.558$ ,  $p < 0.0001$ ). Conversely, within this one sample (i.e., holding climate constant), nasal passage shape was not significantly correlated with either body mass ( $r = 0.168$ ,  $p = 0.261$ ) or BMR ( $r = 0.132$ ,  $p = 0.724$ ). These results support previous suggestions that, within geographically indigenous populations, males and females exhibit similar nasal shapes due to shared climatic conditions, while differing in nasal size due to sexual dimorphism in energetic demands.

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### Canine integration and modularity in a sample of pedigreed *Papio hamadryas*

CHRISTA D. KELLY<sup>1</sup>, LUCAS K. DELEZENE<sup>1</sup>, KATHLEEN S. PAUL<sup>1</sup>, CHARLES C. ROSEMAN<sup>2</sup> and J. MICHAEL PLAVCAN<sup>1</sup>

<sup>1</sup>Department of Anthropology, University of Arkansas, <sup>2</sup>Department of Evolution, Ecology, and Behavior, University of Illinois

Multiple hypotheses address the selective pressures driving primate canine size evolution, as well as the evolution of canine size dimorphism. Historically important ideas posit that canine size should co-evolve with the size of either the incisors or postcanine teeth. However, few studies have considered the covariance of canine size with other dental modules within species and none have assessed the genetic covariance between canine height and incisor and postcanine size. To test the hypothesis that the canine represents a discrete dental module, 17 linear measurements were collected from casted maxillary dentitions of a *Papio hamadryas* sample (females,  $n = 321$ ; males,  $n = 138$ ) for which pedigree information is available. Phenotypic integration was assessed using partial correlations, measuring the degree of association between dental measurements after the effects of sex had been removed. Genetic correlations were estimated using an animal model with sex as a fixed effect. Both phenotypic and genetic correlation matrices show similar patterns and, corroborating previous studies, both reveal an incisor module and a postcanine module, consisting of two submodules. A semi-independent canine module is also apparent, although canine height shows low genetic covariance with other metrics. In addition, this sample shows the highest covariation between homologous dimensions (i.e., length, breadth) among teeth within each module. These results indicate that canine size evolution, particularly canine height, is relatively unconstrained from changes to either the incisor module or the postcanine module.

### Mortality risk and survival in pre- and post-Black Death Denmark

SAIGE KELMELIS<sup>1</sup> and SHARON N. DEWITTE<sup>2</sup>

<sup>1</sup>Anthropology and Sociology, University of South Dakota, <sup>2</sup>Anthropology, University of South Carolina

Previous bioarchaeological research on medieval London populations revealed declines in survivorship before the Black Death (c. 1347-1351), followed by improvements in survivorship following the epidemic, perhaps due to historically documented improvements in standards of living. While these findings have been repeatedly demonstrated among London populations, mortality risks and survival in pre- and post-Black Death populations in other medieval populations are not well understood. This study examines differences in survivorship and mortality risk between

pre- and post-Black Death populations throughout medieval Denmark by applying Kaplan-Meier analysis and Cox proportional hazard analysis to nonadult and adult age estimates and controlling for changes in birth rates. We use skeletal samples from medieval cemeteries from Jutland and Funen dated to one of three periods based on arm burial position: Early Pre-Black Death (c. 1050-1250), Late Pre-Black Death and Epidemic Years (c. 1250-1350), and Post-Black Death (c. 1350-1536). The results indicate that survivorship for all individuals (all ages pooled) decreased prior to the Black Death and increased afterwards ( $p = 0.06$ ) while there were no significant differences in birth rates; similar results were found for a subsample that included only nonadults ( $p = 0.02$ ). Male survivorship appeared to improve more than females after the Black Death. Comparison of the survivorship curves across time periods further suggests that the Black Death may have acted selectively on frail individuals. These results support that there were significant differences in survival and mortality, but not birth rates, between time periods in medieval Denmark similar to populations in medieval England.

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### Temporal variation in Carabelli's trait frequency and lactase persistence

DORI E. KENESSEY and MARIN A. PILLOUD

Department of Anthropology, University of Nevada, Reno

Dental morphology is frequently utilized in biological anthropology to explore human migration and evolution as a proxy for genetic information. While single nucleotide polymorphisms of the EDAR and WNT10A genes have been shown to influence dental morphological variation, the genetic mechanisms underlying dental phenotype frequency and expression remain unknown. Mizoguchi (1993) identified an association between Carabelli's trait expression and the consumption of milk, suggesting that common underlying genetic factors may be at play. Here, we examine whether temporal changes in Carabelli's trait frequency coincide with the prevalence of the European lactase persistence allele (-13,910\*T). Since the British Isles exhibits the highest frequency of this allele (~85-95%), we focus our analyses here.

Data on Carabelli's trait were collected from the literature spanning nine temporal periods (Late Pleistocene/Early Holocene, Neolithic, Bronze Age, Iron Age, Romano-British period, Early Christian period, Medieval period, Postmedieval period, and Modern period). A Kruskal-Wallis test and a Dunn's

post-hoc test were conducted to test for temporal differences. Due to a lack of region-specific data on temporal lactase persistence allele variation, published data were compiled from Europe.

Genotype data show that the derived lactase persistence allele only becomes prevalent (~70%) in Medieval Europe and thereafter. Similarly, Carabelli's trait frequency increases during the Postmedieval and Modern periods ( $p < 0.05$ ). These results tentatively confirm the apparent covariation previously highlighted by Mizoguchi (1993), and suggest a complex evolutionary past for dental morphological traits. Future studies will explore the exact genetic mechanism underlying lactase persistence and Carabelli's trait expression through a genome-wide association study.

### Taxonomic Efficacy of the Macaque Skeleton

BRITTANY KENYON-FLATT<sup>1,2</sup> and NOREEN VON CRAMON-TAUBADEL<sup>2</sup>

<sup>1</sup>Department of Molecular Biomedical Sciences, North Carolina State University, <sup>2</sup>Department of Anthropology, University at Buffalo

Taxonomic classification is fundamental for understanding the natural world, yet current methods for unknown species assessment are based on qualitative methods and focused on craniodental morphology. It is currently unknown how much variation could, or should, exist within a particular genus. Here, we tested whether taxonomy can be accurately predicted from patterns of morphological variation in a geographically widespread taxa, the macaques ( $H_1$ ) and whether postcranial bones reflect subgeneric taxonomy similarly, or better, than the cranium ( $H_2$ ).

Data included 3D scans from nine species (*M. arctoides*, *M. fascicularis*, *M. fuscata*, *M. mulatta*, *M. nemestrina*, *M. nigra*, *M. radiata*, *M. sylvanus*, and outgroup *Trachypitecus cristatus*), for a sample of 297 individuals. Macaque species were chosen for their phylogenetic diversity and their geographic representation. 293 fixed and semi-landmarks were applied to eight skeletal elements for each individual (crania=45; mandible=31; scapula=66; humerus=38; radius=33; os coxa=28; femur=40; tibia=40). A regression analysis was performed to minimize the effects of sexual dimorphism, making the primary input variables regression residuals.

Patterns of variation were analyzed between- and within-species via Canonical Variates Analysis and 2D Multidimensional Scaling. Classificatory ability was tested using Discriminant Function Analysis. Results suggest that different species of macaque monkeys are taxonomically distinct and that the crania and postcrania possess a taxonomic signal. Some bones, like the limb bones, were more useful taxonomically than

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previously realized. Results suggest that taxonomic assessment should be updated to reflect newer methodologies and we argue that these results should inform future studies.

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### Exploring the use of portable X-ray fluorescence (pXRF) for the identification of pathological archaeological bone

NAOMI N. KILBURN<sup>1</sup>, REBECCA L. GOWLAND<sup>1</sup>, HRAFNHILDUR H. HALLDÓRSDÓTTIR<sup>2,3</sup>, RHYS WILLIAMS<sup>2,3</sup> and TIM J.U. THOMPSON<sup>2</sup>

<sup>1</sup>Department of Archaeology, Durham University, <sup>2</sup>School of Health and Life Sciences, Teesside University, <sup>3</sup>National Horizons Centre

The accurate identification of pathological conditions in human skeletal remains is crucial for building an understanding of the past—contributing information about living environment, health, and societal structure. This study assesses the utility of using portable X-ray fluorescence (pXRF), a rapid and non-destructive method of trace element analysis, in the investigation of pathological conditions in archaeological human skeletal remains. The elemental distribution in the femora of 99 individuals (34 adult; 63 non-adult) from the Post-Medieval Coach Lane skeletal collection (Durham University, UK) was determined, and the results examined in relation to rickets, scurvy, cribra orbitalia, and pathological new bone formation. Scatterplots revealed no observable patterns correlated with rickets, scurvy, or cribra orbitalia. Femora with pathological new bone formation had increased levels of geologically abundant elements (silicon, potassium, titanium, aluminum), and decreased phosphorus and calcium values, relative to bones without. There was a strong linear correlation between these elements (Si/P:  $r = -0.84$ ,  $p < 0.05$ ), suggesting the post-depositional exchange of elements. Single cases of “phossy jaw” and neoplastic disease, as well as suspected occurrences of tuberculosis, smallpox, and syphilis, were noted in the sample, with potential alterations in bone chemistry observed for syphilis and neoplastic disease. The complexity of interconnected factors contributing to the elemental content of bone prevents definitive conclusions about the sources of elemental variation. Although the results of this study do not support adding pXRF to the current repertoire of palaeopathological diagnostic techniques, further research could provide greater clarity about its potential use.

### The influence of lunar phase on circadian rhythms in a mobile, non-industrial population: Sleep analysis from a community of BaYaka foragers from the Congo

ERICA KILUUSI<sup>1</sup>, DAVID R. SAMSON<sup>1</sup>, SHEINA LEW-LEVY<sup>2</sup>, MALLIKA S. SARMA<sup>3</sup>, LEE T. GETTLER<sup>4</sup> and ADAM BOYETTE<sup>5</sup>

<sup>1</sup>Department of Anthropology, University of Toronto Mississauga, <sup>2</sup>Department of Psychology, Simon Fraser University, <sup>3</sup>School of Medicine, Johns Hopkins University, <sup>4</sup>Department of Anthropology, University of Notre Dame, <sup>5</sup>Department of Human Behavior, Ecology, and Culture, Max Planck Institute for Evolutionary Anthropology

**Background:** Accounts in Western contexts have linked many human behaviours to the phases of the moon, including restlessness and increased nighttime activity. However, little research on whether moon phase affects sleep patterns has been conducted in foraging populations, whose subsistence practices lead to high levels of environmental exposure. Thus, their sleep may be more influenced by nighttime light exposure. We investigated sleep in the BaYaka, a forager population in Republic of the Congo.

**Methods:** Participants' sleep was measured when they lived in a higher density village setting, as well as a forest camp setting. Objective actigraphy devices were worn for ~7 days each setting ( $n=362$  nights total). Lunar phase data was obtained from the Astronomical Applications Department of the US Navy. We conducted a linear mixed-effects model to determine if sleep variables were influenced by lunar phase. Additionally, we investigated sex differences in central phase measure (CPM), the midpoint of main sleep periods, to assess the potential influence of gender roles in nighttime subsistence activities.

**Results:** A greater lunar phase predicted a later CPM ( $\beta$  estimate = 0.119,  $p < 0.05$ , CI: 0.0012, 0.236). Additionally, CPM was phase delayed in men ( $\beta = 0.112$ ,  $p = 0.05$ ), indicating a later chronotype that could suggest gendered patterns of nighttime hunting or social activities

**Significance:** These findings suggest a link between lunar phase and circadian sleep patterns in subsistence foragers, perhaps reflecting increased activities during greater lunar phases. These results provide insight into the moon's potential influence on human social behaviour.

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### Post-impressionistic Age Estimation? Quantitative analysis of pubic symphysis complexity, curvature, and relief for age-at-death estimation

JIEUN KIM, ANTHONY HARPER and ALEKHYA BOMMIREDDIPALLI

Anatomy, Lincoln Memorial University DeBusk College of Osteopathic Medicine

Age-at-death estimation of skeletal remains is a foundational procedure for reconstructing individual identity and mortality in past and modern populations, and to diagnose age-specific diseases. Recent efforts to mitigate the inherent subjectivity involved with macroscopic age estimation have improved the accuracy and reliability of these estimates using Geometric Morphometric (GM) algorithms and digitized surfaces generated by widely accessible optical scanners. Prior GM aging methods based on (semi)landmark shape analyses on digitized symphyses have reduced within-/between-observer error and increased repeatability in age estimation. Nevertheless, these methods suffer from decreasing age-informative power past mid-life.

This project quantifies three homology-free topographic variables on the symphyseal surface of the pubis and evaluates their usefulness as bony correlates of age-at-death. We analyzed 3D digitized surfaces of the ( $n=56$ ) Suchey-Brooks standard and instructional pubic symphyseal cast sets, and recorded three surface topography metrics that characterize the complexity, curvature, and relief of the symphyseal face; Dirichlet Normal Energy (DNE), Relief Index (RFI), and rotated Orientation Patch Count (OPCr), respectively. Preliminary analysis using linear regression models suggests that statistically significant relationships exist between age-at-death and the three metrics ( $r \approx 0.7$  to  $0.7$ ;  $p < 0.05$ ). R-squared values indicate that 20-50% of this topographic variation can be explained by age. However, DNE requires a drastic truncation of the young or old age groups (i.e., below 30 years or over 50 years). These results demonstrate the three metrics' utility as non-traditional, objective, and quantitative proxies of age-related change of the symphysis when used in combination with other measures/age indicators.

### Critical Pedagogy in the Online Environment

MARC KISSEL<sup>1</sup> and SUSAN BLUM<sup>2</sup>

<sup>1</sup>Anthropology, Appalachian State University, <sup>2</sup>Anthropology, University of Notre Dame

Current research into pedagogy has shown that teaching is not just the dissemination of information. Furthermore, we know that learning happens best in interactions with others. At the same time, it seems that connection with others is more challenging in a totally remote digitally mediated environment. The work of critical digital pedagogy, an extension of Paulo Freire's observations that “There is no such thing as a neutral educational process”, can help to connect students and professors. Scholars spend countless hours critiquing our science and scholarship, but we rarely examine our work in the classroom in the same manner. Because of this, and in light of the so-called ‘pivot’ to online learning necessitated

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by COVID-19, we are often in the position where we feel like we don't know how to properly teach, educate, and mentor students in a digital space. In this poster we present both principles and examples of how anthropology faculty might facilitate connection in order to foster robust learning, even in the less-than-ideal conditions of 2020-21. Examples such as unessays, self-assessment, peer-assessment, and ungrading are provided to help professors create critical learning environments and to allow for real learning to emerge.

### Hair microbiome diversity within and across 12 primate species

CATHERINE E. KITRINOS<sup>1</sup>, RACHEL B. BELL<sup>2</sup>, BRENDA J. BRADLEY<sup>3,4</sup> and JASON M. KAMILAR<sup>1,2</sup>

<sup>1</sup>Department of Anthropology, University of Massachusetts Amherst, <sup>2</sup>Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst, <sup>3</sup>Department of Anthropology, The George Washington University, <sup>4</sup>Center for the Advanced Study of Human Paleobiology, The George Washington University

Primate hair is an important host-pathogen interface home to numerous ecto-parasites. As commensal microbes provide important immune functions for their hosts, understanding the microbial diversity in primate hair could provide insight into primate immunity and disease transmission. While studies of human hair and skin microbiomes show differences in microbial communities across body regions, little is known about the nonhuman primate hair microbiome. In this study, we collected hair samples (n=162) from 8 body regions across 12 nonhuman primate species housed at 3 US institutions to examine how nonhuman primate hair microbial communities differ across body regions, institutions, and species. If environmental and evolutionary factors shape the microbiome, then we would expect significant differences in microbiome diversity across body regions, institutions, and species. We examined differences in species richness and evenness via Kruskal-Wallis tests, with post-hoc analyses investigating pairwise comparisons. We quantified beta diversity using Unifrac distances, a principal coordinates analysis, and a PERMANOVA to test for differences in community composition. We found differences in alpha diversity across species, but not across institutions or body regions. Microbiome composition was significantly distinct across species and primates housed at different institutions, but not across body regions. Our results suggest that the uniformity of microbiome diversity across body sites may be due to their relatively similar hair and skin characteristics compared to humans. Also, hair microbial communities are affected by both

evolutionary and environmental factors. These findings have important implications for understanding the biology and conservation of both wild and captive primates.

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### Daily Physical Activity is Associated with Suppressed Immune Activity in U.S. Adults

CHRIS KLASSON<sup>1</sup>, SRISHTI SADHIR<sup>1</sup> and HERMAN PONTZER<sup>1,2</sup>

<sup>1</sup>Department of Evolutionary Anthropology, Duke University, <sup>2</sup>Duke Global Health Institute, Duke University

The Constrained Total Energy Expenditure (TEE, kcal/d) hypothesis proposes that the body responds dynamically to increased daily physical activity by reducing other expenditure, thereby maintaining TEE within a narrow range. Constrained TEE predicts that greater physical activity will suppress other physiological function (e.g., immune activity, stress reactivity, reproductive investment) but most studies examining these relationships have compared outcomes across populations or relied on self-reported activity. Here, we used the 2003-2005 National Health and Nutrition Examination Survey data to test the prediction that greater daily physical activity, measured with accelerometry, is associated with reduced serum measures of immune system activity in N=4,979 U.S. adults. Consistent with the Constrained TEE hypothesis, individuals with greater daily physical activity had lower C-reactive protein, white blood cell count, lymphocytes, monocytes, segmented neutrophils, and basophils [Adj R<sup>2</sup>: 0.003 to 0.029, p<0.0001 all comparisons] as shown by segmented regression. These relationships were strongest in subjects with low to moderate daily physical activity, but attenuated in subjects with higher activity levels. Results provide further evidence that daily physical activity affects the allocation of energy to other physiological function.

### Sustainability in a multi-level cultural evolutionary framework

MICHELLE ANN. KLINE

Psychology, Center for Culture and Evolution, Brunel University London

Humans are obligatorily cooperative, and in comparison to other animals we cooperate extensively and with unrelated conspecifics. This cooperation enables us to create techniques and technologies that accelerate the speed at which we consume natural resources. Ironically, our cooperative nature has spurred an environmental crisis, culminating in global climate change. Cultural evolutionary theory can guide our understanding of how cooperation and social learning shape social dilemmas, including the overexploitation of global fisheries and historical

changes in fisheries management systems in smaller-scale societies over time. In this paper, I propose a cultural evolutionary explanation for the emergence and persistence of both crises and solutions. Based on this framework, I provide a step-by-step process for designing studies of multi-level cultural systems of resource management, including tradeoffs between validity and control, time scale, and use of qualitative/quantitative methods data collection and analysis. This approach is open to historical data as well as new and existing data sets, case studies, and mathematical simulations. Finally, I present a tutorial and code in the R environment that allows uses to manipulate collected or simulated data in order to explore the empirical implications of group-level sustainable cultural systems. Both the framework and the R-based tool are published openly.

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### These feet are made for walking: an investigation of evolutionary processes underlying hominin foot evolution

KLARA KOMZA<sup>1</sup>, BENICE VIOLA<sup>1</sup>, MICHELLE CAMERON<sup>1</sup> and LAUREN SCHROEDER<sup>2,3</sup>

<sup>1</sup>Department of Anthropology, University of Toronto, <sup>2</sup>Department of Anthropology, University of Toronto Mississauga, <sup>3</sup>Human Evolution Research Institute, Department of Anthropology, University of Cape Town

Plio-Pleistocene fossil hominin foot bones demonstrate a wide range of morphological variability reflective of facultative, habitual and obligate bipedalism. Although selection likely drove much of this variation, the specific evolutionary transitions as well as the individual foot bones that were most strongly influenced by selection are currently unknown. Here, we use tests derived from quantitative genetic theory to investigate the evolutionary processes that shaped metatarsal (Mt) and navicular evolution during major transitions in the hominin lineage. Under a null hypothesis of genetic drift, we expect between- and within-population divergence to be proportional, with a non-proportional relationship indicating that selection played an important role. Using extant human and chimpanzee models as proxies for within-population variability in hominins, we apply these tests between *Australopithecus afarensis* and OH 8 (putatively assigned to *Homo habilis*), and between *H. habilis* and *Homo sapiens*. Results indicate that selection most likely influenced Mt1, Mt4, and navicular diversification between *A. afarensis* and *H. habilis*, but not between *H. habilis* and *H. sapiens*. In contrast, genetic drift could not be rejected in all comparisons of Mt3 morphology. These results reveal a selective influence in the transition from habitual to obligate bipedalism,

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but not between obligate bipeds. Furthermore, consistent non-rejections of genetic drift in the Mt3 reflect its relative morphological stasis over time, and support previous suggestions that its derived morphologies are hominin synapomorphies. These results highlight that different regions of the foot were not equally affected by selection, and that they did not evolve adaptations for bipedalism at once.

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### Scaling of grip strength and body mass in humans

ELAINE E. KOZMA

Development and Regeneration, KU Leuven

Larger people are expected to have absolutely larger muscles and greater grip strength than smaller individuals. However, the proportion of strength to body mass is expected to decrease with body mass due to the allometry of muscles and determinants of muscle strength. The maximum force capacity a muscle can develop is determined by its physiological cross-sectional area (PCSA). If the mechanical advantage of a particular muscle is held constant, grip strength is expected to increase proportionally with PCSA. Under these conditions, isometry predicts that both PCSA and strength scale with mass<sup>0.66</sup>. In this study I assess the scaling of maximum voluntary grip strength as a function of body weight, when controlling for body mass index (BMI) and sex in adults between eighteen and fifty years old using two large scale open source data sets: the United States National Health and Nutrition Examination Survey (NHANES 2011-2012, n=3270) and the Korea National Health and Nutrition Examination Survey (KNHANES 2014, n=2377). Results indicate that BMI has a significant effect on the relationship between strength and body mass. When focusing on individuals with 'normal' BMI (BMI ranging from 18.0 to 24.9), grip strengths scales near isometrically with body mass (scaling with  $M^{0.627 \pm 0.041}$  in NHANES and  $M^{0.541 \pm 0.044}$  KNHANES). I discuss direct implications for the clinical evaluation of strength and for physical exercise rock climbing, a sport requiring grip strength to support one's body weight.

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### Female cooperative labor networks in hunter-gatherers and horticulturalists

THOMAS S. KRAFT<sup>1</sup>, VIVEK V. VENKATARAMAN<sup>2</sup>, KIRK ENDICOTT<sup>3</sup>, SARAH ALAMI<sup>1</sup>, EDMOND SEABRIGHT<sup>4</sup> and MICHAEL GURVEN<sup>1</sup>

<sup>1</sup>Department of Anthropology, University of California, Santa Barbara, <sup>2</sup>Institute for Advanced Study in Toulouse, Toulouse, France, <sup>3</sup>Department

of Anthropology, Dartmouth College, <sup>4</sup>Department of Anthropology, University of New Mexico

Cooperation in food acquisition is a hallmark of the human species. Given that costs and benefits of cooperation vary among production regimes and work activities, the transition from hunting and gathering to agriculture is likely to have reshaped the structure of cooperative subsistence networks. Hunter-gatherers are generally more interdependent and experience higher food acquisition risk than horticulturalists, suggesting that cooperative labor should be more widespread and involve larger groups for hunter-gatherers. Here we examine the dynamics of partner choice and compare female cooperative work networks of Batek hunter-gatherers of Peninsular Malaysia and Tsimane forager-horticulturalists of Bolivia. We find that the semi-autonomous nature of Batek foraging tasks facilitates high daily variation and interconnected network structure, in contrast to Tsimane agricultural activities in which labor is given or received in a more targeted fashion by field owners. Regarding partner choice, female Batek assort preferentially during cooperative gathering expeditions with individuals of different ages (age homophily:  $\beta = -0.03$ ,  $P < 0.001$ ) and close kin ( $\beta = 0.81$ ,  $P < 0.05$ ), whereas male hunting partnerships were not more likely to involve related individuals ( $P > 0.05$ ). Tsimane females also tend to share agricultural labor with kin, but no more so than males. Longitudinal analysis indicates that female cooperative work relationships for both Batek and Tsimane persist over time, with individuals displaying a preference for past partners. These findings have implications for understanding cross-cultural differences in gender relations and highlight both shared patterns and key differences between the labor networks of hunter-gatherers and horticulturalists.

### A 3D quantitative comparative analysis of trapezium and trapezoid morphology in *Gorilla* and *Pan*

ALEXANDRA E. KRALICK<sup>1</sup>, EDEN MACKERETH<sup>2,3</sup> and MATTHEW W. TOCHERI<sup>3,4,5</sup>

<sup>1</sup>Anthropology, University of Pennsylvania, <sup>2</sup>Pathology & Anatomical Sciences, University of Missouri, <sup>3</sup>Anthropology, Lakehead University, <sup>4</sup>Human Origins Program, National Museum of Natural History, <sup>5</sup>Australian Research Council Centre of Excellence for Australian Biodiversity and Heritage, University of Wollongong

African apes are all primarily terrestrial knuckle-walkers but western lowland gorillas (*Gorilla gorilla gorilla*) climb more frequently than do eastern gorillas (*Gorilla beringei*), a consequence of ecological differences in their respective habitats. Although bonobos (*Pan paniscus*) have generally been assumed to be more arboreal than common chimpanzees (*Pan troglodytes*), recent fieldwork suggests this is not true. Here we test whether western lowland gorillas, being relatively

more arboreal, exhibit trapezium morphology that enhances pollical grasping ability in comparison to eastern gorillas, whereas trapezoid morphology should vary less among gorillas given its functional role in weight support during knuckle-walking. In contrast, common chimpanzees and bonobos should be more similar to one another in terms of both trapezium and trapezoid morphology. Using 3D geometric morphometrics in combination with measured angles, relative areas, and curvatures, our results follow some of the expected predictions in that western lowland gorilla trapezia are distinguishable from those of eastern gorillas in ways that are reasonably attributable to pollical grasping. However, several significant differences among gorillas in trapezoid shape were also observed. Both the trapezium and trapezoid of bonobos and common chimpanzees also show multiple distinguishing shape features but the functional significance of these observed differences, if any, remains unclear. Overall, these results underscore the challenges of identifying functionally relevant shape variation in hominoid carpal bones while also highlighting a large amount of unexpected carpal shape variation within African ape taxa that is probably best explained by genetic drift.

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### Stay or Go. Kin network effects on dispersal at marriage for female Savanna Pumé hunter-gatherers

KAREN KRAMER and JOSEPH HACKMAN  
Anthropology, University of Utah

It is now broadly recognized that hunter-gatherers cannot be characterized as patrilocal. Rather the sex that disperses varies considerably across societies (male, female, both or neither), with many groups expressing multiple patterns simultaneously. Nonetheless, most investigations focus on male networks to explain the flexible human pattern of dispersal and post-marital residence. However, this derived feature of human sociality also may benefit females. Mothers may benefit from greater access to food, help, or agonistic support by living in her natal group. Alternatively, decisions to disperse at marriage may also be negatively impacted by band relatedness and partner availability. We use longitudinal data on female kin networks, reproductive histories, camp residence and dispersal for two bands of South American hunter-gatherers to establish band composition over time for women who disperse from their natal community at marriage vs. those who remain and to evaluate whether the density of kin affects maternal fitness outcomes. We find that 1) band relatedness increases from the founder to subsequent generations and differs among women and between bands. Given that variation, analyses show 2) that women who

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disperse from their natal community tend to marry younger but are less related to their spouse's band, have precociously early first births with a higher probably of infant mortality, and have less marriage stability over their reproductive careers. Our results provide evidence that kin camp composition varies over time with migration and dispersal events such that flexible residence and marriage patterns allow women respond beneficially to variation in kin networks.

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### Scaling Climate Change to Human Behavior. Predicting Good and Bad Years for Maya Farmers

KAREN L. KRAMER and JOSEPH HACKMAN  
Anthropology, University of Utah

Human responses to climate variation have a rich anthropological history. However, we know less about how contemporary people living in small-scale societies perceive climate variation vs. change, and what climate data are useful in predicting food production at a scale that affects daily lives. In this analysis, we use longitudinal ethnographic interview and economic data first to ask what are the critical aspects of climate variation that affect the agricultural cycle and food production for Yucatec Maya subsistence farmers. Sixty years of high-resolution meteorological data and crop yield assessments then are used to detect the scale at which climate data predict good and bad crop yields. Finally, we assess long-term changes in climate variables critical to food production. We find that 1) seasonal rainfall variation is most critical to food production; 2) local, daily precipitation averages closely fit the seasonal pattern described by farmers, but is missed at regional, state, annual and monthly scales; 3) at both community- and municipal-levels, heavy late-season rains associated with tropical storms have the greatest negative impact on crop yields; 4) in contrast to regional- and state-level assessments, long-term trends show an increase in rainfall, particularly during key periods of the rainy season. Our findings highlight the need to define climate variables at scales appropriate to human behavior. Course-grained geographic patterns and long-term trends tell us little about attributes that are critical to farmers and food production. However, high-resolution local climate data do capture how seasonal variation shapes human responses.

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### From the Andean Highlands to the Patagonian Archipelagos: Reconstructing population dynamics among pre-Hispanic South American groups

SUSAN C. KUJZMINSKY<sup>1,2</sup> and LUMILA MENÉNDEZ<sup>3,4</sup>

<sup>1</sup>Department of Anthropology and Applied Archaeology, Eastern New Mexico University, USA, <sup>2</sup>Anthropology Department, University of California, Santa Cruz, USA, <sup>3</sup>Department of Anthropology of the Americas, University of Bonn, Germany, <sup>4</sup>Konrad Lorenz Institute, Austria

The prehistory of the Andean region has been integral to understanding early human evolutionary adaptations and the population history of South America. Recently, research elucidating the complexity of human lifeways and migrations have benefitted from genomic and morphological studies. One advantage of skeletal analyses is that since data are collected with non-destructive methods, larger sample sizes that increase population coverage can be used. In this study we employ geometric morphometric methods to investigate population history of the central and southern Andean regions. Although they are often studied separately, these two regions may have been part of an integrated system of trade and caravan networks between the coast and the highlands. Using cranial landmark data from individuals excavated at coast and highland sites in Peru and Chile, we investigate biological relationships over ~9800 years of prehistory in the north, central, and southern Andean coast and highland regions. Principal Components Analysis and computed statistical distances indicate close biological similarities all along of the coast of Peru and Chile, as well as close biological similarities between Patagonians, the central coast, and central highlanders in the southern Andes. In the central Andes, biological affinities between the north coast, central Peruvian coast and central Peruvian highlands support a connection within and between these zonal regions throughout Holocene. This research highlights human interaction through the Holocene, not just within distinct central and southern Andean zones, but also between them, particularly along entire Pacific Coast of Peru and Chile.

### Daily feeding modality and saturation response in the skulls of New Zealand white rabbits (*Oryctolagus cuniculus*)

SUSAN E. LAD<sup>1</sup>, REBECCA J. ANDERSON<sup>1</sup>, HUI DING<sup>1</sup>, WILLIAM W. ABERGER<sup>1</sup>, CARMEN E. ALVAREZ<sup>2</sup>, JONATHAN C. COURI<sup>1</sup>, OLIVIA P. HEMING<sup>1</sup>, DANIEL F. LIGGIO<sup>1</sup>, FREDERICK T. LOCKIE<sup>1</sup>, JENNA M. MCKINNON<sup>3</sup>, HANNAH M. MORRIS<sup>1</sup>, TALIA J. THORNTON<sup>4</sup> and MATTHEW J. RAVOSA<sup>1</sup>

<sup>1</sup>Biological Sciences, University of Notre Dame, <sup>2</sup>Population Biology, Ecology, and Evolution, Emory University, <sup>3</sup>DDS Program, University of

Michigan School of Dentistry, <sup>4</sup>Marian High School, Mishawaka, IN

Protracted cyclical loading engenders a greater osteogenic response in the mammalian chewing apparatus. However, studies using rat ulnae suggest that during cyclical loading there is a saturation point at which bone cells become unresponsive to further stimulation. Renewed responsiveness requires a recovery period of several hours. Here we investigate whether a saturation response occurs in the skull by modulating food access throughout the day, thus altering daily distribution of load cycles. Twenty male New Zealand white rabbits were raised for 48 weeks starting at weaning onset. Ten had continuous access to pellets for 9.5 hours (unimodal group), while another ten had two 2.25-hour periods with food access separated by five hours without food (bimodal group). Post-experiment, all heads were microCT scanned (70kVp, 47µA, 70µm voxel), with cortical areas (Ct.Ar) and thicknesses (Ct.Th) quantified in five regions: mandibular symphysis, corpus, and condyle, and maxillary hard palate and lateral alveolus. After finding no difference in cranial length between groups, all measurements were scaled to mean daily grams of food consumed (175g daily allotment minus grams uneaten). All Ct.Ar comparisons were significant ( $P < 0.05$ ) except for the symphysis and corpus. A number of Ct.Th measurements were significant in all regions. In all comparisons, the bimodal group exceeded the unimodal group, despite the unimodal group consuming more grams/day on average (i.e., greater chewing) ( $P < 0.001$ ). These novel results indicate a saturation response may occur in response to protracted loading in parts of the jaws, and that a recovery period facilitates continued bone growth.

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### Human burials at the Kisesse II rockshelter, Tanzania

MYRA F. LAIRD<sup>1</sup>, ELIZABETH A. SAWCHUK<sup>2,3</sup>, AMANDUS KWEKASON<sup>4</sup>, AUDAX Z.P. MABULLA<sup>4</sup>, EMMANUEL NDIEMA<sup>5</sup>, CHRISTIAN A. TRYON<sup>6</sup>, JASON E. LEWIS<sup>3,7</sup> and KATHRYN L. RANHORN<sup>8</sup>

<sup>1</sup>Integrative Anatomical Sciences, University of Southern California, <sup>2</sup>Anthropology, University of Alberta, <sup>3</sup>Anthropology, Stony Brook University, <sup>4</sup>Archaeology, National Museums of Tanzania, <sup>5</sup>Earth Sciences, National Museums of Kenya, <sup>6</sup>Anthropology, University of Connecticut, <sup>7</sup>Turkana Basin Institute, Stony Brook University, <sup>8</sup>Institute of Human Origins, Arizona State University

The Late Pleistocene and early Holocene in eastern Africa are associated with complex evolutionary and demographic processes that relate to regional population variation today. However, there are relatively few human skeletal remains from this time period. Here we present the skeletal remains from the Kisesse II rockshelter in Tanzania

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that were excavated in 1956, a radiocarbon date for one of the individuals, and cranial and dental metric comparisons to other eastern African populations. We assessed the age, sex, and stature of the Kisesse II individuals. Dental size and a subset of Howell's cranial measurements were collected from the Kisesse II individuals and compared to a sample of modern Africans (cranial  $n = 476$ ) and early Holocene, early pastoralist, and Pastoral Neolithic adults (cranial  $n = 48$ ; dental = 158). Our results suggest a minimum of six individuals in the Kisesse II collections including two adults and four juveniles. While the dating for most of the burials is uncertain, one individual dates to ~7.1 ka suggesting at least one burial is early Holocene in age. Craniodental metric comparisons suggest the Kisesse II individuals present a combination of features that are relatively distinct from other Late Pleistocene and early Holocene eastern Africans, and our findings contribute to a growing body of evidence suggesting eastern African human skeletal remains during this time period exhibit relatively high amounts of morphological variation. However, the Kisesse II individuals also suggest localized morphological homogeneity potentially supporting increased regionalization during the early Holocene.

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### Genetic analyses of the Lomami River Blue Monkey, *Cercopithecus mitis heymansi*, in the central Congo Basin

EMMA R. LARKIN-GERO<sup>1</sup>, AILISSA LEROY<sup>2</sup>, JOHN A. HART<sup>3</sup>, TERESE B. HART<sup>3</sup> and KATE M. DETWILER<sup>1,4</sup>

<sup>1</sup>Biological Sciences, Florida Atlantic University, <sup>2</sup>Anthropology, Santa Ana College, <sup>3</sup>TL2 Project, Frankfurt Zoological Society, <sup>4</sup>Anthropology, Florida Atlantic University

*Cercopithecus mitis* is a polytypic, pan-African guenon species with a complex evolutionary history. Multiple forms of *C. mitis* are found within the Congo Basin, including *C. m. opisthostictus*, *C. m. stuhlmanni* and *C. m. heymansi*. The Lomami River Blue Monkey, *C. m. heymansi*, occurs within the Tshupa-Lomami-Lualaba (TL2) Conservation Landscape and exhibits high pelage variation. A previous Y-chromosomal study (900bp TSPY gene) of *C. m. heymansi* ( $n=5$ ) revealed an affinity between the TL2 population and East African *C. (mitis) albobularis*. By contrast, this relationship was not supported in a mitogenomic study of guenons, which included one *C. m. heymansi* museum skin from north of TL2. Here, we test the pattern found in the mtDNA tree using a larger sample size ( $n=8$ ) that spans the range of *C. m. heymansi* in the TL2 landscape. We included samples of *C. mitis* collected from north and south of TL2 ( $n=5$ ). We sequenced

the *cytb* locus (1,141bp) of the mitochondrial genome and applied Bayesian and maximum likelihood phylogenetic analyses to the data set. Despite the discordance found among mtDNA and Y-chromosome gene trees, *C. m. heymansi* forms highly supported monophyletic clades in both trees. Samples from north and south of TL2 cluster with other *C. mitis* forms, with the latter grouping into a basal clade. These results suggest that *C. m. heymansi* is a distinct lineage within the *C. mitis* radiation. Future genomic analyses are important to understanding the evolutionary history of these populations and discerning their taxonomic classification and conservation value.

### Studying hair morphology in African and African-descendant populations

TINA LASISI

Anthropology, Penn State University

Hair morphology has historically been used as one of the main criteria to classify African and African-descendant (AA) populations as a distinct race.

As a consequence of negative experiences associated with the racist homogenization and devaluation of their hair texture, AA individuals are more difficult to recruit for studies on hair morphology than other populations who have not experienced racial discrimination associated with their hair.

I will present some guidance on best practices for the study of scalp hair morphology, with an emphasis on hair sample collection.

Various hair styles commonly found in AA individuals involve manipulation of the hair using techniques or products that either temporarily or permanently alter the shape of hair fibers. As such, protocols must include clear guidance on participation eligibility and how hair is collected for a range of different hairstyles and hair lengths.

Having members of a study team that can be readily recognized as AA individuals themselves is especially important to establish trust. Equally, anyone interacting with participants should be expected to articulate the purpose of the study in a straightforward manner to assuage concerns on misuses of data concerning the individual, but also misrepresentation of AA peoples as a group.

Finally, I will cover some of the unintended consequences that racist hair terminology has had on AA peoples as regards forensic science and dermatology, as well as ethical considerations for future research on hair, and how lessons learned here may be applied to other racialized phenotypes and populations.

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### Birth canal shape and fetal rotation in *Australopithecus* and Neandertals

NATALIE M. LAUDICINA<sup>1,2</sup> and MATT CARTMILL<sup>2,3</sup>

<sup>1</sup>Biomedical Sciences, Grand Valley State University, <sup>2</sup>Anthropology, Boston University, <sup>3</sup>Evolutionary Anthropology, Duke University

For decades, researchers have sought to understand when and why human childbirth became more difficult than birth in other primates. Previous research utilized human-defined obstetric planes (inlet, midplane, outlet) to evaluate birth mechanisms in fossil hominins. We have previously shown that these three pelvic planes do not accurately indicate points of fetal obstruction. Instead, the whole birth canal must be analyzed to examine how changing dimensions throughout the birth canal affect fetal descent.

In this research, the reconstructed shapes and minimum dimensions of the entire canal in five fossil hominins (A.L. 288-1, Sts-14, Sts-65, MH2, Tabun-1) were compared with estimated fetal dimensions (head and shoulder breadth) in order to identify points of potential obstruction and probable birth mechanisms. Each hominin's birth canal shape is unique and shows multiple points of constriction not captured by the traditional three-plane analysis. Inter- and intraspecific differences indicate that the degree of birth difficulty depends on many factors. In the early australopithecines A.L. 288-1, Sts-14, and Sts-65, the risk of dystocia comes from both the fetal head and shoulders. In the later MH2 specimen (*Australopithecus sediba*), neither the fetal head nor shoulder breadth would have produced obstruction. In the Tabun Neandertal, estimated fetal shoulder breadth, but not head size, exceeds birth-canal dimensions. This research indicates that adaptations to reduce obstetric constraints (cranial molding, pelvic ligamentary relaxation) may have arisen in the hominin lineage considerably earlier than previously thought.

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### Lumbar muscle architecture and function in *Propithecus*

KATHRYN D. LAURIA<sup>1</sup>, FAYE R. MCGECHIE<sup>2</sup>, NEYSA GRIDER-POTTER<sup>3</sup> and CAROL V. WARD<sup>2</sup>

<sup>1</sup>Anthropology, University of Missouri-Columbia, <sup>2</sup>Pathology and Anatomical Sciences, University of Missouri-Columbia, <sup>3</sup>Department of Clinical Anatomy and OPP, Rocky Vista University

The lumbar spine varies among primates with different locomotor specializations, and differences in associated musculature have been described among some taxa. As primarily a vertical clinger and leaper, the sifaka (*Propithecus*) uses its spine in orthograde posture and should undergo significant rotation during locomotion. As such, its lumbar epaxial musculature should

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reflect these behaviors, but the complexity of its lumbar musculature has not been fully characterized. Here we apply novel contrast-enhanced computed tomography and 3D fascicle tracking algorithms to digitally visualize and quantify mechanically relevant aspects of lumbar muscle architecture in a Coquerel's sifaka (*Propithecus coquereli*). The specimen was contrast stained and microCT-scanned (0.12 mm<sup>3</sup> voxels). Data were segmented using Avizo and individual muscle fascicles tracked using the Avizo Xfiber module. These methods not only allow visualization of this complex musculature in 3D for the first time, but orientations and physiological cross-sectional areas of the complex architecture of spinal musculature can be calculated. Variation of fascicle orientation even within muscles can be appreciated. For example, even within the spinalis, generally considered a simple extensor, internal muscle architecture varies, with more craniocaudally oriented fascicles cranially that gain complexity in its caudal region, perhaps related to rotation of the spine. Other muscles vary in fascicle geometry as well. Future work will compare the muscular architecture of *Propithecus* with that of quadrupedal strepsirrhines and with anthropoids to identify variation associated with locomotor specializations. These data will better inform interpretations of vertebral morphology and spinal function in living and fossil primates.

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### Acetabular orientation and pelvic form in hominins and other anthropoids

AUSTIN B. LAWRENCE<sup>1</sup>, ASHLEY S. HAMMOND<sup>2,3</sup> and CAROL V. WARD<sup>1</sup>

<sup>1</sup>Department of Pathology and Anatomical Sciences, University of Missouri, <sup>2</sup>Division of Anthropology, American Museum of Natural History, <sup>3</sup>New York Consortium in Evolutionary Primatology, New York, NY

Hominin pelvic form differs dramatically from that of other primates by having more laterally facing iliac blades, a wider sacrum and a larger, transversely broad pelvic inlet. The orientation of the acetabulum may also differ, plausibly related to differences in load transmission during habitual bipedal posture and locomotion, which may, in turn, affect overall pelvic geometry. We compared acetabular orientation in humans, *Australopithecus* and extant anthropoids using two approaches. First, we measured the 3D orientation of the acetabulum on *in silico* models of individual hipbones aligned to the median plane by registering models to landmark coordinates that had been collected on articulated pelvises. We fit a plane to the acetabular rim and measured its orientation relative to the median, transverse

and coronal planes. Second, we performed 3D geometric morphometric analyses of landmarks collected on whole pelvises and on acetabula alone of 30 extant non-hominin anthropoid species, humans and *Australopithecus afarensis*. Results show the acetabulum opens further anteriorly and inferiorly in hominins compared to other anthropoids. Acetabular orientation is similar among non-hominin anthropoids. Humans and *Australopithecus* have equivalent orientations despite differences in hip joint size, pelvic inlet breadth and iliac morphology. These data suggest that hip joint orientation is independent of these other aspects of pelvic form. Geometric morphometric analyses show that acetabular reorientation in hominins may also influence mediolateral breadth of the lower ilium. These results suggest that the orientation of the acetabulum is a key component in the suite of pelvic characteristics related to habitual bipedality in hominins.

### Heterogeneous frailty and the expression of linear enamel hypoplasia in a genealogical population

JULIE LAWRENCE<sup>1</sup>, CHRISTOPHER M. STOJANOWSKI<sup>1</sup>, KATHLEEN S. PAUL<sup>2</sup>, ANDREW C. SEIDEL<sup>1</sup> and DEBBIE GUATELLI-STEINBERG<sup>3</sup>

<sup>1</sup>School of Human Evolution and Social Change, Arizona State University, <sup>2</sup>Department of Anthropology, University of Arkansas, <sup>3</sup>Department of Anthropology, The Ohio State University

The prevalence of linear enamel hypoplasia (LEH), a dental defect that arises during development, is a key metric for bioarchaeological analyses of past populations. LEH is associated with early life insults, such as nutritional stress or illness, the endurance of which leaves permanent marks on enamel. High prevalence of LEH is often interpreted as evidence that a population experienced environmental hardship and those individuals with LEH were particularly frail. Little is known, however, about the effects of shared genes/environment on LEH variation. This is problematic since bioarchaeological assemblages frequently share a restricted geographic and temporal origin and contain close relatives. To address this issue, we examined dental casts of 239 individuals with known genealogical relationships to evaluate whether LEH prevalence is kin-structured. Narrow sense heritability estimates were moderate but significant for some teeth, including the tooth most commonly affected by LEH, the mandibular canine. Age was a significant covariate that suggested a secular decrease in LEH, although LEH persisted across multiple generations. Further analyses revealed that nearly all heritability was accounted for by a household effect (except in the mandibular canine), indicating that the shared household environment of kin groups can affect a population's LEH prevalence. Kin structure of LEH prevalence calls into question the uncritical use of

this dental defect in the population-level assessment of past environmental stress and disease susceptibility. Bioarchaeologists should consider how kin/household structure may influence LEH prevalence in study populations and exert caution when interpreting LEH as an independent paleopathology marker.

### Uncovering the evolutionary history of the Turkana, a desert pastoralist group

AMANDA J. LEA<sup>1,2</sup>, REBECCA SIFORD<sup>3</sup>, TANYA PHUNG<sup>4,5</sup>, ANGELA TARAVELLA<sup>4,5</sup>, FRANCIS LUTUKOI<sup>6</sup>, SIMON LOWASA<sup>6</sup>, BENJAMIN MUHOYA<sup>6</sup>, CHARLES WAIGWA<sup>6</sup>, SHAWN DAVIDSON<sup>2</sup>, CARLA HANDLEY<sup>3</sup>, JOSEPH KAMAU<sup>7,8</sup>, DINO MARTINS<sup>1,6</sup>, ANNE STONE<sup>3</sup>, SARAH MATHEW<sup>3</sup>, MELISSA WILSON<sup>4,5</sup> and JULIEN AYROLES<sup>1,2</sup>

<sup>1</sup>Department of Ecology and Evolutionary Biology, Princeton University, USA, <sup>2</sup>Lewis Sigler Institute for Integrative Genomics, Princeton University, USA, <sup>3</sup>School of Human Evolution and Social Change, Arizona State University, USA, <sup>4</sup>School of Life Sciences, Arizona State University, USA, <sup>5</sup>Center for Evolution and Medicine, Arizona State University, USA, <sup>6</sup>Mpala Research Centre, Kenya, <sup>7</sup>Institute of Primate Research, Kenya, <sup>8</sup>Department of Biochemistry, School of Medicine, University of Nairobi, Kenya

In a blink of evolutionary time, humans have explored every corner of this planet and have shown an amazing capacity to adapt to extreme conditions; yet, these adaptations remain poorly understood at the genomic level. To address this gap, we are working with the Turkana, a group that inhabits the arid regions around northwest Kenya and consumes a milk- and meat-rich diet as a result of their pastoralist lifestyle. To uncover regions of the genome under positive selection in the Turkana, we compiled a large dataset of 110 high (>20x) and 197 low (~6x) coverage genomes, as well as array data for validation (n=188). We tested for signatures of positive selection across ~8 million variants using the integrated haplotype score, population branch statistic, and BayEnv XtX approaches, and found 8 outlier regions. One of these regions includes a putative enhancer for a kidney-expressed gene involved in fluid balance, the response to dehydration, and the elimination of waste products produced during the breakdown of purine-rich foods such as red meat. By pairing demographic inference with forward-time simulations, we inferred the strength and timing of selection on regulatory variants near this key gene. Further, we are using RNA and serum samples collected from the same individuals to show these regulatory variants are associated with gene expression and kidney-derived metabolite levels. Together, our work provides a comprehensive picture of how the Turkana's unique ecology and lifestyle have shaped their genomes and physiology, providing insight into evolutionary processes and present-day human diversity.

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## Examining Long Bone Phenotypic Plasticity: A Case Study of Skeletal Differences between Northern and Southern Japanese Macaques

ROSE LEACH<sup>1</sup>, DEXTER ZIRKLE<sup>1</sup>, TAKESHI NISHIMURA<sup>2</sup>, RICHARD S. MEINDL<sup>1</sup>, MARY ANN RAGHANTI<sup>1</sup> and CLAUDE O. LOVEJOY<sup>1</sup>

<sup>1</sup>School of Biomedical Sciences, Department of Anthropology, Kent State University, <sup>2</sup>Primate Research Institute, Kyoto University

Neanderthals exhibit a robust somatotype, thick cortical diaphyseal bone, shorter limb, and larger thoraxes, relative to modern humans. While phenotypic differences could be a result of a distinct genome, they may also reflect somatic plasticity in response to colder climates. Geographical rules developed by Bergmann and Allen state that mammals in warmer temperatures have a reduced thorax and longer limbs to aid in heat dissipation, whereas the robust thorax and shorter limbs in cold climates serve to conserve heat. Japanese macaques have a longer period of developmental exposure to their immediate environment and reside in areas of Japan ranging from the colder regions of northern Honshu to the hot climates in southern regions like Yakushima Island, providing an opportunity to examine these theories. Climate may affect Japanese macaque skeletal ontogeny, implying some level of plasticity and/or cold climate adaptation. Therefore, we expect northern Japanese macaques will exhibit significant differences in osteological architecture from southern Japanese macaques. This study sampled adult macaques (*M. fuscata fuscata* and *M. fuscata yakui*, n=85) from the Kyoto University Primate Research Institute Skeletal Collection. Sex-balanced data for each macaque were collected using osteometrics. Preliminary plots show minimal variation in limb length between groups and no clear cline with increasing temperature. The results suggest that the cline does not exist due to the limited range in climate used in the study.

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## Urinary C-peptide is associated with percent body fat in healthy adult premenopausal women

KATHARINE MN. LEE<sup>1,2</sup>, MARY P. ROGERS-LAVANNE<sup>3</sup>, ANDRZEJ GALBARCZYK<sup>4</sup>, GRAZYNA JASIENSKA<sup>4</sup> and KATHRYN BH. CLANCY<sup>2</sup>

<sup>1</sup>Division of Public Health Sciences - Department of Surgery, Washington University School of Medicine, <sup>2</sup>Department of Anthropology, University of Illinois at Urbana-Champaign, <sup>3</sup>Institute for Genomic Biology, University of Illinois Urbana-Champaign, <sup>4</sup>Department of Environmental Health, Faculty of Sciences, Jagiellonian Medical College

Measuring energy status in remote field-based studies can be difficult, but monitoring C-peptide is one proposed method. We measured urinary

C-peptide for one menstrual cycle in 105 healthy pre-menopausal women (age 18-46) from Illinois (n=22) and rural Poland (n=83). Height, weight, and percent body fat were measured at enrollment and at the end of data collection. At enrollment, women weighed 66.2±13.2 kg (mean±SD), had a BMI of 24.3±4.3, and had body fat of 28.5±7.6%. During data collection, change in body size and composition ranged from -3.9 to +4.7 kg, -11.4% to +8.5% body fat, and -1.5 to +1.8 BMI points. Using linear regression and adjusting for age, we examined whether log-transformed C-peptide, averaged across the cycle for each participant, was associated with body weight, BMI, percent body fat, or the change in these measures across the menstrual cycle. Using AIC for model selection, we found that percent body fat at enrollment provided the best fit (overall model p=0.002, adjRsq=0.09), and none of the models that examined change in body size or composition were significant. Thus, in this sample of healthy adult women, C-peptide seems to be most strongly associated with percent body fat, not change in body size or body composition occurring over a time period of approximately 1-2 months.

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## Cross-population comparison of oxytocin receptor gene (OXTR) allele frequencies reveals a signature of local- and species-level selection for enhanced oxytocin signaling in the human brain

MINWOO LEE<sup>1</sup>, JOHN LINDO<sup>1</sup> and JAMES K. RILLING<sup>1,2,3,4,5</sup>

<sup>1</sup>Department of Anthropology, Emory University, <sup>2</sup>Department of Psychiatry and Behavioral Science, Emory University, <sup>3</sup>Yerkes National Primate Research Center, Emory University, <sup>4</sup>Center for Translational Social Neuroscience, Emory University, <sup>5</sup>Silvio O. Conte Center for Oxytocin and Social Cognition, Emory University

Allele frequencies of oxytocin receptor gene (*OXTR*) polymorphisms are known to vary across primate species and across human populations. Yet, specific evolutionary mechanisms and phenotypic correlates of these observed differences are unclear. We hypothesized that *OXTR* variants were selected for their effects on receptor expression in specific brain areas, which in turn biased individuals towards behaviors adaptive in species-specific or population-specific social environments. To test this hypothesis, we first used the Gene-Tissue Expression database (<https://gtexportal.org>) to identify all single-nucleotide polymorphisms (SNPs) in human *OXTR* that influence receptor expression in 10 brain areas. Next, we incorporated the data from the 1000 Genomes project to calculate the frequency of the

high-expressing alleles (HEAs) for each brain area across five geographic population groups (Africa, America, East Asia, Europe, and South Asia; N=2,504). Average HEA frequency was highest in East Asians for the anterior cingulate cortex (ACC), a brain region linked with social sensitivity,  $F_{(4, 2499)}=72.6, p<.001$ . Furthermore, comparing East Asian genomes with other genomes revealed that two of the ACC *OXTR* SNPs were in linkage disequilibrium with SNPs that were under moderate selection. Cross-population differences in ACC HEA frequency correlated with collectivist values ( $r=.56, p<.05$ ), which, in turn, was associated with historical rice farming ( $r=.55, p<.05$ ). We also identified uniquely human HEAs (vs. chimpanzee and Neanderthal genomes) in the substantia nigra, a brain region involved in social reward and motivation. Our findings provide potential evidence of local- and species-level selection on human *OXTR*, favoring enhanced oxytocin signaling in brain areas involved in social behavior.

## Responses to novel food in a group of captive hamadryas baboons (*Papio hamadryas*): The role of sensory cues

SAEIN LEE<sup>1</sup>, YENA KIM<sup>2</sup>, CÉCILE SARABIAN<sup>3</sup> and JAE C CHOE<sup>1</sup>

<sup>1</sup>Laboratory of Behaviour & Ecology, Interdisciplinary program of EcoCreative, Ewha Womans University, <sup>2</sup>Cognitive Psychology Unit, Institute of Psychology, Leiden University, <sup>3</sup>Primate Research Institute, Kyoto University

While foraging, primates rely on multi-sensory cues to evaluate the nutritional value of food and avoid toxicity. To date, food neophobia has mainly been studied in great apes. Thus, the present study examined sensory responses to novel food items in a group of captive hamadryas baboons – a diurnal species mainly known for its reliance on visual and olfactory cues in socio-sexual contexts. We tested 1) which sensory cues are used first and most frequently for detecting novel food, and 2) how their responses to novel food change over time. Due to the difficulty of individual testing, we provisioned novel food items in a group setting and consequently recorded the display of social behaviors during each one-hour test session. We used familiar food (apple) as control item and four novel food (melon, peach, pear, watermelon) with similar nutritional value, as test items. When food items were within visual detection range (10cm), baboons used olfactory cues for the first investigation on novel food. While investigating novel food, baboons used gustatory (bite and lick) cues most frequently, though the frequency of using tactile and gustatory cues was similar to probing familiar food. There was no effect of repeated exposure on the use of sensory cues. Additionally, group members closely observed each other during novel food testing. Our results indicate that baboons use multi-sensory cues and social

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information in a foraging context, which contrasts with the previous findings of using/investigating only a single sensory channel in foraging and other contexts.

### Scaling of sexual size dimorphism in thick-tailed galagos (*Otolemur crassicaudatus*)

STEVEN R. LEIGH<sup>1</sup>, MICHELLE L. SAUTHER<sup>1</sup>, FRANK P. CUOZZO<sup>2</sup> and ADRIAN S. TORDIFFE<sup>3</sup>

<sup>1</sup>Anthropology, University of Colorado Boulder, <sup>2</sup>Lajuma Research Station, Lajuma Research Station, Louis Trichardt (Makhado), Limpopo, South Africa, <sup>3</sup>Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, South Africa

Sexual size dimorphism (SSD) in strepsirrhine primates is limited relative to anthropoid primates. However, galagos exhibit modest levels of sexual size dimorphism, with males about 15-20% heavier than females, depending on species and resulting from bimaturism.

Here, we analyze ontogenetic allometry in thick-tailed bushbabies/galagos (*Otolemur crassicaudatus*) to explore allometric bases of SSD. We predict that ontogenetic scaling, or projection of scaling relations seen in females to male size ranges, will account for SSD. Morphometric analyses are based on measurements of animals from Lajuma, South Africa (N= 47 females, 50 males, 37 measurements). Regressions measure scaling relations between somatometrics and overall size measures as well as scaling relations among variables.

Sexual size dimorphism occurs in numerous dimensions, although at lower levels than for body mass. While allometries overlap extensively, regressions diverge late in development, suggesting that ontogenetic scaling does not account fully for SSD body dimensions. Relative to overall size, male regressions have lower allometric coefficients than females, even though males reach larger adult masses.

Divergence of allometric relations between sexes produces relatively small body dimensions in male galagos. Bimaturism in mass growth probably exceeds bimaturism in skeletal dimensions, suggesting that males "fill-out" late in ontogeny. Exaggerated skeletal features produced either through positive male allometry or significantly extended growth that characterize some anthropoid primates are not apparent. We discuss the implications of this finding in terms of sexual selection, and consider functional consequences of sex differences in mass relative to skeletal dimensions.

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### Evolution of de novo microRNA Genes in the Human Lineage

NATHAN H. LENTS<sup>1</sup>, HUNTER R. JOHNSON<sup>2</sup>, BEATRIZ MERCADO<sup>1</sup>, JOSÉ GALVÁN<sup>1</sup>, JESSICA BLANDINO<sup>1</sup>, SAMANTHA VEE<sup>1</sup> and WILLIAM HIGGINS<sup>1</sup>

<sup>1</sup>Sciences, John Jay College, The City University of New York, <sup>2</sup>Mathematics and Computer Science, John Jay College, The City University of New York

In a search for human-specific genetic elements, using whole chromosome alignments, our laboratory has discovered a region on human chromosome 21 that is markedly distinct from anything found in other extant apes. Within this region are eight microRNA (miRNA) genes, in three distinct families, that appear to have no functional orthologs in other ape species. Upon closer inspection by synteny analysis, this region of the chromosome has undergone repeated rounds of segmental duplication, which has likely driven the proliferation of these orphan miRNA genes. Reconstruction of the ancestral state of this region reveals an array of ribosomal RNA (rRNA) genes or pseudogenes, raising the possibility that these human-specific miRNA genes evolved through duplication and diversification of ancestral rRNA genes. The region is also enriched in sequence motifs associated with meiotic recombination, suggesting a possible molecular mechanism for the segmental duplications that occurred and gave rise to the new miRNA genes over the past six million years. Attempts to date the duplication events and age the new miRNA genes have given mixed results, but the miRNA genes appear shared in the available ancient genomes from Neanderthal and Denisovans. An analysis of the gene ontology of the predicted targets of these new miRNA genes reveal potential roles in nervous system development and functioning and thus the unique evolutionary trajectory of the human lineage.

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### Pushing Through The Pandemic: The Impacts Of Covid-19 On Maternity Care, Anxiety, And Childbirth Experiences In The United States

KYLEA L. LIESE and JULIENNE N. RUTHERFORD  
Human Development Nursing Science, University of Illinois Chicago

Within an unprecedented matter of days in Spring 2020, the COVID-19 pandemic upended long-established best practices for obstetric care. Changes in standard prenatal appointments and fluctuations in hospital policies threatened pregnant people with the prospect of birthing alone and/or being separated from their newborn. It is unknown the extent to which these changes

impact pregnant people's anxiety during pregnancy and beliefs in the fundamental "safety" of birthing in hospitals. We launched a national online survey of pregnant people's prenatal experiences, garnering a sample of over 4,800 predominantly white, highly educated, higher income respondents, representing all fifty states. In bivariate regression models, increased prenatal changes and hospital safety precautions predicted increased anxiety (respectively  $\beta=0.05$ ,  $p=0.001$ ,  $r^2=0.005$ ;  $\beta=0.13$ ,  $p<0.001$ ,  $r^2=0.06$ ). In multiple regression models accounting for education, race, and insurance status, both prenatal changes and hospital precautions remained significant (overall model  $p<0.0001$ ,  $r^2=0.07$ ). Black respondents experienced significantly more changes in prenatal care ( $n$ =Pearson's  $\chi^2(30)=42.86$ ,  $p=0.01$ ). Qualitative responses elucidate how the accumulation of changes in care intended to protect pregnant people, their new infants, and their families from COVID-19 may themselves be imposing an additional burden of maternal stress. Our preliminary findings speak to the negative impact of the pandemic on pregnancy for highly resourced white pregnant people, but we don't know the extent to which Black pregnant people and other POC are affected by these significant changes to the experience of pregnancy, changes that will likely remain in place for some time as the pandemic enters subsequent phases.

### Evidence of Stress in Native American Populations of Florida: Investigations into the Microstructure of Enamel

KAITLYN LISEBY<sup>1</sup> and SCOTT W. SIMPSON<sup>2</sup>

<sup>1</sup>Department of Biology, Case Western Reserve University, <sup>2</sup>Department of Anatomy, Case Western Reserve University School of Medicine

Native Americans of Florida experienced stress associated with changes in subsistence practices, population density, and disease throughout history that was exacerbated by the arrival of the Spanish colonists. The Native American dental remains used in this study originated from archaeological sites in Florida ranging from an Early Archaic hunter-gatherer population (7100 B.C.-5800 B.C.) to sedentary, maize agriculturalist populations (A.D. 1000-1700) that included the arrival and occupation of the Spanish. Two types of developmental defects of enamel, pathological striae and linear enamel hypoplasias, were examined to gauge the physiological stresses experienced by these populations.

Native Americans who experienced Spanish colonialism during the Early and Late Mission Periods possess the highest frequencies of pathological striae. Early Archaic Native Americans of the Hunter-Gatherer Period possess low frequencies of pathological striae and the highest frequencies of linear enamel hypoplasias. Pathological striae formed at significantly earlier ages than linear enamel hypoplasias for both tooth types across

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all time periods. In maxillary central incisors, 74% of pathological striae formed between 0.75 and 2.5 years of age, while 94% of linear enamel hypoplasias formed after 2.5 years of age. In mandibular canines, 75% of pathological striae formed before 2.5 years of age, while 87% of linear enamel hypoplasias formed after 2.5 years of age. It is believed that the pathological striae resulted from acute episodes of weaning diarrhea and other diseases resulting in severe dehydration. It is also believed that the linear enamel hypoplasias resulted from prolonged periods of malnutrition and seasonal stress.

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### A Virtual Anthropological Approach to Examining Sexual Dimorphism in the Pelvis

HELEN LITAVEC (BRANDT)

Anthropology, Binghamton University

The pelvis is an area frequently used for the estimation of sex due to the numerous morphological differences between males and females. These differences have been notably observed in the shape of the greater sciatic notch, subpubic concavity, and obturator foramen. Although these differences have been documented previously, one common drawback of prior studies has been their inability to use quantitative methods to observe these morphological differences and to discover where exactly these subtle nuances lie. Virtual methods are particularly useful in these circumstances. This pilot study will examine these three locations using three-dimensional (3D) models, virtual landmarks, and a Procrustes Analysis of Fit. Eighteen individuals were examined from the Binghamton University Skeletal Collection. The pelvises were scanned using a NextEngine 3D Laser scanner and the shapes were analyzed using Landmark Editor by IDAV. Landmark coordinates were placed and subsequently uploaded into MorphoJ, where a Procrustes Fit and Principle Components Analysis (PCA) were conducted. The results indicate that there are quantitatively identifiable morphological differences between male and female pelvises in these areas, supporting previous research. To test if these observed differences were statistically significant, a Discriminant Function Analysis (DFA) was conducted and demonstrated that the majority of pelvises were able to be correctly classified using this method. In sum, these results illustrate that this technique could assist anthropologists in classifying a pelvis of unknown sex using an objective, computer-based method. In the future, it is hoped that this method can be tested on a larger sample size.

### COVID-19 Related Health Concerns and Grief during the Perinatal Period: Potential impacts on Maternal Mental Health

CINDY H. LIU<sup>1,2</sup>, CARMINA ERDEI<sup>1</sup> and LEENA MITTAL<sup>2</sup>

<sup>1</sup>Pediatric Newborn Medicine, Brigham and Women's Hospital/Harvard Medical School, <sup>2</sup>Psychiatry, Brigham and Women's Hospital/Harvard Medical School

**Background:** Approximately 116 million births will have taken place worldwide during the COVID-19 pandemic by the end of 2020. The perinatal period is a vulnerable period for mothers, especially during the pandemic, given likely increases in worry and grief, and elevated mental health symptoms.

**Methods:** The Perinatal Experiences and COVID-19 Effects (PEACE) Study assesses self-reported data on the mental health and well-being of U.S. pregnant and postpartum women during the COVID-19 pandemic. We measured COVID-19-related health worries and grief experiences, and current mental health symptoms (depression, generalized anxiety, and PTSD) in 1,123 U.S. women from May 21 to August 17, 2020.

**Results:** Among our respondents, 36.4% reported clinically significant levels of depression, 22.7% reported clinically significant levels of generalized anxiety, and 10.3% reported clinically significant levels of PTSD. Women with pre-existing mental health diagnoses were 1.6-to-3.7 more likely to score at clinically significant levels of depression, generalized anxiety, and PTSD. Approximately 18% reported high levels of COVID-19-related health worries and were 2.6-to-4.2 times more likely to score above the clinical threshold for mental health symptoms. Approximately 9% reported high levels of grief and were 4.7-to-5.5 times more likely to score above the clinical threshold for mental health symptoms.

**Conclusions:** Perinatal women with pre-existing mental health diagnoses are more vulnerable to elevated symptoms during the COVID-19 pandemic. COVID-19-related health worries and grief experiences may increase the likelihood of mental health symptoms among those without pre-existing mental health concerns. Providers should develop strategies for addressing health-related worry and grief within their practice.

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### Dental topography, shear crest lengths, and macrowear in the Miocene catarrhine *Rangwapithecus*: implications for dietary inference

ELLIS M. LOCKE

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

*Rangwapithecus gordonii* is a medium-sized nyanzapithecine catarrhine from the early Miocene of western Kenya, characterized by mesiodistally elongate molars with crenulated enamel and long shear crests. Previous analyses of *Rangwapithecus* molar morphology inferred a folivorous adaptation, but dental microwear results suggest that *Rangwapithecus* and all other African Miocene catarrhines were generalized frugivores. While shearing quotient studies are restricted to unworn teeth, dental topography (DT) provides a toolkit for measuring aspects of shape (e.g. sharpness, complexity, and relief) from digital models of tooth crowns regardless of wear stage. Additional GIS-based methods provide a means of measuring shear crests from worn specimens. The pattern of wear-mediated change in DT and shear crests has been shown to provide insight into dietary behavior in some primates.

I apply these methods to a wear series of lower m2s of *Rangwapithecus* ( $n=10$ ). The pattern of DT and shear crest change in *Rangwapithecus* is compared with wear series of wild-shot specimens of *Pan troglodytes schweinfurthii* ( $n=21$ ), which consumes primarily fruit, and *Gorilla gorilla gorilla* ( $n=20$ ), which seasonally consumes leaves and herbaceous vegetation as fallback foods. Although linear regressions show few differences in the pattern of wear-mediated DT change between *Pan* and *Gorilla*, they have little overlap in DT values at any wear stage. Across all wear stages, *Rangwapithecus* m2s are not significantly different from *Gorilla* but exhibit significantly sharper occlusal surfaces with higher slope, greater relief, and longer shear crests than *Pan*. These results affirm previous suggestions that *Rangwapithecus* had a diet that included herbaceous vegetation.

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### The relationship between arboreality and climate variables in lactating female chimpanzees at Gombe National Park, Tanzania

VICTORIA A. LOCKWOOD<sup>1</sup>, ELIZABETH V. LONSDORF<sup>2</sup>, MARGARET A. STANTON<sup>3</sup>, SEAN M. LEE<sup>1</sup> and CARSON M. MURRAY<sup>1</sup>

<sup>1</sup>Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, Washington, DC, <sup>2</sup>Department of Psychology and Biological Foundations of Behavior Program, Franklin and

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Marshall College, Lancaster, PA, <sup>3</sup>School of Social and Behavioral Sciences, University of New England, Biddeford, ME

A key transition in human evolution is the shift to bipedal locomotion. The arboreal, terrestrial, or combined origins of bipedalism have been debated, with chimpanzees (*Pan troglodytes*) often used as a referential model for understanding hominin locomotor capabilities. Understanding the environmental predictors of arboreality in extant chimpanzees can provide additional insight on the potential arboreal capabilities of fossil hominins. Previous research on the predictors of arboreality have been biased towards males and relatively little is known about how female arboreality relates to climate. Female chimpanzees, particularly mothers, face different pressures than males due to offspring investment and differing social strategies. In this study, we ran a linear mixed model to investigate how arboreality relates to temperature, wet/dry season, and age in chimpanzee mothers at Gombe National Park, Tanzania, using 6 years of behavioral data (2011 – 2016). Season ( $F = 8.536$ ,  $df = 1$ ,  $p = 0.004$ ) and age ( $F = 6.528$ ,  $df = 1$ ,  $p = 0.029$ ) were both significant predictors of the proportion of time spent arboreal, while maximum temperature (range 20-38 degrees Celsius) was significant at the  $p < 0.10$  level ( $F = 3.772$ ,  $df = 1$ ,  $p = 0.053$ ). Arboreality decreased with both increasing age and increasing temperature and mothers spent a greater proportion of time arboreal during the wet compared to the dry season. These results demonstrate seasonal differences in arboreality alongside the effect of increasing age. Future work will investigate how infant age affects arboreality and infant carrying behavior in an arboreal context.

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## Biological distance in the Eastern Adriatic: a preliminary analysis

TISA N. LOEWEN<sup>1</sup> and MALLORY J. ANCTIL<sup>2</sup>

<sup>1</sup>Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona State University, <sup>2</sup>Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

The Iron Age (~600-200 BCE) peoples of the Eastern Adriatic (modern day Croatia and Bosnia Herzegovina) shared trade networks, material practices, and by 10 CE were united under the Roman Empire. These local cultural groups interacted with the surrounding Roman, Greek, and Celtic peoples through both collaboration and war. Although these peoples maintained distinct material culture and customs, later Roman interventions raise questions about the impact of cultural exchange on biological population

structure. Studies have been conducted for the well-known Roman, Greek, and Celtic populations; though there are no biodistance studies of the inhabitants that populated the lands between. This study provides a preliminary analysis in the region through examination of the phenetic diversity among the neighboring groups before Roman disruption at the end of the Iron Age. Specifically, this analysis tests the hypothesis that the imperial and cultural exchanges were accompanied by biological changes. Previously published ASUDAS dental non-metric trait frequencies of 18 regional samples from Roman, Greek, and Celtic populations (N=1856) were compiled. Data from 32 dental traits were analyzed using the mean measure of divergence distance statistic to yield inter-sample phenetic affinities. The MDS plot (eigenvalue-based GoF 0.83) shows overall phenetic heterogeneity between the Roman, Greek, and Celtic populations; therefore, continuity among these groups is not supported. The two traits driving the intersample variation are Anterior Fovea LM1 (39.4 MD) and Lingual Cusp variation LP2 (22.2 MD). This study warrants future work incorporating the local populations that resided between these groups as they shared imperial cultural influence.

## Addressing the shifting legacies of US racism through active and engaged science communication

JUSTIN LUND

Anthropology, University of Oklahoma

Anthropology is well aware of the complex relationship between the colonization of the Americas and the imported models of racism. For much of the public, however, these realities are only now becoming apparent. The pandemic and the events that lead to the racial unrest of 2020 have highlighted for many people some of the more problematic aspects of our colonial history and how those past events continue to negatively impact our society. Here, I demonstrate the shifty nature of racialized politics and how they impact the field of anthropological genetics. I share my perspective and concern as an Indigenous anthropologist on recent rhetoric and research in and on Indian Country. As stewards of valuable knowledge on race, Anthropology has failed to educate the public, and anthropologists may be politically unequipped to do so. By recognizing the political nature of science, we should also come to recognize our role as unwitting politicians. Future efforts to educate will move beyond the colonial academy and find direct avenues to foster discussions with those who need the power of knowledge most.

## Evolutionary patterns of relative turbinate size across Euarchontoglires

INGRID K. LUNDEEN<sup>1</sup> and ADDISON D. KEMP<sup>2</sup>

<sup>1</sup>Department of Anthropology, University of Texas at Austin, <sup>2</sup>Department of Integrated Anatomical Sciences, University of Southern California

The olfactory system has long been presumed to exhibit some level of reduction in crown primates. This hypothesized reduction would apply to both the olfactory bulb of the brain and the turbinates, the bones within the nasal fossa that support both the olfactory and respiratory epithelium. Though turbinate size can be used as a proxy for the functional importance of olfaction, comparative study of this feature has received significantly less attention. Compared with non-primate euarchontans, primates have reduced relative olfactory turbinal surface area, suggesting a reduction in olfactory sensitivity from the primitive euarchontan condition to the crown primate condition. Here, we test this hypothesis using an expanded euarchontoglian comparative sample that includes dermopterans (n=2), primates (n=51), rodents (n=69), and scandentians (n=10). Turbinal surface area was quantified for all taxa using micro-CT scan data, then scaled to body mass to look at general patterns in both respiratory and olfactory turbinal size among euarchontoglires. This analysis reveals a strong relationship between body mass and turbinate size in all taxa. While haplorhine primates have relatively small olfactory turbinates, strepsirrhine primates, rodents, and dermopterans all have similar relative turbinate sizes. Scandentians have relatively large olfactory turbinates for a given body size suggesting that rather than representing the ancestral condition in euarchontans, they may be derived in terms of their investment in olfactory anatomy. This study highlights the importance of exploring patterns in data at multiple taxonomic scales.

## It's Lit: Campfire Relaxation as a Preadaptation for Television Viewing

CHRISTOPHER LYNN and ALEX SENTS

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.

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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.

### CT and TT phenotypes are associated with poor pregnancy outcomes when compared with CC phenotypes

CAROLINE MACLEAN, LUCIO REYES, MIGUEL DIMANLIG and LORENA MADRIGAL

Human Ecology and MicroEvolutionary (HEME) Center for the Study of Health Inequalities, Department of Anthropology, University of South Florida

Effects of the MTHFR C677T allele on reproduction include multiple complications. We compare frequency of fetal loss of CC, CT, and TT mothers using data collected from existing literature. **The ultimate purpose** of our project is to understand the evolutionary reasons why some populations maintain high T-allele frequencies with such deleterious effects on fertility. Data were taken from studies which included participants experiencing embryonic, fetal, or perinatal loss (cases). We also included studies which reported control groups. **The data:** Four comparable studies include cases and controls (Mehandjiev et al. 2019; Lee et al., 2013; Pogliani et al. 2010 Hwang et al. 2017). Total number of participants in these studies is 1418. Four studies that do not include controls are (Turgal et al. 2018, Mehandjiev et al. 2019; Kedar and Chandel, 2019; Makino et al., 2004). Total sample size of participants in these studies is 1027. **Results:** Frequency of the phenotypes does not differ between cases and controls (data not shown). However, observed and expected frequency of fetal loss differs significantly among the three phenotypes ( $X^2 = 228, 2, p < 0.001$ ). **Discussion:** Participants who carry the CT or TT phenotype were not significantly different from controls who did not experience fetal loss. The three phenotypes differ significantly in their frequency of embryonic, fetal, or perinatal loss. These studies took place in Eurasia. The populations with the highest T frequency are

the Indigenous people of Central America and Mexico. A cross-cultural approach to the study of this polymorphism demands a representative study of human diversity.

### Lifelong relationships: genomic data use after completion and publication of a study

RIPAN S. MALHI

Anthropology, University of Illinois Urbana-Champaign

Although not legally required, some human paleogenomics researchers adhere to an ethical standard to engage linked Indigenous communities (or at a minimum gain consent from the community/ies) for planned genomic analysis of ancient Ancestors. Once these studies have been completed, articles on the research studies are usually published in peer review journals and the data generated on the ancient individuals are uploaded to public databases. Some reasons often given by researchers for the use of public databases are so that the data is freely available to be confirmed as authentic by members of the ancient DNA community and so future studies can use the data in a comparative fashion to address questions of interest. However, as new analytical methods are developed, the potential to address novel or previously undiscussed questions, with low coverage paleogenomic data, grow. This means that the data may be used in a manner not consistent with the original agreement with the linked Indigenous community(ies) and may have social implications for those communities. As a result, researchers who generate and disseminate paleogenomic data of Ancestors have a lifelong duty to make sure that such data is used appropriately in accord with the decisions of the linked communities. To aid in this duty, I discuss the use of biocultural labels and databases with Indigenous oversight as ways to maintain the sovereignty of Indigenous communities while still having paleogenomic data accessible for research purposes.

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### The gut microbiome of common marmosets (*Callithrix jacchus*) living in an extremely hot and dry Caatinga environment

ELIZABETH K. MALLOTT<sup>1,2</sup>, PAUL A. GARBER<sup>3</sup>, ANNA C. MCKENNEY<sup>4</sup>, PETER M. FINNEGAN<sup>2</sup>, JULIO CESAR BICCA-MARQUES<sup>5</sup>, ANTONIO SOUTO<sup>6</sup>, NICOLA SCHIEL<sup>7</sup> and KATHERINE R. AMATO<sup>2</sup>

<sup>1</sup>Department of Biological Sciences, Vanderbilt University, <sup>2</sup>Department of Anthropology, Northwestern University, <sup>3</sup>Department of Anthropology, University of Illinois at Urbana-Champaign, <sup>4</sup>Department of Natural Resources and Environmental Sciences, University of Illinois at

Urbana-Champaign, <sup>5</sup>Escola de Ciências, Pontifícia Universidade Católica do Rio Grande do Sul, <sup>6</sup>Departamento de Zoologia, Universidade Federal de Pernambuco, <sup>7</sup>Departamento de Biologia, Universidade Federal Rural de Pernambuco

Many factors shape the gut microbiome of nonhuman primates, including diet, seasonality, reproductive status, age, group membership, sex, and pathogen exposure. Assessing the relative contributions of multiple factors is important for understanding host-environment-microbiome interactions. Here, we examine if season and group membership influence the gut microbiome composition and function of common marmosets living in a hot and dry Caatinga environment in northeastern Brazil (mean annual rainfall=337mm). In this habitat, marmosets experience heat and water stress, especially during the dry season. Between 2015 and 2016, we collected 60 fecal samples (dry season=36, wet season=24), extracted DNA, and performed 16S rRNA gene sequencing and shotgun metagenomic sequencing. While season did not have a strong effect on gut microbiome composition based on weighted UniFrac distances (PERMANOVA:  $R^2=0.02, p=0.18$ ), group membership explained 33% of the variation in community composition (PERMANOVA:  $R^2=0.33, p<0.01$ ). In contrast, when examining gut microbiome function, while group was not associated with changes in gene family composition and pathway abundance (PERMANOVA: both  $R^2=0.39, p=0.29$ ), season was associated with variation in microbiome function (PERMANOVA:  $R^2=0.13, p=0.06$ ;  $R^2=0.16, p=0.05$ ). Specifically, there was an increase in the abundance of carbohydrate and vitamin biosynthetic pathways during the dry season (LDA scores > 2.0). In sum, group membership has a stronger modulating effect on gut microbiome composition than season in this population and increases in the abundance of carbohydrate and vitamin biosynthetic pathways may help marmosets to cope with seasonal changes in diet, thermal environment, and water stress in this extremely dry environment.

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### Tooth crown mineralization and mandibular stiffness in growing lemurs

NANAMI MANO<sup>1</sup>, CHRISTOPHER J. VINYARD<sup>2</sup>, VALERIE B. DELEON<sup>3</sup> and TIMOTHY D. SMITH<sup>1</sup>

<sup>1</sup>School of Physical Therapy, Slippery Rock University, <sup>2</sup>Department of Anatomy and Neurobiology, Northeast Ohio Medical University, <sup>3</sup>Department of Anthropology, University of Florida

Strepsirrhines vary in pace of dental maturation and weaning age. Here, dentocranial data from late fetal to juvenile ages are compared in *Lemur catta* and *Varecia* spp., species with widely

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different dental eruption schedules and moderately divergent diets. Amira software was used to measure crown volume of dp4 as well as M1 and create cross-sectional slices of the mandible at the level of dp4. The cross-sectional area (CSA) and maximum bending resistance (Imax) were determined using BoneJ. Based on the specimens of known age, M1 is poorly mineralized at birth in *Varecia*. The volume of a one-month-old specimen was only 0.5% of the adult crown compared to ~25% in *Lemur*; less disparity exists for dp4 with 30% in *Varecia* compared to 43% in *Lemur*. In late fetuses, M1 is the smaller cusp, but overtakes dp4 volume as head size increases; this occurs more rapidly (at smaller head sizes) in *Lemur*. Thus, M1 mineralization is far more rapid in *Lemur*. CSA and Imax share a linear relationship with palatal length (proxy for snout length) in *Lemur*. In contrast, preliminary results on *Varecia* suggest the mandible, like crown volume, follows an exponential growth curve evidenced by delayed growth relative to *Lemur*, followed by rapid growth related to load resistance. Results imply mandibular load resistance and cusp mineralization follows a shared developmental trajectory at specific dental levels. We hypothesize the more rapid development of tooth crowns and mandibular stiffness in *Lemur* compared to *Varecia* may relate to a greater dietary dependence on leaves.

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### Family-focused COVID-19 research: leveraging tools and insights from biocultural anthropology

MELANIE A. MARTIN<sup>1,3</sup>, BEATRICE Q. CAFFE<sup>2</sup>, AMANDA KUNKLE<sup>1</sup>, ELEANOR BRINDLE<sup>3</sup>, DAN T.A. EISENBERG<sup>1,3</sup> and COURTNEY L. MEEHAN<sup>2</sup>

<sup>1</sup>Department of Anthropology, University of Washington, <sup>2</sup>Department of Anthropology, Washington State University, <sup>3</sup>Center for Studies in Demography and Ecology, University of Washington

Globally, COVID-19 infection and mortality rates have been lowest in pediatric groups, however, the social and behavioral effects of containment have had outstanding impacts on families with infants and young children (IYC). Barriers to testing and inclusion of IYC in COVID-19 research has stymied our understanding of the disease and evidence-based public health, educational, and economic responses to the pandemic. For example, in many studies, differential transmission risks and protective immune responses among IYC are not described, and infectious outcomes of all children under age 18 are analyzed together. Studies promoting the benefits of saliva sampling in place of nasopharyngeal swabs for wider viral surveillance have often not considered the logistical challenges posed by IYC for this methodology.

In July of 2019, we began recruiting COVID+ U.S. mothers for a study of IYC health and infectious outcomes in relation to household exposures and feeding, sleep, and care practices. In this talk, we discuss protocols developed for survey and no-contact biomarker collection from mothers and IYC during and following maternal infection. We further discuss how household composition and infectious dynamics influenced maternal decisions or abilities to self-isolate and take other recommended precautionary measures related to IYC care and feeding. As of this writing, COVID-19 infections are rising in younger age groups owing to changing behaviors and exposures among demographic groups. Our participants' experiences underscore the need for research methodologies and public health recommendations that specifically consider the diverse challenges faced by families with IYC.

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### Ongoing evolution of the FADS locus from the Paleolithic to the present-day

IAIN MATHIESON

Department of Genetics, University of Pennsylvania

The FADS genes play an important role in the synthesis of long-chain plasma unsaturated fatty acids, critical for many cellular and organismal processes including cell membrane formation. A derived haplotype at this locus is strongly associated with lipid levels and related phenotypes in present-day populations and has fluctuated in frequency over human evolutionary timescales likely in response to changes in diet. Using both ancient and present-day genetic data we are able to reconstruct the history of this haplotype across a broad range of human populations, including at least four independent episodes of selection.

In particular, we show that after ancient selection for the derived allele predating the out-of-Africa bottleneck, the ancestral allele was selected in Upper Paleolithic Eurasia. Later, the derived allele was again selected independently in Holocene Europe and East Asia, with a selection coefficient of 0.7-0.8%. This recent selection was likely associated with the independent development of agriculture in both regions. Finally, we show that the recent episode of selection in Europe is still ongoing today, with a similar selection coefficient—over the past 50 years, carrying the derived allele is associated with an approximately 0.74% increase in number of children ever born in a Northern European cohort. The unique evolutionary history of this functionally important variant underscores the value of combining the study of ancient and present-day DNA to understand adaptive evolution in our species.

### Gender reversals in social networks based on prevailing kinship norms in the Mosuo of China

SIOBHÁN M. MATTISON<sup>1,2</sup>, ADAM Z. REYNOLDS<sup>1</sup>, RUIZHE LIU<sup>1</sup>, GABRIELLE D. BACA<sup>1</sup>, MENG ZHANG<sup>3</sup> and CHUN-YI SUM<sup>4</sup>

<sup>1</sup>Anthropology, University of New Mexico,

<sup>2</sup>Anthropology, National Science Foundation,

<sup>3</sup>Cultural Heritage and Museology, Fudan

University, <sup>4</sup>College of General Studies, Boston University

Kinship is hypothesized to structure access to social support, yet how it does so remains unresolved. Kin are more readily available to women with uxorilocal residence than with virilocal residence and vice versa for men, which is expected to produce differences in social support networks. In particular, gender-biased residence patterns might be expected to produce broader networks for females in matriliney and the reverse in patriliney [H1]. Alternatively, if men leverage social capital more than women regardless of residence, we may see that [H2] males have broader networks or more centralized positions in both contexts. We compare these hypotheses using tools from social network analyses and data on male and female social networks in matrilineal and patrilineal Mosuo communities. In support of H1, we find that female networks are broader (have higher edge-density) than male networks in the matrilineal community, while the reverse is observed in the patrilineal community. Additionally, we find that female networks are more degree centralized in matrilineal communities whereas male networks are more degree centralized in patriliney. These results support the idea that the access to kin affects social support networks, which may have important consequences on health and well-being.

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### Phylogenetic analysis of sex-biased natal dispersal in primates

KEELY Q. MAYNARD and STEPHANIE A. POINDEXTER

Anthropology, University at Buffalo

The evolution of dispersal patterns in primates has been related to behavioral flexibility, as populations adapt to changing social and ecological pressures. Behavioral flexibility is constrained by the evolutionary history of the taxa limiting behavioral adaptation to a certain point. We aim to investigate the ancestral state of natal dispersal to understand the evolutionary history and limitations on dispersal patterns. We expand upon previous research by including more taxa with a particular focus on strepsirrhines. Due to the prevalence of male-biased dispersal in other mammalian species, we hypothesize that the ancestral characteristic for primate natal

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dispersal is male-biased dispersal and female philopatry. We collected data on natal dispersal patterns, social structure, and reproductive strategies in 61 primates. We ran a maximum likelihood (ML) ancestral character estimation. The ML model ( $L_x = -57.5$ , rate = 4.48, SE = 1.07) provided weak support in favor of our hypothesis of male-biased dispersal as the ancestral characteristic. Using *phylo.D*, we calculated the phylogenetic signal (D) for each dispersal pattern. Both sex-biased ( $F - D_{\text{estimate}} = 0.284$ ,  $p = 0.008$ ;  $M - D_{\text{estimate}} = 0.187$ ,  $p < 0.0001$ ) are significantly conserved under Brownian evolution. Therefore, we tested if dispersal constrains the evolution of reproductive and social behaviors. We found that there was a negative evolutionary correlation between bisexual dispersal and the promiscuous mating system (Likelihood Ratio Test = 9.822,  $p = 0.04$ ). Our results confirm previous research that dispersal patterns are a constraining variable on behavioral flexibility.

### Allopregnanone Serum Concentrations in Term and Preterm Birth: An Exploratory Study

GABRIELLA B. MAYNE<sup>1</sup>, UWE CHRISTIANS<sup>2</sup>, DANA DABELEA<sup>3</sup>, K. JOSEPH HURT<sup>4</sup> and ANNA G. WARRENER<sup>1</sup>

<sup>1</sup>Department of Anthropology, University of Colorado, Denver, <sup>2</sup>C42 Clinical Research & Development, Department of Anesthesiology, University of Colorado Anschutz Medical Campus, <sup>3</sup>Lifecourse Epidemiology of Adiposity and Diabetes (LEAD) Center, University of Colorado Anschutz Medical Campus, <sup>4</sup>Department of Obstetrics & Gynecology, Maternal Fetal Medicine and Reproductive Sciences, University of Colorado School of Medicine

Preterm birth (<37 weeks' gestation) is the leading cause of infant morbidity and mortality in the US and is associated with substantial racial/socio-economic disparities. Maternal stress is a key variable affecting maternal-placental-fetal-neuroendocrine system plasticity. Allopregnanone, a "stress-responsive" neuroactive steroid, plays a role in stress pathophysiology, and animal models demonstrate an association between low ALLO and reduced gestational length. Therefore, we hypothesized that ALLO is lower in women who deliver preterm in a nested case-control study using banked serum samples. We included healthy, low-risk women with singleton pregnancies and excluded subjects with major medical illness, preeclampsia, hypertension, or diabetes. We matched preterm cases with term controls (1:1) by gestational age (GA) at first blood draw and least difference in time between first and second blood draw (N=27 per group). We performed a new high-performance liquid chromatography tandem mass spectrometry assay to quantify ALLO at two points in gestation (sample 1 mean GA 16.85 weeks, range 12.43-25 weeks; sample 2 mean GA 26.51 weeks, range 22.3-32

weeks). Statistical tests were ANOVA and T-test. There was no significant difference between term and preterm delta ALLO (3.45± 2.71 ng/ml vs. 2.97± 1.75 ng/ml,  $p = .446$ ), and thus our findings do not support our hypothesis. Age, socio-economic status and self-reported race/ethnicity were not significantly related to ALLO. However, there was a strong inverse relationship between maternal pre-pregnancy BMI and ALLO ( $p < 0.001$ ). This inverse relationship suggests maternal energetic status plays an important role in determining ALLO variation during pregnancy and warrants further investigation.

### Prevalence of stress and disease indicators by sex and age-at-death in a medieval cemetery (11<sup>th</sup>-12<sup>th</sup> c) from Giecz, Poland

REBECCA C. MAYUS<sup>1,2</sup>, GIUSEPPE VERCELLOTTI<sup>2,3</sup>, HEDY JUSTUS<sup>2</sup> and AMANDA AGNEW<sup>1,2</sup>

<sup>1</sup>Skeletal Biology Research Laboratory, The Ohio State University, <sup>2</sup>Anthropology, The Ohio State University, <sup>3</sup>Institute for Research and Learning in Archaeology and Bioarchaeology, Columbus, Ohio

The formation of the Polish state in the 10<sup>th</sup> c CE led to major changes in the daily lives of medieval Poles, including the implementation of feudalism and the adoption of Christianity. Examination of skeletal indicators can reveal the effects of socio-cultural changes on human health, and whether experiences differed based on an individual's identity within their community. The objective of this research was to determine whether patterns of skeletal stress varied among individuals interred at the 11<sup>th</sup> to 12<sup>th</sup> c CE cemetery of Giecz, Poland based on sex and age-at-death. 140 adult skeletons (89 male, 51 female) were examined for presence/absence of the following indicators: cribra orbitalia, porotic hyperostosis, linear enamel hypoplasia, caries, abscesses, antemortem tooth loss, periostitis, and degenerative joint disease. Additionally, stature was estimated from femoral length using population-specific equations. With the exception of sexual dimorphism in stature, indicators did not reveal significant differences by sex, suggesting similar levels of stress were experienced by both males and females. Caries, abscesses, antemortem tooth loss, and degenerative joint disease prevalence increased with age, likely reflecting natural senescence processes rather than population-specific stressors. A positive association between stature and age was found, which may indicate individuals with higher frailty died at younger ages. Alternatively, this trend may reflect cultural buffering of certain individuals throughout their entire lifespan, allowing taller stature and longer lives. Future research will examine severity of paleopathology indicators and incorporate mortuary evidence to determine whether subtler trends exist within the assemblage.

### Revised estimates of stature-at-death and body proportions for KNM-WT 15000 (*Homo erectus*)

ROBERT C. MCCARTHY<sup>1</sup>, DALYA KANANI<sup>1</sup>, DEBORAH L. CUNNINGHAM<sup>2</sup> and DANIEL J. WESCOTT<sup>2</sup>

<sup>1</sup>Department of Biological Sciences, Benedictine University, <sup>2</sup>Department of Anthropology, Texas State University

The only reasonably-complete specimen of early *Homo erectus*, KNM-WT 15000, is a juvenile requiring extrapolation to predict adult body size and shape. Recent adult body size reconstructions have relied on limb bone lengths either directly as a "starting point" for growth projection or indirectly as the basis for estimating stature-at-death. One previous study found a considerable discrepancy between regression estimates of stature-at-death from limb bones (154–169 cm) and anatomical estimates (141–147 cm). New insights on the structure of KNM-WT 15000's vertebral column, thorax, and pelvis along with methodological innovations make this an opportune time to reconsider anatomical reconstruction as a method for addressing questions about KNM-WT 15000's stature-at-death, body proportions, and ontogeny.

We adjusted KNM-WT 15000's vertebral heights to account for missing ring epiphyses using data from a small sample of subadult modern human skeletons. We used existing regression equations to estimate talocrural height, cervical vertebral length, and total vertebral length; reconstructed living height from skeletal height using anatomical and regression-based methods; and reconstructed anterior trunk height using equations from the biomedical literature.

New stature-at-death point estimates (143–146 cm) and confidence intervals (138–150 cm) agree remarkably well with previous anatomical estimates but do not overlap with larger estimates based on limb bone lengths. Compared to adult and juvenile modern humans, KNM-WT 15000's limbs were disproportionately long in relation to the trunk, suggesting either that limb:trunk proportions differed in *H. erectus* or that KNM-WT 15000's trunk growth followed a delayed schedule compared to modern human standards.

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### Life Aquatic: Taphonomic Change Documented in Florida's Waterways

SHANNON MCCARTY and HEATHER WALSH-HANEY

Department of Justice Studies, Florida Gulf Coast University

Humans continue to modify their environment after death as their corporal remains become host to numerous organisms that in turn modify their host. Forensic anthropologists evaluate these postmortem changes to estimate time since

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death (TSD), identify the scene, and reveal the postmortem "life" of the remains. Meta-analyses of forensic cases as well as controlled animal experiments in aquatic environments is limited. This study aims to delineate the aquatic taphonomic modifications to human remains recovered from bodies of water within Florida. Through the Human Identity and Trauma Analysis Lab, we evaluated 58 forensic anthropology cases from aquatic environments. Twenty-four evidenced aquatic taphonomic change. These human remains were discovered in canals, culverts, harbors, and beaches with an TSD that ranged from one day to over 75 years. We grouped the aquatic organisms into adhering marine taxa, such as barnacles and serpulid worms versus bioerosion scavengers like sharks and fish. We expected the taphonomic changes from adhering organisms to be significantly associated with longer TSD estimates while the bioerosion scavengers would be strongly associated with shorter TSD estimates. We performed a chi-square test and revealed significance ( $p < 0.05$ ) between TSD and both groups of aquatic organisms. While our sample size barely met the assumptions intrinsic to chi-square analysis, the descriptive statistics supported our hypothesis. Consequently, this study highlights the need for further research with the goal of providing more reliable future forensic anthropological analyses.

### Future Directions in Anthropological Pedagogy: Insights into the role of technology in teaching anthropological genetics from the Covid-19 pandemic

KATIE MCCORMACK and JADA BENN-TORRES  
Anthropology, Vanderbilt University

The shift to distance learning in response to the ongoing COVID-19 pandemic required university instructors to navigate novel technologies and teaching strategies in order to redesign courses that effectively promote student engagement with material and accurately evaluate learning. This ongoing experiment in online pedagogy has raised numerous questions about how to create an environment conducive to collaborative learning without face-to-face instruction. Although distance learning is largely framed as temporary and necessarily inferior to in-person instruction, the challenges presented by this undertaking are also an opportunity to reexamine the role of technology in undergraduate education. In this presentation, I offer some considerations on the future of pedagogy within anthropological genetics, reflecting on insights as a trainee working as a teaching assistant during this period of change and uncertainty in education. Specifically, I focus on how online learning can better facilitate student participation relative to in-person lectures. Although this effect has not been universal, distance learning has the potential to facilitate interactions between students and the

instructor that are more engaging and less intimidating. Digital formats can also integrate a variety of online resources that reinforce understanding of subjects that are difficult to grasp in traditional lecture settings. These considerations of participation and clarification are particularly important given the diversity of student backgrounds and the interdisciplinary nature of the field as a whole. Although many eagerly await the return to widespread in-person instruction, the successes and limitations of distance learning should inform how we use technology to engage with students moving forward.

### An X/Y chromosome quantitative PCR protocol for assessing secondary DNA transfer: Implications for forensic cases

SAMANTHA M. MCCRANE<sup>1,2</sup> and CONNIE J. MULLIGAN<sup>1,2</sup>

<sup>1</sup>Anthropology, University of Florida, <sup>2</sup>Genetics Institute, University of Florida

Primary touch DNA is deposited when individuals shed DNA-containing skin cells or sweat directly onto an object. There is also the possibility of secondary DNA transfer when an individual's DNA is transferred via an intermediary to an object that the individual never directly touched. These forms of touch DNA are increasingly cited as evidence in criminal court proceedings despite a lack of thorough understanding of the factors that affect touch DNA transfer. The high cost of forensic DNA kits and capillary-based DNA analysis systems is one barrier to further research. This study utilized a cost-effective X/Y chromosome quantitative PCR protocol to test forensically relevant factors. Specifically, a male and then a female held an AR-15 gun grip for 5 minutes, after which the gun grip and the female's hand were independently wet swabbed. Fluorescently-tagged sex determination markers were used to detect primary DNA transfer (X or Y markers on the gun grip) and secondary DNA transfer (Y markers on the female's hand). Self-reported age, sex, and presence/absence of skin conditions that enhance skin sloughing were recorded for all participants and tested for association with DNA transfer. In preliminary studies, individuals with eczema or psoriasis deposited primary touch DNA in significantly more trials than individuals without any skin condition. Our finding suggests that these skin conditions increase the probability of touch DNA transfer. A better understanding of secondary DNA transfer is critical to guard against wrongful convictions, especially since many skin conditions disproportionately affect already marginalized groups.

### 3D Functional Anatomy of Nuchal Musculature in Primates

FAYE MCGECHIE<sup>1</sup>, NEYSA GRIDER-POTTER<sup>2</sup>, THIERRA K. NALLEY<sup>3</sup>, ELLE FRICANO<sup>3</sup>, KEVIN M.

MIDDLETON<sup>1</sup>, CASEY M. HOLLIDAY<sup>1</sup> and CAROL V. WARD<sup>1</sup>

<sup>1</sup>Pathology and Anatomical Sciences, University of Missouri, <sup>2</sup>Department of Structural Medicine, Rocky Vista University, <sup>3</sup>Department of Medical Anatomical Sciences, Western University of Health Sciences

The nuchal region is important for understanding variation in postural and locomotor behaviors within primates. To date, there has not yet been a quantitative study of comparative nuchal muscle functional morphology, partly due to the complexity of this musculoskeletal system. We applied novel methodologies to visualize and compare nuchal musculature among taxa to explore the relationship between trunk posture, head turning behaviors, and forelimb-dominated below branch suspensory behaviors on the head and neck musculature across primate taxa. Contrast-enhanced CT imaging, 3D muscle fascicle-tracking, and 3D muscle visualization were all used to compare the attachment sites, orientations, and estimates of force for 19 muscles across five species that displayed contrasting positional behaviors. Ternary diagrams were used to compare the force generating capability and orientation of muscle bellies. Results show that most muscle forces scale isometrically, but musculature varies according to neck function. Suspensory species have a more dorsoventrally oriented cranial belly of the trapezius than non-suspensory taxa. Orthograde primates tend to have a relatively less powerful longissimus capitis compared to pronograde primates. *Carlito*, notable for its dramatic head turning behaviors, has a more transversely oriented and more powerful sternocleidomastoid in addition to more powerful obliquus capitis superior muscle. The latter is also seen in *Propithecus*. These findings support the hypothesis that the moment-generating capacities of key nuchal muscles are related to posture and locomotion in primates. Therefore, osteological correlates of observed variation in nuchal musculature can be useful for reconstructing behavior in fossil primates.

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### Noxious Smoke and Silent Killers: Pollutant Exposure during England's Industrial Revolution

SARA A. MCGUIRE<sup>1</sup>, MARK HUBBE<sup>1</sup>, ALI POURMAND<sup>2</sup> and WILLIAM J. PESTLE<sup>3</sup>

<sup>1</sup>Department of Anthropology, The Ohio State University, <sup>2</sup>Neptune Isotope Lab, Department of Marine Geosciences, Rosenstiel School of Marine and Atmospheric Science, University of Miami, <sup>3</sup>Department of Anthropology, University of Miami

The consequences of industrialization in England include an increase in exposure to pollution and the deterioration of urban environments. Growing

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industrial cities especially saw an increase in pollution, as compared to the more rural agrarian countryside, so often assumed to have provided a comparatively clean and idyllic escape from the noxious fumes of industry. This study examines subsets of two historic English populations (Barton-upon-Humber, n = 40; South Shields, n = 54) from the Industrial period (c. 1760 AD to 1850 AD) to examine pollutant exposure in environments that are midway along the spectrum between rural villages and industrial cities. Trace element analysis was used to examine exposure to pollutants that transfer into bones and are retained postmortem (arsenic, barium, and lead). The results of elemental analysis for 94 individuals were contrasted according to collection using Kruskal-Wallis tests. All trace element values fell within ranges of dangerous exposure levels (arsenic =  $1.00 \pm 1.05$  ppm; barium =  $63.77 \pm 41.89$  ppm; lead =  $36.52 \pm 31.37$  ppm). Moreover, individuals from the larger and more industrial town of South Shields had significantly higher values for arsenic ( $p < 0.001$ ) and barium ( $p = 0.013$ ), while individuals from the smaller and more rural town of Barton-upon-Humber had significantly higher values for lead ( $p = 0.020$ ). As such, this research provides evidence that exposure to pollutants may not have been confined to industrial cities, and that at least the individuals from Barton-upon-Humber were not necessarily protected by their more rural and agrarian environment.

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### Is Sleep Disturbance in Menopause Explained by Evolutionary Mismatch? Evidence from Three Cohorts of Guatemalan Maya

LEELA MCKINNON<sup>1</sup>, DAVID R. SAMSON<sup>1</sup>, CHARLES L. NUNN<sup>2,3</sup>, AMANDA ROWLANDS<sup>4</sup>, KATRINA G. SALVANTE<sup>4</sup> and PABLO A. NEPOMNASCHY<sup>4</sup>

<sup>1</sup>Department of Anthropology, University of Toronto Mississauga, <sup>2</sup>Department of Evolutionary Anthropology, Duke University, <sup>3</sup>Duke Global Health Institute, Duke University, <sup>4</sup>Maternal and Child Health Laboratory, Faculty of Health Sciences, Simon Fraser University

Improvements in nutrition, sanitation, and healthcare have dramatically extended the human lifespan, resulting in a higher proportion of women having significant lifespans beyond menopause. Women undergoing menopause in Western contexts often report considerable sleep disturbance. These menopause-associated sleep disruptions may reflect evolutionary mismatch. In particular, nuclear family living in Western societies often results in decreased inter-generational social integration, a situation that is in contrast to the high levels of sociality and group living of human ancestral environments.

To better understand sleep patterns associated with menopause in non-Western populations, we investigated sleep in Guatemalan Maya women spanning a life history range from puberty to menopause (age range: adolescent girls=12-16 years, younger adult women=34.4-43.7 years, menopausal women=46-80 years). We tested the hypothesis that menopausal women living in societies with less social isolation and more inter-generational family support and allomaternal care – as in this Maya population – show sleep characteristics that differ from Western populations. Thus, we predicted that menopausal women will not exhibit shorter or less efficient sleep than younger adult women or adolescents. Consistent with this prediction, we found that menopausal women's sleep was longer (mean=6.85 hours, SD=0.95) and more efficient (mean=80.86%, SD=7.88) than younger adult women's sleep (mean duration=6.45 hours, SD=1.08; mean efficiency=77.35%, SD=9.15), and in fact was more similar to adolescent sleep (mean duration=7.08 hours, SD=0.86; mean efficiency=80.82%, SD=4.73). Our results suggest that poor sleep is not a universal consequence of menopause, and that a cultural consideration of social integration is critical to understanding aging and sleep health.

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### Retrofit, Reform, Re-envision: Lessons Learned While Engaging with Pregnancy Registries

MONICA R. MCLEMORE<sup>1</sup>, YALDA AFSHAR<sup>2</sup>, IFEYINWA V. ASIODU<sup>1</sup>, BRITTANY D. CHAMBERS<sup>3</sup>, HENDRIX E. ERHAHON<sup>1</sup>, VALERIE FLAHERMAN<sup>4</sup>, STEPHANIE GAW<sup>5</sup> and VANESSA JACOBY<sup>5</sup>

<sup>1</sup>Family Health Care Nursing Department, University of California, San Francisco, <sup>2</sup>Department of Obstetrics and Gynecology, University of California, Los Angeles, <sup>3</sup>Department of Epidemiology and Biostatistics, University of California, San Francisco, <sup>4</sup>Department of Pediatrics, University of California, San Francisco, <sup>5</sup>Department of Obstetrics, Gynecology, and Reproductive Sciences, University of California, San Francisco

The COVID-19 pandemic has laid bare the core issues that intersect the social, clinical, economic and structural determinants of health. In the context of the current Black Maternal Health crisis and COVID-19, it was essential to document the impact COVID-19 has on people with the capacity for pregnancy, particularly for Black, Indigenous, and People of Color (BIPOC) and queer communities. In March 2020, the Pregnancy CoRonaVirus Outcomes RegIsTrY (PRIORITY) launched. PRIORITY is a nationwide study of 1,300 pregnant or recently pregnant people who are either under investigation for COVID-19 or have been confirmed to have COVID-19. First, PRIORITY was retrofitted with a reproductive health equity and birth justice CORE to establish authentic and

transparent community engagement to ensure data integrity and full participation of people experiencing the greatest burdens of COVID-19. Next, in an attempt to reform health services provision and public health measures for BIPOC communities, the CORE recruited and convened a national community advisory council purposively structured to represent BIPOC people from diverse backgrounds and from diverse geographical locations to assist in decision-making and regional recruitment across the United States. Finally, to reimagine the power of the registry study design, the research priorities of affected communities was implemented to reinforce or shift the focus of the study to amplify, capture, and reflect the questions most important to BIPOC communities. Lessons learned establishing the CORE, retrofitting it to PRIORITY and actionable next steps will be described in this session.

*The PRIORITY registry study has multiple funding sources that can be found on the websites here, priority.ucsf.edu/our-supporters-0*

### Big leapers and small climbers: Does size matter?

ALLISON MCNAMARA<sup>1</sup> and MICHELLE BEZANSON<sup>2</sup>  
<sup>1</sup>Anthropology, University of Texas at Austin,  
<sup>2</sup>Anthropology, Santa Clara University

Primatologists who examine positional behavior depend on body mass estimates to predict positional outcomes. Fleagle and Mittermeier (1980) provided a rich context for the interpretation of positional behavior. In their model, smaller primates were expected to leap more and larger primates were expected to climb more. Since their important publication, most examinations of positional behavior include or entirely focus their discussion on body mass predictions. We present a comparative analysis of the relationship between body mass and locomotion and discuss how various methods of studying locomotion and body mass influence results. We reviewed 43 peer reviewed papers on positional behavior published from 1996-2016 covering 61 primate species. We compiled proportions of locomotor modes that were reported, and then tested if published body mass predicted the top locomotor mode reported in the publication. Quadrupedalism is the most common locomotor mode used among primate species, therefore we analyzed the odds that a species exhibited leaping or climbing more than quadrupedalism based on its body mass. Results indicate that there is a significant inverse relationship between body mass and leaping being the number one locomotor mode reported for a species. Interestingly, the odds of a species using any other locomotor mode more frequently than quadrupedalism did not have a significant relationship with body mass. This analysis indicates that the relationship between locomotion and body

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mass is not straightforward and is influenced by a multitude of factors including environment, taxonomy, observational methods, and how body mass is measured, estimated, and reported.

### New hominin remains from the Leado Dido'a area of Woranso-Mille, Ethiopia

STEPHANIE M. MELILLO<sup>1</sup>, LUIS GIBERT<sup>2</sup>, BEVERLY Z. SAYLOR<sup>3</sup>, ALAN DEINO<sup>4</sup>, MULUGETA ALENE<sup>5</sup>, TIMOTHY M. RYAN<sup>6</sup> and YOHANNES HAILE-SELASSIE<sup>7</sup>

<sup>1</sup>Department of Human Evolution, MPI-EVA, <sup>2</sup>Departament de Mineralogia, Petrologia i Geologia Aplicada Facultat de Ciències de la Terra, Universitat de Barcelona, <sup>3</sup>Department of Earth, Environmental and Planetary Sciences, Case Western Reserve University, <sup>4</sup>Berkeley Geochronology Center, <sup>5</sup>School of Earth Sciences, Addis Ababa University, <sup>6</sup>Department of Anthropology, Pennsylvania State University, <sup>7</sup>Department of Physical Anthropology, Cleveland Museum of Natural History

Fossils discovered at Woranso-Mille, Ethiopia have challenged the idea that *Australopithecus afarensis* was the sole hominin present in the Afar Depression during the ca. 3.5-3.3 Ma period. However, the extent of spatial and temporal overlap among hominin taxa remains unclear. Jaws and teeth attributed to *Australopithecus deyiremeda* and the taxonomically unattributed Burtele foot were recovered from >3.47-3.33 Ma strata in the Burtele area of Woranso-Mille that are contemporaneous with *A. afarensis* specimens from Maka, Dikika and Hadar. Yet evidence of *A. afarensis* at Woranso-Mille during this period was limited.

Here, we describe new hominin fossils from a collection locality in the Leado Dido'a area of Woranso-Mille (LDD-VP-1), which lies just 3.5 km southeast of Burtele. Geochemical identification of a Sidi Hakoma Tuff (SHT) correlate and measurements of paleomagnetism were combined to date the LDD-VP-1 strata to 3.41-3.33 Ma.

We assign most specimens in the LDD-VP-1 sample to *A. afarensis*, based on diagnostic morphology and metric comparison of the mandible, maxilla, canines and premolars. These specimens fall largely within the range of variation previously documented for *A. afarensis*, but increase the frequency of some rare morphological variants. However, one isolated third molar is extremely small and its taxonomic affinity is currently unknown. The value added with this sample lies in its contribution to controlling for spatiotemporal differences among site-samples in the *A. afarensis* hypodigm, and its contemporaneity with non-*A. afarensis* specimens at Burtele.

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### The differential influence of climate on cranial variation in North and South Americans: an integral approach combining morphometric, genetic, and environmental data

LUMILA P. MENENDEZ<sup>1,2</sup>, ALEXANDRA GROSHEVA<sup>3</sup>, TAYISIA SYUTKINA<sup>4</sup>, TSUNEHICO HANIHARA<sup>5</sup>, MARK HUBBE<sup>6</sup> and ANDREJ EVTEEV<sup>7</sup>

<sup>1</sup>Department Anthropology of the Americas, University of Bonn, <sup>2</sup>Evolutionary Anthropology, Konrad Lorenz Institute for Evolution and Cognition Research, <sup>3</sup>Vavilov Institute of General Genetics, Russian Academy of Science, <sup>4</sup>Institute of Ethnology and Anthropology, Russian Academy of Science, <sup>5</sup>Department of Anatomy, Kitasato University School of Medicine, <sup>6</sup>Department of Anthropology, Ohio State University, <sup>7</sup>Anuchin Research Institute and Museum of Anthropology, Moscow State University

The main factors behind cranial variation of humans in the Americas have been discussed for a century and a half. In spite of this, comprehensive studies combining morphological, genetic, and environmental data in an extensive sample and wide geographic area are still lacking. This paper analyzes the influence of climate on cranial variation in high latitude populations living in temperate to cold environments of North and South America. For this, we compiled morphometric data from publicly available databases (Debets, Pucciarelli), paired it with climatic and genomic data, and applied an exhaustive set of statistical methods (Partial Least Square, Spatial Autoregression Analysis, and Mantel tests). Our results indicated that populations living at cold regions are characterized by an increment in nasal height, facial and orbital heights and widths, decrease in facial protrusion, as well as larger cranial vaults. Both correlation matrices and linear regression methods showed that a moderate to large amount of this variation could be accounted as a result of climatic impact on morphology. Populations from southern South America present the strongest climate signal (PLS, SC=29.4%). The southern South Americans show more pronounced facial changes (Mantel,  $r=0.43$ ,  $P<0.01$ ; SAR,  $r=0.75$ ;  $P<0.01$ ), while the populations living at cold climates in North America exhibit most of the changes in the cranial vault (Mantel,  $r=0.24$ ,  $P=0.07$ ; SAR,  $r=0.50$ ,  $P=0.20$ ). Overall, those changes are supported by physiological, morphometric, genetic, and ecological predictions; and we conclude that they could be explained as the result of local evolutionary processes and cultural adaptations as well.

This project was developed thanks to a visiting (AE) and a postdoc fellowship (LPM) provided by the Konrad Lorenz Institute for Evolution and Cognition Research (KLI, Klosterneuburg).

### Contrasting craniodental lesion rates in platyrrhines

MATTHEW MERWIN<sup>1</sup>, CLAIRE A. KIRCHHOFF<sup>1</sup>, D. REX MITCHELL<sup>2</sup>, SIOBHÁN B. COOKE<sup>3,4</sup> and CLAIRE E. TERHUNE<sup>5</sup>

<sup>1</sup>Department of Biomedical Sciences, Marquette University, <sup>2</sup>Center for Anatomical Sciences, University of North Texas Health Science Center, <sup>3</sup>Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, <sup>4</sup>New York Consortium in Evolutionary Primatology Morphometrics Group, <sup>5</sup>Department of Anthropology, University of Arkansas

As demonstrated in humans, craniodental pathologies reflect dietary, ecological, and social adaptations, but such studies on non-human primates are rare. We compare rates of craniodental lesions in five platyrrhine species: *Alouatta seniculus* ( $n=48m$ , 58f), *Ateles geoffroyi* ( $n=26m$ , 26f), *Cebus capucinus* ( $n=48m$ , 42f), *Sapajus apella* ( $n=51m$ , 52f), and *Saimiri boliviensis* ( $n=37m$ , 36f). Each adult specimen was evaluated for temporomandibular joint (TMJ) osteoarthritis, antemortem tooth loss, periodontal disease, caries, pulp cavity exposure, abscesses, tooth crowding/malocclusion, craniofacial trauma, and other pathologies using standard criteria. Fisher's exact tests for relationships between lesions, sex, and species differences were carried out in SPSS. *Alouatta* exhibits sex differences in rates of pulp cavity exposure ( $p=0.023$ ) and dental abscesses ( $p=0.018$ ); *Sapajus* in the rate of other pathologies ( $p=0.01$ ). Differences in pathology rates for monkeys with versus without TMJ osteoarthritis were observed for caries (*Saimiri*,  $p=0.022$ ), pulp cavity exposure (*Saimiri*,  $p=0.003$ ), dental abscess (*Saimiri*,  $p=0.022$ ), and other trauma (*Sapajus* females,  $p=0.038$ ). Also of note are differences in lesion rates between taxa. *Alouatta* males often differed from the other samples, including the lesion rates for pulp cavity exposure ( $p=0.023-0.001$ ), dental abscesses ( $p=0.024-0.004$ ), and trauma ( $p=0.035-0.029$ ). *Ateles* also differed from other samples, including for TMJ osteoarthritis ( $p=0.043$ ), periodontal disease ( $p=0.044-0.012$ ), abscesses ( $p=0.016-0.009$ ), and dental crowding ( $p=0.025$ ). Interestingly, these differences may fall more closely along taxonomic lines, with *Alouatta* (males) and *Ateles* differing from *Cebus* and *Sapajus* rather than one another. Future directions include incorporating pathology analysis with tooth wear and craniodental morphometrics.

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### Ulna curvature in *Sahelanthropus*, the StW 573 ("Little Foot") *Australopithecus*, and other early hominins

MARC R. MEYER<sup>1</sup>, ISABELLA FX. ARAIZA<sup>2</sup> and SCOTT A. WILLIAMS<sup>3,4</sup>

<sup>1</sup>Anthropology, Chaffey College, <sup>2</sup>Anthropology, University of California, Riverside, <sup>3</sup>Center for the Study of Human Origins, Department of

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**Anthropology, New York University, <sup>4</sup>New York Consortium in Evolutionary Primatology**

Discoveries of ulnae for early hominins such as the TM 266-01-050 *Sahelanthropus tchadensis* and the StW 573 ("Little Foot") *Australopithecus* are welcome additions to the early hominin fossil record. Significant curvature of the ulna is a normal anatomic feature among extant apes and many early hominins that has been linked to locomotor behaviors involving the forearm. Here we employ elliptical Fourier shape analysis to quantify ulnar curvature in extant apes ( $n = 46$ ), early hominins ( $n = 9$ ), and *Homo sapiens* ( $n = 30$ ) to better understand forearm functional morphology across the sample.

The significantly curved and gracile StW 573 ulna falls within the morphospace of *Pongo*, and well outside the distribution of *H. sapiens* the human clinical sample. Falling closest to the U.W. 101-499 *H. naledi* and KNM-BK 66 *H. erectus* fossils, its high degree of midshaft curvature and gracility also distinguishes it from *Pan*, *Gorilla*, and the more robust and curved *Sahelanthropus* and *Paranthropus* fossils. The curvature of both the TM 266-01-050 and StW 573 is greater than observed in *A. afarensis*, *A. sediba*, and the KNM-WT 15000 *H. erectus*, which are all more similar to modern humans. We discuss the functional implications of forearm curvature across taxa, and also address whether the Little Foot ulna reflects traumatic bowing of the left forearm resulting from a childhood fall, as suggested by previous work.

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## Reliability of wet versus dry bone CT scan-based quantification of cortical area measurements

JULIA L. MEYERS and HUGO FV. CARDOSO  
Archaeology, Simon Fraser University

The proliferation of Computed Tomography (CT) technology in bioarchaeology research has allowed for specimen to be studied in a non-destructive manner, and by an increasingly large group of researchers through digital access programs. The methods used to study CT scans of bioarchaeological specimen were largely developed by and adapted from clinical CT research, which often utilizes bone that is still imbedded in muscle and fat, and thus has not undergone any taphonomic processes. The goal of this research project is to examine how measurements of cortical bone area taken from CT scans differ between wet and dry bone through quantification of intraobserver error. Cortical area measurements were taken from images isolated from CT scans from the Luis Lopes Identified Skeletal Collection (early 20<sup>th</sup> century) and pre-autopsy CTs from the Office of the Medical Examiner in New Mexico (early 21<sup>st</sup> century). Five individuals

with corresponding ages, ranging from 1 to 15, were selected from each sample. Two sets of cross-sectional cortical bone measurements were taken using the BoneJ plugin in ImageJ software. Mean residuals and mean absolute residuals of error were calculated from the difference between the two sets of cortical bone area measures. Initial results indicate a smaller error in dry bone, potential due to the border between the cortical bone and the exterior in the CT image being clearer than in bone situated in tissue. The results of this research will help evaluate the applicability of methods developed in clinical settings for CT analysis on dry bone samples.

## Patterns of health condition and social complexity in the Iron Age "Picenes" population from Novilara (Central Italy, 8<sup>th</sup>-7<sup>th</sup> c. BC)

MARCO MILELLA<sup>1</sup>, MICHAEL A. BECK-DE LOTTO<sup>2</sup>, CHIARA DELPINO<sup>3</sup>, SANDRA LÖSCH<sup>1</sup> and ZITA LAFFRANCHI<sup>1,4</sup>

<sup>1</sup>Department of Physical Anthropology, Institute of Forensic Medicine, University of Bern - Bern - Switzerland, <sup>2</sup>Department of Cultural Heritage: Archaeology, History of Art, Cinema and Music, University of Padua - Padua - Italy, <sup>3</sup>Superintendence of Archaeology, Fine Arts and Landscape for the Provinces of Frosinone, Latina and Rieti, SABAP - Italy, <sup>4</sup>Department of Legal Medicine, Toxicology and Physical Anthropology, Faculty of Medicine, University of Granada - Granada - Spain

The comparison of "biological" and "social" status in the past is a central topic in bioarchaeological studies. For the Italian Iron Age, previous research comparing skeletal and funerary variables depict a multifaceted scenario consistent with nuanced biocultural patterns. This calls for new studies on a broader series of archaeological contexts and skeletal series. Here, we contribute new data about the biological correlates of social differentiation during the Italian Iron Age by comparing paleopathological and funerary variables in the Picene necropolis of Novilara (Marche region, 8<sup>th</sup>-7<sup>th</sup> c. BC). This context is one of the largest Picene necropolises in the Italian Peninsula and one of the most important funerary sites of the Italian Early Iron Age. The skeletal sample for this study includes 139 individuals (M:69, F: 34, 31 nonadults). Frequencies of lineal enamel hypoplasia, cribra orbitalia, porotic hyperostosis, and periosteal reaction are used to approximate non-specific stress, and are compared with a subset of 7 archaeological variables (e.g. type and amount of grave goods) by means of Fisher tests and Mann-Whitney tests.

Results show no link between age, sex, and paleopathological variables. The latter show however a subtle pattern when considered along funerary

features. Individuals featuring more complex funerary treatment show in average, in both sexes, a lower incidence of stress-related skeletal and dental changes.

This study agrees with previous reconstructions suggesting a complex link between biological and social status among Italian Iron Age communities, and stimulates new reflections regarding the theoretical and methodological issues affecting this types of studies.

## Using the Patella to Estimate Sex in a Terminal Classic Maya Bone Deposit of Commingled Human Remains

KATHERINE A. MILLER WOLF  
Anthropology, University of West Florida

Ucanal was a major Maya center during the Terminal Classic period (830-1000 CE) with complex social, political, and economic relationships emerging after the "collapse" of the Classic Maya civilization. Recent excavations revealed unusual and surprising mortuary patterns that deviate from other cities. Most notably, large deposits of bone have been recovered spread across plaza floors and in dense, concentrated groups. Deposits contain isolated human skeletal remains that were relatively easy to remove from the body of a living or recently deceased person like teeth, the patella, and bones of the arms, hands, and feet. Moreover, many of the bones show evidence of subsequently being 'worked' and in the process of being transformed into another object – something most often seen with faunal remains. Given the unique nature of this assemblage, a primary objective was to estimate sex and age of the isolated elements to reconstruct what may have occurred at the site. A total of 31 patella from Ucanal were examined and six metrics were collected from each bone (e.g. Buikstra and Ubelaker, 1994; Sakae, 2008), verified with IOE data, and statistically evaluated to reveal sexual dimorphism among the patella (t-test and Mann-Whitney's U). The method was verified with comparative samples of patella from collections derived from other regional sites (Ambergris Caye, San Juan, Cac Balam, and Ek Luum). Sex can be estimated from the patella alone for the ancient Maya samples and the method has great potential use for isolated, poorly preserved remains from other similar contexts.

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## ABSTRACTS

### Metatarsal Torsion in Relation to Longitudinal Arch Height in Modern Humans

CATHERINE K. MILLER<sup>1,3</sup>, AMBER N. HEARD-BOOTH<sup>2</sup> and JEREMY M. DESILVA<sup>1</sup>

<sup>1</sup>Anthropology, Dartmouth College, <sup>2</sup>Radiology, Michigan State University College of Human Medicine, <sup>3</sup>Ecology, Evolution, Environment, and Society, Dartmouth College

A defining morphology of the modern human foot is the presence of a longitudinal arch. However, this feature is difficult to identify in the fossil record, and thus the evolutionary history of the human longitudinal arch remains unclear. It has been suggested that the degree of metatarsal torsion of the second (Mt2) and third (Mt3) metatarsals, and of the fourth metatarsal (Mt4) is associated with the presence of a medial and lateral longitudinal arch respectively. That is, a greater degree of external torsion in the metatarsals is associated with a higher longitudinal arch. To test this hypothesis, we conducted an intraspecific study in which torsion was measured in 20 modern human second, third, and fourth metatarsals digitally extracted from MRI scans using OsiriX. Torsion was compared to arch height, which was quantified as relative navicular height in each individual. We found no relationship between arch height and torsion of the Mt2 ( $r=0.000$ ). Arch height was statistically, but negatively, correlated with Mt3 torsion ( $r=0.522$ ;  $P=0.02$ ). While arch height was slightly correlated with external torsion of the Mt4, it was not statistically significant ( $r=0.28$ ; one-tailed  $P=0.12$ ). These results indicate that metatarsal torsion alone is not a reliable predictor of arch height and therefore caution should be used when inferring arch height from isolated hominin metatarsals. Future studies should look at the combined effects of torsion with other anatomies of the foot and take into account variables such as shoe type if working with shod populations.

### Dietary histories in early China: gender and food in five communities spanning the Eastern Zhou and Han Dynasties (ancient Zhengnan City, China)

MELANIE J. MILLER<sup>1</sup>, YU DONG<sup>2</sup>, BOWEN YANG<sup>2</sup>, KATE PECHENKINA<sup>3</sup>, WENQUAN FAN<sup>4</sup> and SIÁN HALCROW<sup>1</sup>

<sup>1</sup>Anatomy, University of Otago, New Zealand, <sup>2</sup>Institute of Cultural Heritage, Shandong University, China, <sup>3</sup>Anthropology, Queens College CUNY, <sup>4</sup>Research Division of Shang and Zhou Dynasties, Henan Provincial Institute of Cultural Relics and Archaeology, China

Stable isotope analysis of human skeletal samples allows bioarchaeologists to study dietary patterns with biosocial variables such as age and sex. Furthermore, combining results from tooth and bone from the same individual can provide fine-grained dietary histories from discrete periods of

life. Previous bioarchaeological isotopic research studied two mortuary groups buried in the ancient city of Zhengnan on the Central Plains of China during the Eastern Zhou Dynasty (771 – 221 BCE), and identified dietary differences between females and males, suggesting this period was significant in the emergence of gender inequalities in ancient China. This project expands that research with individuals from three newly studied mortuary populations ranging from the Eastern Zhou to the Han Dynasty period and from both urban and rural settings near ancient Zhengnan city (modern-day Xinzheng). Using a life-course approach, we applied an incremental dentin sampling method on an early-forming tooth from 38 adult individuals to investigate breastfeeding, weaning, and childhood diet, in conjunction with a bone sample, which records diet from the final decade before death. Across these five mortuary groups we see that males consumed greater amounts of millet than females, who consumed more wheat, soy, and other  $C_3$ -foods, and that gendered eating began in childhood. Here we examine dietary patterns over individual lifetimes, particularly in relation to gender and social inequality. Further, historical research has indicated that wheat consumption increased during the Han Dynasty, and isotopic analysis of individuals and groups can help reveal the timing and the tempo of wheat adoption.

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### Adult mortality from infectious disease and childhood stress markers on the North American Great Plains

JOCELYN D. MINSKY-ROWLAND  
Anthropology, Howard Community College

Childhood skeletal stress markers have consistently been used by anthropologists to estimate selective mortality in adulthood. The current project questions whether skeletal stress markers (linear enamel hypoplasias, cribra orbitalia, porotic hyperostosis or short stature) increased risk of death, from an infectious disease (treponematoses or tuberculosis), among the historic Arikara Native Americans, from four archaeological sites in South Dakota (AD 1600-1832). Three-hundred and seventy-one discrete, adult, individuals were skeletally complete enough to be statistically analyzed for age, sex, the presence of at least one skeletal stress marker and one infectious disease. Risk of death was investigated using Kaplan-Meier estimates and cox proportional hazards in SPSS version 22. The analyses were conducted separately by sex. No statistically significant results were found for individuals with and without an infectious disease or skeletal stress marker. However, age-specific mortality patterns are visible on the Kaplan-Meier survivorship curves. Among

females without an infectious disease, individuals with a skeletal stress marker exhibit increased survivorship after age 40. For females with an infectious disease, individuals with a skeletal stress marker die earlier in life than those females without a skeletal stress marker. Regardless of infection status, males without a skeletal stress marker exhibit increased survivorship, after age 40, compared to those with a stress marker. Thus, skeletal stress markers affected risk of death, from an infection, for females, but not for males. These results support earlier research suggesting that childhood stress markers differentially affected the sexes in this sample, and may extend to adult mortality from infectious disease.

### Preliminary comparisons of cross-sectional geometry and histology between 20<sup>th</sup> century and late medieval human midshaft femora

JUSTYNA J. MISZKIEWICZ<sup>1,2</sup>, RITA HARDIMAN<sup>3</sup>, AMY J. VASSALLO<sup>4</sup>, BRENDAN BAYLISS<sup>1</sup> and PATRICK MAHONEY<sup>2</sup>

<sup>1</sup>School of Archaeology and Anthropology, Australian National University, <sup>2</sup>School of Anthropology and Conservation, University of Kent, <sup>3</sup>Melbourne Dental School, University of Melbourne, <sup>4</sup>Women's Health Program, The George Institute for Global Health

Variation in human cortical bone histology is an indicator of bone health that can relate to lifestyle. This preliminary study compares histology and cross-sectional geometry between femora from three adult males dating to the late Medieval period (11<sup>th</sup>-16<sup>th</sup> century) in England and the late 20<sup>th</sup> century in Australia. The Australian femur was a post-mortem sample from a physically active 47 year old of poor nutritional tendencies. The Medieval individuals were 35-50 years old and represented low and high socio-economic status (SES) lifestyles.

Stature, midshaft femur circumference, maximum and minimum bending strength ( $I_{max}$ ,  $I_{min}$ ,  $I_{max}/I_{min}$ ), polar torsion ( $J$ ), total and cortical area (CA, TA, CA/TA), secondary osteon population density (OPD), area (On.Ar), and Haversian canal area (H.Ar) were recorded in each femur. Descriptive and hierarchical cluster analysis was conducted. A total of 1099 secondary osteons from cross-section anatomical axes were examined for between-individual linkages.

Femora from the Medieval males had a greater circumference,  $I_{max}$ ,  $I_{max}/I_{min}$ ,  $J$ , CA, TA when compared to the modern, albeit taller individual, suggesting they developed with increased biomechanical input. The lowest OPD, H.Ar, and On.Ar values were from the low SES Medieval individual, possibly due to strenuous occupations and poor health. The closest link in On.Ar ( $AC = 8.354$ ,  $9.843$ ) occurred between the two Medieval individuals. However, H.Ar of the high SES Medieval individual that was likely more sedentary clustered

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(AC = 9.946, 16.904) with the Australian physically active male. These initial data suggest differences in bone remodeling and strength between the archaeological and modern samples.

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### Committed to justice, struggling to teach: The experiences of social justice educators in spring 2020

TIFFANY MITCHELL PATTERSON<sup>1</sup>, CHRIS SEEGER<sup>2</sup> and KATE MCGRATH<sup>3</sup>

<sup>1</sup>Department of Curriculum & Instruction/Literacy Studies, West Virginia University, <sup>2</sup>Department of Education and Human Development, University of Virginia, <sup>3</sup>Anthropology, The Ohio State University

The spring of 2020 posed an unprecedented set of challenges for K-12 educators, including the abrupt transition to remote learning in response to the Covid-19 pandemic, and a national reckoning with racism, galvanized by the unjust killings of Breonna Taylor, George Floyd, and others. The purpose of this study is to understand the experiences and teaching practices of K-12 social justice educators during remote learning in the spring of 2020. This study reports the results of a survey of 90 self-identified social justice K-12 educators. Exploratory factor analysis results suggest a 12 item, two-factor solution: (a) confidence in social justice teaching, and (b) social justice teaching practices. MANOVA results indicate that participants who teach in high poverty schools have similar confidence levels in social justice teaching as teachers in wealthier schools, but high poverty school teachers were more likely to experience challenges with implementing social justice teaching practices, including difficulties with curriculum design. These initial findings highlight the need for further research in order to understand the systemic forces and challenges teachers face in high poverty schools exacerbated by the COVID-19 pandemic. We provide preliminary strategies for overcoming these challenges, highlighting examples of teaching for social justice that are particularly relevant for social studies (K-12), science (K-12), and biological anthropology (university) classrooms. The quantitative factor analysis results will be used to inform the subsequent qualitative phase of a mixed methods study about the experiences of social justice educators in 2020.

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### Familial hypercholesterolemia and atherosclerosis: new insights from an old mutation

BRAXTON D. MITCHELL

Medicine, University of Maryland School of Medicine

The Lancaster Amish are a founder population who settled in Lancaster, PA in the early 1700s. Due to this migration bottleneck event and genetic drift, there is high enrichment of the *APOB* R3527Q mutation, a known cause of familial hypercholesterolemia. While the frequency of this mutation is 0.06% in the overall European population, it is 6.7% in the Amish. Due to high levels of LDL cholesterol (LDL-C), *APOB* carriers experience elevated levels of coronary artery calcification (CAC), placing them at high risk for early heart disease.

The high frequency of *APOB* R3527Q in the Amish offers unique opportunities to test novel hypotheses about the consequences of elevated LDL-C on cardiometabolic health. For example, Mendelian randomization approaches enable testing causal relationships between LDL-C and other metabolic conditions, including diabetes and bone health. Detailed studies of *APOB* R3527Q carriers may also provide novel insights into the development of atherosclerosis. Our Amish cohort includes 110 *APOB* carriers in whom we have performed detailed imaging studies to measure CAC. Although *APOB* carriers have a 9-fold higher odds of having significant CAC than noncarriers, there is considerable variability in CAC levels among *APOB* carriers. In fact, there is a subset of ~20% of *APOB* carriers who, despite lifelong high levels of LDL-C, have CAC scores as low as or lower than that of age- and sex-matched noncarriers. Detailed studies comparing *APOB* carriers with very low and very high CAC scores may unmask the identify of nonlipid factors that protect against the development of atherosclerosis.

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### Where only the strong survive: Excluding damaged/pathologic specimens may result in sampling biases in shape analyses

D. REX MITCHELL<sup>1,2</sup>, CLAIRE A. KIRCHHOFF<sup>3</sup>, SIOBHÁN B. COOKE<sup>4</sup> and CLAIRE E. TERHUNE<sup>1</sup>

<sup>1</sup>Department of Anthropology, University of Arkansas, <sup>2</sup>Center for Anatomical Sciences, University of North Texas Health Science Center, <sup>3</sup>Department of Biomedical Sciences, Marquette University, <sup>4</sup>Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Many geometric morphometric studies analyze shape data obtained from dry bone specimens. However, these can sometimes exhibit signs of postmortem damage (e.g., cracks, breakages), perimortem damage (e.g., bullet wounds, cuts),

and/or antemortem pathology (e.g., healed breakages, dental disease). Specimens with conditions like these are often sidelined by researchers, but the impact this selection process has on shape analyses has not been tested. We collected 3D landmark data from the cranium and mandible of 100 crab-eating macaques (*Macaca fascicularis*), some of which exhibited mild to severe cases of damage and/or pathology. Two researchers independently identified specimens they would likely exclude from testing because of severe damage/pathology. Analyses of shape variation reveal a potential bias in this selection process: for this species, large males were more likely to be excluded because these individuals commonly exhibit severe cases of damage and pathology (e.g., healed fractures, broken teeth, etc.), likely associated with aggressive behaviors. We suggest that excluding damaged/pathologic specimens from datasets may inadvertently ignore demographic-specific shape variation from groups more likely to exhibit severe pathologies and could therefore be limiting the represented range of true intraspecific variation. We further found that including these specimens had little impact on dominant predictors of shape; however, they did have some influence on less statistically important trends in shape variation. Hypotheses concerning highly significant predictors and shape associations of gross morphology may therefore benefit from the inclusion of these individuals; however, studies analyzing finer-scale aspects (e.g., subregions, modules) will likely be affected by their presence.

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### Sex differences in play style among wild East African chimpanzees (*Pan troglodytes schweinfurthii*)

ISABELLE G. MONROE<sup>1</sup> and KRIS H. SABB<sup>1,2</sup>

<sup>1</sup>Anthropology, University of New Mexico,

<sup>2</sup>Anthropology, Tufts University

Play behavior may function as preparation for adult social behavior by providing a platform to practice skills that are integral to adult survival and reproduction, including sex-typed social strategies. Chimpanzee males are both more aggressive than females and more reliant on same-sex social bonds. Therefore, we predicted that young males would use more rough play behaviors than females, especially when playing with other males. Second, we predicted that males would be more likely to use play faces, a cooperative signal that may signify friendly intentions. To test these predictions, we analyzed 156 video-recorded dyadic play bouts among immature chimpanzees (under 10 y.o., n=32) of the Kanyawara community in Kibale National Park, Uganda. For each video, we recorded the sexes of the players and scored whether or not players used rough behaviors, like

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biting and wrestling, and play faces. When males played with other males, they bit one another nearly twice as often (prop.=0.46) compared to female-only (prop.=0.26, Fisher's Exact probability test,  $p=0.02$ ) and mixed-sex bouts (prop.=0.28,  $p=0.04$ ). However, compared to male- (prop.=0.14) and female-only bouts (prop.=0.08), mixed-sex bouts were the most likely to include wrestling (prop.=0.21,  $p=0.03$ ). As expected, male-only bouts also included more play faces (prop.=0.75) than female-only (prop.=0.62) or mixed-sex bouts (prop.=0.63), however this difference was not significant ( $p=0.2$ ). Thus, immature chimpanzees' play style foreshadowed sex differences in adult social behavior in some expected ways, but not others. Our findings may reflect that rough play has benefits for both sexes of chimpanzees.

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### Using phenotypic integration to understand the evolution of the cercopithecoid maxillary dentition

TESLA A. MONSON<sup>1</sup>, MARIANNE F. BRASIL<sup>2,3</sup>, CHRISTOPHER A. SCHMITT<sup>4</sup>, CATHERINE E. TAYLOR<sup>2,5</sup>, RYAN YOHLER<sup>2,5</sup> and LESLEA J. HLUSKO<sup>2,5</sup>

<sup>1</sup>Department of Anthropology, Western Washington University, <sup>2</sup>Human Evolution Research Center, Berkeley, <sup>3</sup>Berkeley Geochronology Center, Berkeley, <sup>4</sup>Department of Anthropology, Boston University, <sup>5</sup>Department of Integrative Biology, University of California Berkeley

Many traits of the primate dentition are heritable and vary significantly across taxa making them highly utile in taxonomic designations of fossil species. The heritability and taxonomic discriminatory power of mandibular postcanine dental proportions (as captured by the molar module component, MMC, and the premolar-molar module, PMM) have been well tested in primates, bats, and more broadly across boreoeutherians. However, these genotype:phenotype traits have not yet been assessed in the maxillary dentition. As many fossils consist solely of maxillary dentition, validating MMC and PMM in the maxilla generates a valuable tool for taxonomic investigation in the fossil record. We assessed variation in maxillary MMC and PMM using data from a sample of  $n=695$  extant cercopithecids, spanning 19 species. Our results demonstrate that MMC and PMM have strongly conserved phylogenetic signal in the maxilla and vary significantly across extant primates. Given the strong taxonomic power of maxillary MMC and PMM, we turned our attention to postcanine dental variation in the Plio-Pleistocene African fossil record ( $n=102$  fossil cercopithecids). We find that fossil *Cercopithecus*, *Colobus*, and *Papio* have MMC and PMM values that directly align with their extant counterparts,

whereas values for fossil *Theropithecus* fall well outside those of extant gelada baboons. Using these powerful dental phenotypes, we also discuss the systematics of fossils classified as *Parapapio* and *Procercocebus*. Together, the data presented from extant and fossil cercopithecids demonstrate the significant phylogenetic conservation of maxillary dental proportions and provide a novel method of investigating variation in the primate fossil record.

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### Cranial shape allometry in anthropoid primates

ISABEL J. MORMILE<sup>1</sup> and CHRISTOPHER J. PERCIVAL<sup>2</sup>

<sup>1</sup>Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, <sup>2</sup>Department of Anthropology, Stony Brook University

The platyrrhine clade is often said to be particularly dolichocephalic (the condition of having an anteroposteriorly long neurocranium relative to cranial breadth), and dolichocephaly has been shown to scale negatively with body size in New World Monkeys. However, the allometry of neurocranial shape has not been formally investigated in Old World Monkeys or hominoids, leaving it uncertain whether increased dolichocephaly is an artifact of small body size across anthropoids, or unique to small-bodied platyrrhines. A dolichocephaly ratio of neurocranial length (glabella-lambda) and breadth (bi-parietal distance) was collected for 450 adult non-human primates, including specimens of both sexes and from most anthropoid subfamilies. This was regressed against body size using GLS pANCOVA, a method which combines generalized least squares analysis and phylogenetic analysis of covariance to determine if certain clades deviate from allometric predictions, and at what taxonomic levels these deviations occur. Our results indicate that, contrary to expectations, body size alone cannot explain variation in dolichocephaly across anthropoid taxa. Small catarrhines are not significantly more dolichocephalic than large-bodied catarrhines, and atelids consistently group with catarrhines in both degree and allometry of dolichocephaly. Extreme dolichocephaly appears to be restricted to cebids such as *Saimiri*, *Aotus*, and the callitrichines, suggesting an allometric grade shift between platyrrhines and catarrhines, and potentially a functional basis for neurocranial shape in small-bodied platyrrhines.

### Shearing ratios of Aycross anaptomorphine omomyids: Support for a middle Eocene refugium habitat

PAUL E. MORSE<sup>1,2</sup>, MICHALA K. STOCK<sup>3</sup>, RICHARD F. KAY<sup>1,4</sup> and BLYTHE A. WILLIAMS<sup>1</sup>

<sup>1</sup>Department of Evolutionary Anthropology, Duke University, <sup>2</sup>Florida Museum of Natural History, University of Florida, <sup>3</sup>Department of Sociology and Anthropology, Metropolitan State University of Denver, <sup>4</sup>Division of Earth and Ocean Sciences, Nicholas School of the Environment, Duke University

Anaptomorphine omomyids are a common component of early Eocene Wasatchian North American Land Mammal Age (NALMA) faunas, but waned in both abundance and diversity during the middle Eocene Bridgerian NALMA as closely related omomyines diversified and became more abundant. This turnover in faunal composition has been linked to warming climate regimes that permitted northward migration of omomyines during the Watchian-Bridgerian transition, forcing endemic anaptomorphines into marginal habitats. One exception to this pattern is the anaptomorphine-dominated fauna of the Bridgerian Aycross Formation, Bighorn Basin, WY, which has been interpreted as an upland refugium for anaptomorphines, including *Gazinius* and *Strigorhysis*. Under a refugium scenario, the ecology of Aycross anaptomorphines should have been similar to that of their earlier, basin floor relatives, whereas ecological pressures from a less suitable habitat would have likely produced adaptive shifts in morphology. One avenue of characterizing the ecology of extinct species is to quantify relative shearing crest length (shearing ratios), to form an analogy with modern taxa of known feeding behaviors. Using high resolution  $\mu$ CT scans, we calculated M<sup>1</sup> shearing ratios of *Gazinius* and *Strigorhysis* and compared them to the late-Wasatchian anaptomorphine *Absarokius* and modern prosimians. All fossil specimens had shearing ratios similar to extant frugivores, with *Gazinius* exhibiting relatively longer crests than *Strigorhysis*. Neither Aycross anaptomorphine differed significantly from the range of shearing ratios exhibited by *Absarokius*, consistent with the hypothesis that their upland environment did not pose a severe ecological departure from that encountered by anaptomorphines when they were the dominant omomyids on the landscape.

### Nature and nurture: Association of MAOA, 5-HTTLPR, and COMT genetic variants and resilience with psychosocial stress outcomes in Syrian refugee and Jordanian youth

CONNIE J. MULLIGAN<sup>1,2</sup>, CHRISTOPHER J. CLUKAY<sup>1,2</sup>, ANTHONY MATARAZZO<sup>1,2</sup>, KRISTIN

# ABSTRACTS

HADFIELD<sup>3,4</sup>, LISA NEVELL<sup>1,2</sup>, RANA DAJANI<sup>5</sup> and CATHERINE PANTER-BRICK<sup>6</sup>

<sup>1</sup>Department of Anthropology, University of Florida, <sup>2</sup>Genetics Institute, University of Florida, <sup>3</sup>School of Psychology, Trinity College Dublin, <sup>4</sup>Trinity Centre for Global Health, Trinity College Dublin, <sup>5</sup>Department of Biology, Hashemite University, <sup>6</sup>Department of Anthropology, Yale University

Early childhood trauma can have profound and lifelong effects on adult mental health and psychosocial wellbeing. Arguments abound on whether such effects are mediated by genetics or the environment. We tested the effects of both genetics and the environment in a case:control study of Syrian refugee and Jordanian non-refugee youth, who were differentially exposed to trauma. Specifically, we tested for direct and interactive effects of genetic variants in three genes implicated in response to early life adversity (*MAOA*, *5-HTTLPR*, and *COMT*) with traumatic exposures and a new measure of resilience on six psychosocial and mental health outcomes. We collected buccal samples and survey data on trauma, resilience, and the six outcomes in 417 Syrian refugee and 306 Jordanian youth at three time points over one year. Variants in all three genes showed an association with resilience on two stress measures; *MAOA* and *5-HTTLPR* variants and resilience were associated with symptoms of psychosocial stress on the Perceived Stress Scale (PSS) and *COMT* variants and resilience were associated with post-traumatic stress symptoms (CRIS-8). In all three cases, the genetic variants showed protective effects in individuals with high resilience; gene x environment effects were identified in *5-HTTLPR* and *COMT* and an additive effect in *MAOA*. No effects of trauma were identified in our models that included genetic variants and resilience. Our study suggests that both nature (protective alleles in three genes) and nurture (protective effect of resilience) play an important role in psychosocial stress in youth who have experienced high levels of trauma.

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## Differences in how women walk while carrying infant-sized loads

MARCIE J. MYERS<sup>1</sup>, LANA PROKOP<sup>2</sup>, MACKENZIE ESS<sup>1</sup>, TAYLOR GENTZ<sup>1</sup> and LAKEN MULLER<sup>1</sup>

<sup>1</sup>Biology, St Catherine University, <sup>2</sup>Nutrition 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.

## Race(ism), Risk, and Accountability: Human Subjects Research, Community Belonging, and Power in Field Research

ROBIN G. NELSON

Anthropology, Santa Clara University

Historically, social science research has largely been extractive with researchers benefitting professionally by collecting information from less advantaged communities on topics ranging from individual health to foraging patterns. In many cases, study participant communities rarely benefitted overtly from engagement with these scholars. While some local communities have established their own standards for how and when to engage with outside researchers, biological anthropologists have yet to fully interrogate how their identity and positionality influence data collection and analysis. In this paper, I examine the influence of the identity and professional status, and thus positionality of the researcher, on the risks of data collection, costs of the study, and benefits experienced by both the researcher and the study community. Using qualitative analyses of data gathered from publications by human biologists, evolutionary anthropologists, and human behavioral ecologists working with living human populations, I identified three salient factors: duration of time working with a study community, ethical considerations as discussed explicitly in the text, and perceived and actual benefits to the study communities as detailed in writing. This paper highlights how researcher relationship to and long-term engagement with their study community influences the often hierarchical power dynamics between researchers and

their participants. Embeddedness within research communities requires collaborative efforts which upend conventional researcher-subject power dynamics, and influences who gains access to what kinds of data, particularly those of a sensitive nature.

## Paleoproteomics contribution to differential diagnosis of human bone remains

RICARDO NEME TAUILL<sup>1</sup>, VIVIAN SCHEINSOHN<sup>2</sup>, DENISE EVANS<sup>3</sup>, PAULA MIRANDA<sup>4</sup>, SILVIA MORENO<sup>1</sup> and FABIAN CRESPO<sup>5</sup>

<sup>1</sup>Centro de Estudios Químicos y Biológicos por Espectrometría de Masa, Universidad de Buenos Aires/CONICET, Argentina, <sup>2</sup>Instituto Nacional de Antropología y Pensamiento Latinoamericano, Universidad de Buenos Aires/CONICET, Argentina, <sup>3</sup>Instituto Nacional de Antropología y Pensamiento Latinoamericano, ANCYPT, Argentina, <sup>4</sup>Instituto Nacional de Antropología y Pensamiento Latinoamericano - Banco Nacional de Genética, Argentina, <sup>5</sup>Anthropology-Center of Archaeology and Cultural Heritage, University of Louisville, KY, USA

Differential diagnosis in archaeological human bones is problematic since diseases have overlapping macroscopic manifestations. In this paper, we explore if paleoproteomics can inform about the presence and distribution of certain proteins in bones and its correlation with different pathological and metabolic states. Using a minimum invasive protocol we collected samples and conducted a proteomic study on 2 human bones from Cueva de Plaza (CDP) site (Patagonia, Argentina) and another bone from a modern collection: a phalanx with macroscopic osteological alterations (sampling the affected and unaffected areas) from CDP, another phalanx of a subadult individual from an osteological reference collection with no visible lesions, and a last fifth metatarsal from another individual of the same archaeological site. For higher protein yield we explored alternative protocols before running the samples in a nHPLC-ESI-Orbitrap mass spectrometer. Data required meticulous interpretation with modified criteria from the classical shotgun experiments. We have obtained proteins in all samples, most of them related to the analyzed tissue (collagens, fibronectin, cartilage, bone, muscle, and blood proteins) and, to a lesser extent, proteins associated with inflammatory responses and other metabolic pathways. Our preliminary analysis confirms the power of proteomics and bioinformatics protocols to inform paleopathology and help on the differential diagnosis of human bone remains.

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### Changes in seasonality of birth across two centuries in a rural Polish community

ILONA NENKO<sup>1</sup>, MICHAEL BRIGA<sup>2</sup>, AGNIESZKA MICEK<sup>3</sup> and GRAZYNA JASIENSKA<sup>1</sup>

<sup>1</sup>Department of Environmental Health, Jagiellonian University Medical College, <sup>2</sup>Department of Biology, University of Turku, <sup>3</sup>Department of Nursing Management and Epidemiological Nursing, Jagiellonian University Medical College

Human birth and the associated conception seasonality are ubiquitous phenomena, usually suggested to be driven by social and climatological factors. In contrast, energetic factors that influence female fecundity are often neglected but can be crucial. In the past, rural societies, had high energy expenditure during summer (harvest and haying season) and compared to fall and winter when women were less involved in farm work. Such intense physical work can affect birth seasonality through suppressing ovarian function.

Here we tested the hypothesis that conception seasonality peaked in autumn using over 200 years of birth data in an agricultural rural Polish community containing 26,957 birth records from 1782 and 2004, with an average of 119 births per year. We identified the average dominant seasonality in successful conceptions and, because agricultural activity diminished with time, tested whether there was a changing conception seasonality.

We found strong evidence for conception seasonality over the 200-year period which declined with time. Contrary to our expectation, on average the dominant seasonality of successful conceptions peaked in spring, which was driven the first 150 years of data, while from the 1950 onwards this peak gradually moved towards summer. Instead, there was a winter peak of successful births in the 18<sup>th</sup> and 19<sup>th</sup> century which moved to spring in the late 20<sup>th</sup> century. We discuss possible causes for these results and their implications for our understanding of the seasonality of human behaviour and reproduction.

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### Staging areas in the settlement of the Americas: Linguistic evidence

JOHANNA NICHOLS

Slavic Languages, University of California, Berkeley, Linguistic Convergence Lab, Higher School of Economics, Moscow

The southward and eastward expansion of the human frontier from Beringia through the Americas was neither gradual nor direct. Evidence from grammatical structure and linguistic phylogeny in North America reveals two kinds of slowdown points (all among Anderson's staging areas): (1) First stops. Entrants from Beringia stopped in the first rich places, flourished, and left

disproportionately many descendents there; later entrants found those places claimed and moved on, fanning out. (2) Second-choice staging areas, settled as next best choice, with accordingly less competition. Descendents are expected to preserve the possibly idiosyncratic profile of their first claimants, a subset of dispersing post-initial entrants.

Thus, reversing usual assumptions, linguistic descendents of earliest entrants cluster closest to Beringia. First stops surveyed here are the Pacific Northwest coast (southeastern Alaska to Puget Sound) and the lower Columbia. Second-choice areas, rich non-coastal wetlands at least through early postglacial times, are the Colorado delta, the western Columbia Plateau, and the Lower Mississippi Valley (a convergence of post-Clovis inland southward spread trajectories). 12 phonological and grammatical features, all fairly stable and slow-changing, are surveyed densely in these areas and compared to overall subcontinental, continental, Pacific Rim, and world frequencies. The results support the expected archaic Eurasian-like profile in the first stops and individual idiosyncratic profiles in the second choices – which, as long-standing staging areas, appear to have contributed the two major western North American possible language macrofamilies and the major diffused grammatical features. A hypothesis is that genetic (and archaeological) distributions follow the linguistic ones.

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### Neanderthal cold adaptation: insights from seasonal patterns of brown adipose tissue activity in humans

ALEXANDRA NICLOU<sup>1</sup> and CARA OCOBOCK<sup>1,2</sup>

<sup>1</sup>Department of Anthropology, University of Notre Dame, <sup>2</sup>Eck Institute for Global Health, University of Notre Dame

Brown adipose tissue (BAT) generates heat under mild cold conditions, and cold climate populations exhibit greater BAT activity than temperate climate populations. BAT's non-shivering thermogenic capacities suggest an adaptive potential in modern humans and Neanderthals. However, current understanding is limited to climate specific variation of BAT activity. The present study examined the seasonal differences in BAT activity in an Albany, NY group (N=75, female n=46, ages: 18-63). BAT activity was inferred comparing metabolic rate and supraclavicular skin temperature at thermoneutrality and after cooling in the winter and summer. In winter, heat dissipation in the supraclavicular area, was significantly greater after cooling than in the summer (+4.0%,  $P < 0.05$ ). Metabolic rate increased, though not to a significant degree, in the winter compared to summer (+4.0%,  $P=0.87$ ), suggesting an increase in BAT activity efficiency associated with acclimatization

to seasonal temperatures. In the winter, BAT may have been activated for several months allowing for the activation of cost-efficient mechanisms over time. Given the consistent warm temperatures of summer, BAT activity acclimatization was unnecessary. Findings of possible seasonal patterns of BAT activation combined with previous evidence for greater BAT activity in cold-adapted individuals suggest BAT may have played a significant role in Neanderthal adaptation to cold. We propose that cost-effective heat production of BAT at chronic cold exposure posed a significant advantage in Neanderthal cold adaptation, allowing them to survive and thrive in extreme environments.

### Social identities of subadults based on mortuary treatments: A study of west-central tennessee archaic period sites

CHRISTOPHER E. NICOSIA

Geography and Anthropology, Louisiana State University (LSU)

There has been little research on the mortuary practices within the Middle (8900-5700 BC) to Late Archaic (5700-3200 BC) periods in the southeastern US, particularly with respect to subadults. For this study, the adult and subadult skeletal sample (n=231) examined comes from seven Archaic period sites: 1) Oakview Landing, 2) Cherry, 3) Eva, 4) McDaniel, 5) Kays Landing, 6) Big Sandy, and 7) Ledbetter Landing formally located along the lower Tennessee River Valley of west-central Tennessee. The biological sex of a subadult is difficult to assess because there are very few sexually dimorphic skeletal characteristics detectable before puberty. However, recent methodologies, such as dentition, humeral head diameter, distal humeral morphology, and the pelvis have sex-assessment accuracies that prove to be archaeologically useful. Along with biological sex, this project sought to identify suites of sex-specific grave accompaniments. The West-Central Tennessee Archaic period results reflected the initial analysis of exploring the mortuary treatment and biological sex of subadults in the Middle and Late Archaic periods. Due to many grave goods exhibiting single occurrence associations with some of the subadult burials across the sites, it was particularly difficult to be certain which grave good displayed a sex-specific male or female pattern. However, with grave goods that did present a pattern in the sample, out of 48 younger subadults that exhibited grave good associations 19 had sex-correlated associations, equaling to 35%. Additionally, the study sheds light on various details concerning subadult identities in the Shell Mound Archaic.

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## To industry and back again: Anthropological genetics outside of the academy

MARIA A. NIEVES-COLÓN

Astrea Forensics, Claret Bioscience LLC, School of Human Evolution and Social Change, Arizona State University

Due to the fiscal uncertainty caused by the COVID-19 pandemic, many academic institutions announced hiring freezes with indeterminate end dates. This uncertainty has narrowed the academic job market for anthropological geneticists. For example, during the 2019-2020 academic year, 30 tenure-track positions in Biological Anthropology were announced on the Academic Jobs Wiki. Ten job ads explicitly stated interest in field or lab-based genetics research. As of October 2020, only one of three academic positions listed on the same website explicitly states interest in anthropological genetics. Postdocs and graduate students about to enter the job market are uniquely impacted by the increasing uncertainty of academic employment. These challenges are magnified for trainees from under-represented groups or with dependent families who may lack the support or financial means to remain in low paying transitional positions. In this context of uncertainty, anthropological geneticists may consider multiple and flexible career paths, within and outside of academia. In this presentation I will discuss my own experience with a flexible career path that included employment in the biotechnology industry. I will describe the factors that led me to look for non-academic positions and my experience interviewing for and working with a forensics startup company. I will detail how my training as an anthropological geneticist did (and did not) prepare me for non-academic employment and how industry experience better equipped me for a tenure-track position. This presentation will highlight how the transferable skillset of anthropological geneticists can be leveraged by students and postdocs for flexible career paths.

## Socioeconomic and stress-related impact of COVID-19 on mothers of Mexican descent in Southern California

AMY L. NON<sup>1</sup>, ELIZABETH S. CLAUSING<sup>1</sup>,  
SANDRALUZ LARA-CINISOMO<sup>2</sup> and KIMBERLY L.  
D'ANNA HERNANDEZ<sup>3</sup>

<sup>1</sup>Anthropology, University of California, San Diego,  
<sup>2</sup>Kinesiology and Community Health, University of  
Illinois, <sup>3</sup>Psychology, California State University, San  
Marcos

Racial and ethnic minorities in the US have disproportionately suffered from the coronavirus pandemic. As of October 2020, Latinos represent 28.4% of COVID-19 U.S. cases, but comprise only 18.5% of the population. This higher burden of infections, along with associated fears and stigmas, can have severe socioeconomic and

mental health consequences, particularly among Latina mothers. We investigated COVID-related changes in socioeconomic status, worries over COVID stigma, and COVID-related stress among mothers of Mexican descent (mean age 31 years, with children up to 6 years old) living in Southern California (n's range 93-202). Surveys were administered by email within 5-16 weeks of the March 19<sup>th</sup> stay at home order in California. Preliminary results suggest severe socioeconomic constraints have increased exposure risk during quarantine (eg. 88% report at least one person working outside of the home, 85% of employed women unable to work from home, 96% of employed continuing to work because they have no choice to pay their bills). Women also report severe socioeconomic impact of COVID (e.g. 38% unemployed; 62% have partners working fewer hours, due to COVID). Many women also report at least some concern that if they contract COVID, they will experience stigma/exclusion from family members (59%), a family member will be deported (28%), they will lose their children (35%), or not be able to care for their children (89%). We will discuss implications for the mental health of this vulnerable population, and for the process of conducting research during a pandemic.

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## Episodes of fruit scarcity lead to muscle wasting in wild Bornean orangutans

CAITLIN A. O'CONNELL<sup>1</sup>, ANDREA L. DIGIORGIO<sup>1,2</sup>,  
ALEXA D. UGARTE<sup>1</sup>, SRI SUCI UTAMI ATMOKO<sup>3</sup> and  
ERIN R. VOGEL<sup>1</sup>

<sup>1</sup>Anthropology, Rutgers University, <sup>2</sup>Writing  
Program, Princeton University, <sup>3</sup>Faculty Biology,  
Universitas Nasional

Animals have evolved a vast array of mechanisms to cope with seasonality. Even in the tropics where seasonal changes are less apparent, primates respond to variation in food availability by adjusting their diet, social behavior, and activity patterns. Despite this, primates may experience deficits in meeting their energy requirements. Bornean orangutans face pronounced low fruit periods, and experience negative energy and protein balance during these times. Given the severity and unpredictability of fruiting, we examined the possibility that wild orangutans experience muscle wasting during low fruit periods at the Tuanan Research Station in Central Kalimantan, Indonesia. Utilizing a method that was validated in wild chimpanzees, we use urinary creatinine standardized by specific gravity as a non-invasive measure of muscle mass to compare flanged males (N=31), unflanged males (N=15), adult females (N=32), and immature orangutans (N=29) during high (408 samples) and low (811 samples) fruit periods. Preliminary analyses revealed that during episodes of fruit scarcity, muscle mass declined across all age-sex classes ( $\beta=-11.863$ ,  $t=4.329 \pm 2.74$ ,  $p<0.001$ ).

As expected, we found that flanged male orangutans had greater muscle mass compared to adult females ( $\beta=9.232$ ,  $t(1137)=2.070$ ,  $p<0.05$ ), but contrary to the findings from chimpanzees, the other age-sex classes did not differ. These findings add to growing evidence that orangutans are characterized by unique metabolic plasticity shaped by their environment. We also raise questions surrounding male bimaturism and the body composition of flanged males, who are twice the size of adult females and are expected to have more muscle mass than unflanged males.

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Studies

## A new three-dimensional musculoskeletal model of the pelvis and lower limbs of *Australopithecus afarensis*

MATTHEW C. O'NEILL<sup>1</sup>, AKINORI NAGANO<sup>2</sup> and  
BRIAN R. UMBERGER<sup>3</sup>

<sup>1</sup>Department of Anatomy, Midwestern University,  
<sup>2</sup>Department of Sport and Health Science,  
Ritsumeikan University, <sup>3</sup>School of Kinesiology,  
University of Michigan

Integrated experimental-modeling studies of human and bipedal chimpanzee walking have provided important insights into the mechanics, energetics and control of bipedal locomotion. These studies can provide context for interpreting optimization-based predictive simulations generated from robust 3-D musculoskeletal models of fossil hominins, provided the models are of similar complexity. Here, we substantially revise, expand and update the *Australopithecus* (*Au.*) *afarensis* model of Nagano et al. (2005) to facilitate new comparative computational studies of human, ape and fossil hominin musculoskeletal function. A new generic model of the *Au. afarensis* pelvis and lower limbs was created in SIMM. The pelvis, femur and some foot bones were replaced with full 3-D reconstructions or isolated elements from similarly sized *Au. afarensis* specimens, necessitating modifications to the hip, knee and ankle geometries. The number of Hill-type muscle models was expanded from 26 to 34 per limb, with origins, insertions and via points reassigned based on skeletal landmarks and published studies of fossil specimens. 3-D joint motion was added to the lower back, coupled femur-tibia translation added to knee rotation and flexion-extension expanded at the ankle. The resulting hip, knee and ankle dimensionless muscle moment arms were predicted and compared to human and chimpanzee models. This *Au. afarensis* model is directly comparable to existing human and chimpanzee models for movement analyses. It can be scaled to represent the full body size

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range of the species and reconfigured for different muscle-tendon designs. The model is amenable to testing a wide range of hypotheses regarding *Au. afarensis* locomotor capabilities.

### Transnational and Cross-generational Cuban Genealogies: discourses on race and ancestry through biological narratives

ELIZABETH OBREGON

Anthropology, University of Illinois at Chicago

In this paper, I bring attention to the role of biology and genetics in racial formation processes within the intimate genealogical memories of transnational (across Cuba and Miami) and cross-generational Cuban families (Cuban-born and U.S.-born Cuban Americans in Miami). Due to the growing scholarly interest on how genetic ancestry tests impact conceptualizations of race, my paper aims to make two key contributions. First, it illustrates the diverse ideas of race among Cubans and the Cuban American diaspora. Second, my data offers pre-existing conceptualizations of race, ancestry, and genetics among a diverse sample prior to even engaging with genetic ancestry tests. My ethnographic interviews suggest that genealogical narratives are a dynamic site to negotiate identity (bio)politics for these Cuban families—with general trends falling along transnational and generational lines. Despite Cuba's official rhetoric as a racial democracy, where *all* Cubans are racially heterogeneous and everyone is equal, my data illustrates how biological narratives become a mechanism for island Cuban and Cuban-born Miamians to reinforce racial difference and maintain racial distance in ways that are non-counterrevolutionary. And though all my interlocutors, across Cuba and Miami combined both socio-constructivist and essentialist ideas of race, it was the U.S.-born who were overtly critical of essentialist race-thinking—even though it was primarily the U.S.-born who were enthusiastic about using genetic ancestry test kits to understand their “true (ethnoracial) self.”

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### Reindeer herders from northern Finland exhibit high total energy expenditure but low caloric intake during the annual herd round up

CARA OCOBOCK<sup>1,2</sup>, PÉIVI SOPPELA<sup>3</sup>, MINNA TURUNEN<sup>3</sup>, VILLE STENBÉCK<sup>4,5</sup>, KARL-HEINZ HERZIG<sup>4,6</sup>, REBECCA RIMBACH<sup>7,8</sup> and HERMAN PONTZER<sup>7</sup>

<sup>1</sup>Department of Anthropology, University of Notre Dame, <sup>2</sup>Eck Institute for Global Health, University of Notre Dame, <sup>3</sup>Arctic Centre, University of Lapland, <sup>4</sup>Research Unit of Biomedicine, Medical Research Center, University of Oulu, <sup>5</sup>Biocenter Oulu,

<sup>6</sup>Department of Gastroenterology and Metabolism, Poznan University of Medical Sciences,

<sup>7</sup>Department of Evolutionary Anthropology, Duke University, <sup>8</sup>University of Witswatersrand

High levels of total energy expenditure (TEE, kcal/day) have been documented among numerous human populations such as tropical climate horticulturalists and high-altitude agriculturalists. However, less work has been conducted among highly physically active cold climate populations to better understand the metabolic outcome of dual thermoregulatory and activity demands. Here we examined TEE among reindeer herders (20-62 years, N=24, 5 females, 19 males) in northern Finland during the physically demanding annual reindeer herd round up in October 2018. During this time, herders complete tasks such as searching for and moving reindeer, often over long distances; separating and slaughtering reindeer; preparing products; and herding and feeding released reindeer. TEE was measured among all participants with the flex-heart rate (flex-HR) method and among a subset of participants with the doubly labeled water (DLW) method for 6-14 days; self-documented dietary intake was also calculated during this time. For DLW measured TEE, herders expended a mean of 4155±1001 kcal/day. There was no significant difference in TEE between the sexes or between the DLW and flex-HR methods ( $p>0.1$  in both instances). Herder mean caloric intake was 1718±709 kcal/day, and was significantly lower than TEE ( $p<.001$ ). The high TEE among herders in combination with low caloric intake reflect the extreme demands placed on herders during the annual herd round up. Our work provides critically needed metabolic data on physically active cold climate populations, which expands our current understanding of variation in human TEE.

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### Evolutionary history of Latin Americans and Native Americans and its effect on phenotypic traits.

TIMOTHY D. OCONNOR, DOUGLAS LOESCH, ROLAND LABOULAYE, JENNIFER FRENCH, DIEGO VELIZ and VICTOR BORDA

Institute for Genome Sciences, University of Maryland School of Medicine

Native Americans and Latin Americans, a group with substantial Native American ancestry, are underrepresented in genomic studies as they only represent about 1.5% of individuals. Further, there is a unique and complex history in different parts of Latin America which has shaped the genomes of these populations. Here, we will present recent findings on the estimation of this demographic history and how this has shaped the genetic variation for these people. Starting in Peru, we will discuss the complex history of the Inca,

European colonialization, and present-day groups. This history plays a role in our understanding of the genetic risks and variation associated with phenotypic traits such as Parkinson's Disease Risk, height, and others. A concerted effort to bring together genomic resources for this group is underway and we will present the first findings of the Genetics of Latin American Diversity (GLAD) database. This is a retrospective collection of publicly available Latin American and Native American genomes of about 100K individuals. We will highlight the fine-scale population structure of GLAD as well as identify Latin American populations that remain nearly absent genomic studies. We will also show examples of how this resource can improve the detection of phenotypic traits for future studies by utilizing summary statistics and advanced machine learning models.

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### Age-related changes in temporal lobe dimensions in *Saguinus oedipus*

LANRE S. OLADIPUPO<sup>1</sup>, VALERIE B. DELEON<sup>2</sup> and TIMOTHY D. SMITH<sup>1</sup>

<sup>1</sup>School of Physical Therapy, Slippery Rock University, <sup>2</sup>Department of Anthropology, University of Florida

This study tests the association of brain growth and synchondroseal fusion in the cranial base in the cotton-top tamarin (*Saguinus oedipus*). Recently, we demonstrated the timing at which bilateral synchondroses of the sphenoid bone fuse differed among primates such as greater bushbabies (*Otolemur crassicaudatus*) and *S. oedipus*. In order to describe the relationship of brain growth and timing of synchondroseal fusion, we reconstructed and measured endocasts of the cranial cavity in the *S. oedipus* at three stages: birth, one-month, and adult. We used Amira 2019.1 software to segment endocranial contours and reconstruct endocasts; the endocasts were measured in maximum bilateral widths at the level of the foramen ovale and foramen magnum. Overall anteroposterior length of the right temporal lobe was also measured. Our findings indicated that the relative width of temporal lobe at the middle cranial fossa (maximum width in coronal section at foramen ovale / AP length) increases across age while the same ratio at the level of the posterior cranial fossa stays the same. Therefore, the largest change in bi-temporal lobe width occurs after the bilateral sphenoidal synchondroses begin to fuse, at about one-month of age in these tamarins. These results indicate that the most profound changes in neurocranial bilateral proportions may relate to bone modeling in response to brain growth, rather than activity at growth centers.

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## The Strepsirrhine and Tarsier Genome Sequencing Initiative: Conservation Genomics of the Non-Anthropoid Primates

JOSEPH D. ORKIN<sup>1</sup>, LUKAS F. K. KUDERNA<sup>1</sup>, MARTA GUT<sup>2,3</sup>, IVO GUT<sup>2,3</sup>, JULIE HORVATH<sup>4,5,6</sup>, MAREIKE C. JANIAK<sup>7</sup>, STEFAN MERKER<sup>8</sup>, ANDREW KITCHENER<sup>9</sup>, LUCA POZZI<sup>10</sup>, GUOJIE ZHANG<sup>11,12,13,14</sup>, CHRISTIAN ROOS<sup>15</sup>, JEFFREY ROGERS<sup>16</sup>, KYLE KAI-HOW FARH<sup>17</sup> and TOMAS MARQUES-BONET<sup>1,18,19,2</sup>

<sup>1</sup>Institute of Evolutionary Biology, Universitat Pompeu Fabra-CSIC, <sup>2</sup>CNAG-CRG, Centre for Genomic Regulation (CRG), Barcelona Institute of Science and Technology (BIST), Baldori i Reixac 4, 08028 Barcelona, Spain, <sup>3</sup>Universitat Pompeu Fabra (UPF), Barcelona, Spain, <sup>4</sup>Genomics & Microbiology Research Lab, North Carolina Museum of Natural Sciences, Raleigh, North Carolina, USA, <sup>5</sup>Department of Biological and Biomedical Sciences, North Carolina Central University, Durham, North Carolina, USA, <sup>6</sup>Department of Evolutionary Anthropology, Duke University, Durham, NC, <sup>7</sup>School of Science, Engineering & Environment, University of Salford, Salford, UK, <sup>8</sup>Department of Zoology, State Museum of Natural History Stuttgart, Germany, <sup>9</sup>Department of Natural Sciences, National Museums Scotland, Edinburgh, UK, <sup>10</sup>Department of Anthropology, University of Texas at San Antonio, San Antonio, TX, USA, <sup>11</sup>Section for Ecology and Evolution, Department of Biology, University of Copenhagen, Copenhagen, Denmark, <sup>12</sup>Center for Excellence in Animal Evolution and Genetics, Chinese Academy of Sciences, Kunming, China, <sup>13</sup>State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China, <sup>14</sup>China National Genebank, BGI-Shenzhen, Shenzhen, China, <sup>15</sup>German Primate Center, Leibniz Institute for Primate Research, Göttingen, Germany, <sup>16</sup>Human Genome Sequencing Center, Baylor College of Medicine, Houston, Texas, <sup>17</sup>Illumina Artificial Intelligence Laboratory, Illumina Inc, San Diego, CA, USA, <sup>18</sup>Institució Catalana de Recerca i Estudis Avançats (ICREA), Barcelona, Spain, <sup>19</sup>Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, Spain

Tremendous effort has been made to study the ecology and evolution of strepsirrhines and tarsiers. However, in comparison to the anthropoids, they remain relatively understudied. This disparity is particularly evident in the field of genomics. While the number of non-anthropoid genome studies has increased in recent years, genomic resources are only available for a small number of species. This relative dearth of information has limited the extent to which the remarkable ecological, phenotypic, and demographic diversity of these primates can be studied. As part of the Primate Sequencing Conservation Initiative, we have sequenced whole genomes from 102 individuals in 59 species (37 Lemuroidea, 17 Lorisioidea, and 5 Tarsiiformes) to high coverage (average of ~30X). The majority of these individuals are wild-born, and from species for which whole genomes have never been sequenced.

Using this broad panel of genomes, we examine patterns of genetic diversity, demographic history, phylogeny, and genetic introgression, observing a wide range of variation. Secondly, we examine the role of local adaptation to eco-geographic regions of Madagascar. We also identify relationships between digestive and chemosensory genes and ecological variation. In particular, we focus our efforts on the families Lemuridae and Indriidae from which we have sequenced most commonly recognized species. We provide new insights relevant to the ecology and evolution of these understudied primates and valuable genomic resources for ongoing conservation efforts.

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## Exploring the potential of pulp stones in reconstructing diet: A comparative study of carbon and nitrogen stable isotopes in pulp stones and incremental dentine

BRETT OSTRUM<sup>1</sup>, DARREN R. GRÖCKE<sup>2</sup> and JANET MONTGOMERY<sup>1</sup>

<sup>1</sup>Archaeology, Durham University, <sup>2</sup>Earth Sciences, Durham University

Pulp stones, mineralized masses that may form inside the dental pulp chamber, have primarily been studied from a clinical perspective, with research concentrating on their morphology, prevalence, and possible etiologies in modern populations. The potential of pulp stones to reveal information about past populations, however, has been relatively understudied. Here, we investigate whether pulp stones from three Early Neolithic (c. 3720–3650 cal BC) individuals from the Whitwell Long Cairn (Derbyshire, England) can provide dietary information through carbon ( $\delta^{13}\text{C}$ ) and nitrogen ( $\delta^{15}\text{N}$ ) isotope analysis, and evaluate if the results can be used in conjunction with those from incremental dentine samples to extend the life histories of these individuals. Six molars (two per individual) were analyzed, four of which contained pulp stones. Collagen was extracted from one-millimeter dentine increments and a portion of each pulp stone. For the dentine samples, the mean  $\delta^{13}\text{C}$  value was  $-21.5 \pm 0.2\text{‰}$  and the mean  $\delta^{15}\text{N}$  value was  $9.9 \pm 0.5\text{‰}$ . The pulp stones had comparable  $\delta^{13}\text{C}$  values ranging from  $-21.6$  to  $-21.4\text{‰}$ , and  $\delta^{15}\text{N}$  values ranging from  $9.1$  to  $9.8\text{‰}$ . Pulp stones from two individuals likely reflect diet from a time period later than their dentine increments. For the third individual, it could not be determined when their pulp stones formed relative to their dentine samples. This study demonstrates that pulp stones can provide dietary information and, when coupled with

isotopic results from incremental dentine, may in some cases extend the life histories of individuals beyond the timeframes provided by primary dentine.

## 13,000-years of climate change and food-security-risk management of Great Plains foragers and farmers 13,000-years of climate change effects on diet, foraging risk, and demography of Great Plains foragers and farmers

ERIK R. OTAROLA-CASTILLO<sup>1</sup>, MELISSA G. TORQUATO<sup>1</sup> and MATTHEW E. HILL<sup>2</sup>

<sup>1</sup>Anthropology, Purdue University, <sup>2</sup>Anthropology, University of Iowa

**Introduction:** The management of food-security-risk is a significant global challenge. Estimates reveal that nearly 1 in 9 people is undernourished worldwide. Predictions show that drastic climate changes will adversely impact food source availability and further exacerbate malnutrition worldwide. Managing food-security-risk resulting from climate change is not a new problem for humans. Our ability to survive through climate change has been a feature of human evolution. Despite this, the impact of climate on prehistoric small-scale societies' food-security-risk management is not widely known.

**Methods:** We applied multivariate optimization to evaluate whether resource diversity was a strategy used to mitigate food-security-risk and examined the impact of climate variation and food-security-risk on the diet patterns from multiple archaeological sites from the North American Great Plains and bordering regions (>2,600).

**Results:** There is significant variation in behaviors to manage food-security-risk across time on the Great Plains. For example, during ~8.5-6 thousand years BP (cal) these data show a striking increase in food-security-risk ( $t$ -ratio=2.53,  $p<0.05$ ). The patterning corresponds to the Holocene Climatic Optimum, a period on the Great Plains when resources were likely scarce. Bayesian modeling results show that food-security-risk, annual temperature, precipitation, and temperature seasonality impacted dietary diversity. Statistical interactions show that Great Plains people alternated between generalist-specialist strategies to deal with fluctuations in climate associated food-security-risk.

**Conclusion:** Spatio-temporal results show that Great Plains people responded to climate change and food-security-risk by adjusting their dietary diversity. These results contribute insight into the impacts of climate changes on human-environment interactions over the past 13,000 years.

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### Association between parity and tooth loss among northern Nigerian Hausa women

ELIZABETH O. OZIEGBE<sup>1,2</sup> and LYNNE A. SCHEPARTZ<sup>2,3</sup>

<sup>1</sup>Faculty of Dentistry, Obafemi Awolowo University,  
<sup>2</sup>Anatomical Sciences, Univ. Witwatersrand,  
<sup>3</sup>Museum of Archaeology and Anthropology,  
University of Pennsylvania

**Introduction:** Female reproduction is associated with physiological and nutritional demands that can negatively effect health and may be cumulative when parity is high. Maternal oral health is likely to be similarly affected, although this has not been adequately tested using high parity women and investigating key potential confounders.

**Objective:** To determine the relationship between parity level and tooth loss in a population with many high parity women while considering age, duration of reproduction and age of first birth, education, SES, BMI, sugar intake, caries, periodontal disease, oral hygiene and dental care.

**Materials and methods:** The cross-sectional study design involved 612 Hausa women of all parity levels aged 13-65 years. Women with  $\geq 5$  children were considered high parity. All teeth present, excluding third molars, were recorded. Missing teeth were noted excluding agenesis or traumas. SES and oral health practices were collected using a structured interviewer-administered questionnaire. Associations with tooth loss were evaluated through ANOVA, post hoc analyses and Student's t-tests. Effect sizes were used to interpret the magnitude of differences. Binomial regression was performed to determine the factors that contributed to tooth loss.

**Results:** Hausa women had a low prevalence of tooth loss (14.1%), despite poor oral hygiene and limited use of dental facilities. Older and higher parity women experienced significantly more tooth loss ( $p=0.00$ ). Increased duration of reproductive years was significantly related to fewer remaining teeth.

**Conclusion:** Higher parity was related to significantly greater tooth loss. Women with  $\geq 5$  children experienced more tooth loss than age mates with fewer children.

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### Migration and biological continuity in central Mexico during the Classic-Epiclassic transition

SOFÍA I. PACHECO-FORÉS<sup>1</sup> and CHRISTOPHER M. STOJANOWSKI<sup>2</sup>

<sup>1</sup>Anthropology Department, Hamline University,  
<sup>2</sup>School of Human Evolution and Social Change,  
Arizona State University

Archaeologists have long debated the role of migration in the cultural development of pre-Hispanic central Mexico. Archaeological models suggest that central Mexico experienced

increased migration during the Epiclassic period (600-900 CE) and that migrants may have originated in northwestern Mexico. While previous biodistance analyses of Classic and Postclassic populations have come to similar conclusions, none have incorporated Epiclassic skeletal populations. This study uses multi-scalar biodistance analyses of Epiclassic populations to directly evaluate archaeological Epiclassic migration models within central Mexico. Finite mixture and relationship (R) matrix analyses of cervicometric tooth dimensions are used to reconstruct patterns of biological affinity among Classic and Epiclassic Mesoamerican populations ( $n=333$ ), including at the central Mexican Epiclassic shrine site of Non-Grid 4 where biogeochemical analyses identified large numbers of migrants. Estimated inter-site genetic distances demonstrate support for some degree of both biological continuity and extra-local gene flow within central Mexico during the Classic-Epiclassic transition. Furthermore, genetic distances and finite mixture posterior probabilities indicate central Mexican Epiclassic populations were biologically diverse, originating from various source populations throughout Mesoamerica, including the Bajío region, the Malpas Valley, and the Oaxaca Valley. Results suggest that a perspective of biological admixture may be more appropriate to understand central Mexican population structure during the Classic-Epiclassic transition. Moreover, analyses support previous archaeological migration models positing Epiclassic migrants into central Mexico originated in northwestern Mexico, but also find evidence of migrants originating from previously unanticipated locales like southern Mexico.

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### Do captive lemurs have mites (Class: Arachnida)?

LISA PACIULLI, DAVID DENTON, MCKENZIE NALLEY and TAEIM KWON

Biological Sciences, North Carolina State University

Mites are small arthropods belonging to the class Arachnida. They are distantly related to spiders and scorpions. Mites can cause asymptomatic or symptomatic reactions in their hosts, with extreme cases causing and/or exacerbating disease. Nonetheless, there have been few studies on the relationship between mites and non-human primates (NHP), including lemurs. Therefore, in this study, captive lemur hair was examined for the presence of mites. The hypothesis was that some lemur species would have a higher density of mites than other species, and that the sex or age of lemurs would affect mite presence. The study was conducted under the Duke Lemur Center (DLC) Institutional Animal Care and Use

Committee (IACUC) blanket protocol. Hair from six facial and eight limb regions of lemurs undergoing medical attention that differed by genus and species was examined under a compound light microscope. Fifteen lemurs from nine different species were sampled from varying sex and age classes. The results showed that there were no statistical associations between lemur sex or age and mite presence. Also, five lemurs had mites, and crowned lemurs (*Eulemur coronatus*) had more mites than the other species. It is unclear why crowned lemurs had more hair mites than the other species sampled. The information from this study will not only contribute to the lack of knowledge on non-human primate mites, but also provide insight into the relationship between mites and lemurs. Future research should include genetics to identify mite species, as well as the health of lemurs with mites.

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### Evidence of Trophy Taking Behavior in Prehistoric Japan

BRIAN D. PADGETT<sup>1,2</sup> and NORIKO SEGUCHI<sup>3,4</sup>

<sup>1</sup>Scientific Analysis Directorate, Defense POW/MIA Accounting Agency (DPAA), <sup>2</sup>Department of Anthropology, The Ohio State University, <sup>3</sup>Department of Anthropology, The University of Montana, Missoula, <sup>4</sup>Faculty of Social and Cultural Studies, Kyushu University

Skeletal evidence of violent trauma has been recognized in human remains from the Yayoi period of Japan (~900 BCE – 250 CE), with wounds resulting from arrows, bronze swords, and other weapons, but details on the enactment, motivations, or symbolism of violence have not been explored. During a re-examination of skeletal remains recovered from Yayoi sites in Kyushu, several cases of unusual perimortem defects to crania were observed. A forensic approach, in combination with culturally contextualized considerations, was applied in the examination of the remains. Interpretation of the skeletal evidence suggests that human heads were occasionally taken as trophies and mounted for display.

Non-random patterns of skull burials and headless burials were observed that suggest that victims tended to be middle-aged male adults, some of whom were in a suboptimal physical condition at the time of death. Observations of cranial defects suggest multiple methods of trophy display were practiced. Furthermore, two cases suggest that heads were sometimes returned to the home group for interment with the postcranial remains. These patterns suggest that victims were political leaders of subordinated groups.

Intergroup conflict for political power was part of the process leading to an emergent state society. This research contributes to our understanding

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of violent conflict in Japanese prehistory. This violence and the associated symbolism of dominance and subordination may have played important roles in the consolidation of political power, as well as in the ethnogenesis of the Yamato people, the predominant ethnic group in Japan today.

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### Livelihood diversity and childcare in a foraging population, the Agta of Palanan, Philippines

ABIGAIL E. PAGE<sup>1</sup>, ANUSHÉ HASSAN<sup>1</sup>, MARK DYBLE<sup>2</sup>, DANIEL SMITH<sup>3</sup> and ANDREA B. MIGLIANO<sup>4</sup>

<sup>1</sup>Department of Population Health, LSHTM, <sup>2</sup>Department of Anthropology, University College London, <sup>3</sup>Department of Anthropology, University of Bristol, <sup>4</sup>Department of Anthropology, University of Zürich

A wide range of cross-cultural, contemporary and historical studies have highlighted that mothers are not alone in raising their children. Fathers, grandmothers, older siblings and non-kin are all pointed to as key allomothers (non-maternal caregivers). Nonetheless, little exploration has occurred into why we see such diversity in allomothers. Arguably, human cooperation evolved as a response to environmental and resource unpredictability, promoting cooperation when individuals could not reliably reproduce on their own. Wide cooperative childcare networks, thus, can be understood as a form of risk transfer (an informal insurance network) associated with an unpredictable foraging livelihood. When individuals settle, farm and increase storage and wealth (risk retention) they may rely on their own ability to absorb losses and remove themselves from wider cooperative networks. Thus, who provides childcare may be a function of how individuals deal with risk, a hypothesis we test in data from the Agta (78 mother-child dyads), a diverse Philippine population who demonstrate variability in mode of subsistence, degree of mobility and household wealth. Using mixed-effect models on childcare observations, we found that fathers and older siblings invested significantly less in foraging households. Likewise, households with increased wealth received less childcare from distant and non-kin. Thus, foraging was associated with wider, less related cooperative networks while settled cultivation was associated with childcare from within the nuclear family. This finding supports our hypothesis that different forms of livelihoods promote different types of risk mitigation. Overall, our results reinforce the necessity of exploring diversity in who supports mothers raising children.

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### Infant Feeding during the COVID-19 Pandemic in the U.S

AUNCHALEE EL. PALMQUIST<sup>1</sup>, CAROLYN FOX<sup>2</sup>, STEPHANIE CHUNG<sup>1</sup>, CECILIA TOMORI<sup>3</sup> and E.A. QUINN<sup>2</sup>

<sup>1</sup>Department of Maternal and Child Health, University of North Carolina at Chapel Hill, <sup>2</sup>Anthropology, Washington University in St. Louis, <sup>3</sup>Population, Family and Reproductive Health, John Hopkins University

When SARS-CoV-2 appeared in the United States, a combination of unclear guidelines and unknown information made it difficult for parents of infants and young children to make informed decisions about infant feeding. 1726 parents in the USA completed an online survey between 03/25/20 – 04/20/20 about the impact of COVID-19 on their infant feeding decisions. The majority of participants were White (87%), a well known bias of online survey research. Mean maternal age was 32 years; mean infant age was 7 months.

The majority (95%, n=1642) were providing their infants with some human milk. Of parents who were breastfeeding, 29.9% (n=461) reported an increase in nursing frequency due to being home more, and 14.2% (n=219) of parents changed their weaning or feeding plans due to COVID-19; with the overwhelming majority (95%) weaning later than planned. Opened ended questions exploring maternal decision making found that the desire to provide protective antibodies to infants were primary reasons for delaying human milk cessation.

Parents had also heard conflicting information about the risks or benefits of providing human milk during COVID-19 and expressed a desire for more information. While 8.7% (n=150) had COVID-19 symptoms, only 3.8% (n=67) were able to get a positive COVID-19 test. Of those with confirmed positive COVID-19 tests, the majority (65.6%) continued direct breastfeeding; 15% were pumping and using human milk and 10% had stopped breastfeeding/expressing human milk.

COVID-19 led parents to reassess their lactation plans, and parents reported stress and concerns about contradictions in the COVID-19 guidelines.

### Ratios of Dental Surface Concavity and Convexity: Implications for Dental Topography Analyses

JAMES D. PAMPUSH<sup>1,2</sup>, PAUL E. MORSE<sup>3,4</sup>, EDWARD J. FUSELIER<sup>5</sup> and RICHARD F. KAY<sup>3,6</sup>

<sup>1</sup>Exercise Science, High Point University, <sup>2</sup>Physician Assistant Studies, High Point University, <sup>3</sup>Evolutionary Anthropology, Duke University, <sup>4</sup>Florida Museum of Natural History, University of Florida, <sup>5</sup>Mathematical Sciences, High Point University, <sup>6</sup>Division of Earth and Ocean Sciences, Nicholas School of the Environment, Duke University

Among dental topography metrics, Dirichlet normal energy (DNE) seems to best quantify occlusal sharpness, which presumably translates into DNE's success in sorting primate molar morphology into traditional heuristic dietary categories. Despite DNE's successful application to prosimian and monkey dentitions, some confounding results have emerged from its application to hominid teeth. One potentially complicating factor is its inability to distinguish concave from convex surface curvature. Sorting the surface contributions according to curve inflection boundaries should make the metric more reflective of dietary adaptation, since the deep recesses (sulci) of the concave portions of the surface are unlikely to aid in food-breakdown, despite their large contributions to DNE values. Here we present a modification to DNE that allows users to sort convex from concave components of DNE. We show that this modification has minimal impacts on many prior studies of molars using DNE, because for most primates, occlusal convexity dominates the DNE signal. In contrast, hominid molars have much larger contributions from concave aspects of the occlusal surface due to their deep sulci and crenulated enamel. After accounting for inflection boundaries, hominid convex DNE is more similar to the bunodont dentitions of omnivores rather than the high-crowned dentitions of monkey and strepsirrhine folivores. Explanations for the relatively large contribution from hominid occlusal concave areas include: [1] deeper sulci due to inflated relative enamel thickness; [2] an allometric effect concentrated on occlusal sulci; and/or [3] an adaptive response to hard object feeding. Future hominid studies should differentiate the surface inflection components of DNE.

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### Islands and Bubbles: Lessons from the 1918-19 Influenza Pandemic

JOSEPH M. PARISH  
L'nu, Political, and Social Studies, Cape Breton University

A century after the worst global pandemic in memory, we are visited by a virus that has thrown the world into chaos. Public health warnings and how populations interpret them demonstrate the impact socio-cultural behaviours have on epidemics. Contact rates are not governed by biological mechanisms – they are only made possible through them.

This poster explores the initial findings of a multi-year project focussed on the 1918-19 influenza pandemic on Cape Breton Island, Canada. Early indications from this study suggest that a natural population bubble caused by the island environment of Cape Breton may have had a similar effect in 1918-19 to what we are witnessing in

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today's pandemic. However, deaths from related respiratory infections were unaffected or even declined in the period following the pandemic. The records also show that the traffic of military personnel may have negatively contributed to the arrival of the pandemic.

Data for this project were drawn from the Nova Scotia civil registrations, which were re-started in 1908, and are publicly available. The website hosting the records is designed for genealogical research, so a workaround was created to access each record individually. Almost 5,500 records were transcribed completely for 1918-1919 for all four counties and for 1920-1924 for two of the four counties. Each contains up to 49 fields of entry including sex, age, cause of death, birthplace, length of illness, and address. The data were analysed for cause of death information and reported with mortality curves for age and month of death.

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### Bioarchaeology and forensic anthropology and as unique expertises

NICHOLAS V. PASSALACQUA<sup>1</sup>, MARIN A. PILLOUD<sup>2</sup> and DEREK CONGRAM<sup>3</sup>

<sup>1</sup>Anthropology and Sociology, Western Carolina University, <sup>2</sup>Anthropology, University of Nevada - Reno, <sup>3</sup>Colombia, International Committee of the Red Cross,

Over the past several decades, various methods have been developed addressing applications and research agendas within bioarchaeology and forensic anthropology, with differing foci based on the nature of these disciplines. These differing research agendas have increasingly diverged into academic programs and graduate advisors specializing in bioarchaeological or forensic anthropological approaches. In doing so, bioarchaeology and forensic anthropology have slowly deviated in terms of professional conferences attended, academic advisors and institutions, bodies of literature, venues of publication, and professional memberships. Through this divergence, they have become more and more isolated from each other, developing separate communities of practice.

The goal of this presentation is to consider both bioarchaeology and forensic anthropology as unique disciplines following Collins and Evans' (2007) model of expertise, where disciplinary experts are those with "Contributory Expertise". Contributory experts are those that are able to interact with other individuals at a complex level and able to perform complex disciplinary tasks competently (Collins et al., 2016). Within this model, both bioarchaeology and forensic anthropology share many lower-level expertises, representing what Collins and Evans (2007) refer to as primary source knowledge. However,

as specialization increases, there is decreasing overlap in expertise. These distinctions in knowledge area and expertise are important, as without the appropriate the appropriate amount of expertise, practitioners perform tasks inappropriately and/or incorrectly. The only way to develop contributory expertise is through enculturation and as Collins and Evans (2007) point out, lacking such enculturation at the level of contributory expertise leads to overconfidence and poor performance.

N/A

### Maternal behavior and glucocorticoid levels shape infant development in wild olive baboons

SAM K. PATTERSON<sup>1</sup>, KATIE HINDE<sup>1,2</sup>, ANGELA B. BOND<sup>2</sup>, BENJAMIN C. TRUMBLE<sup>1,2</sup>, AMY LJ<sup>3</sup>, SHIRLEY C. STRUM<sup>4,5</sup> and JOAN B. SILK<sup>1</sup>

<sup>1</sup>School of Human Evolution and Social Change, Arizona State University, <sup>2</sup>Center for Evolution and Medicine, Arizona State University, <sup>3</sup>Department of Anthropology, Stony Brook University, <sup>4</sup>Department of Anthropology, University of California, San Diego, <sup>5</sup>Uaso Ngiri Baboon Project, Kenya

Mammalian mothers provide offspring with critical behavioral and physiological signals that allow offspring to adaptively calibrate development in relation to environmental cues. Such signals are hypothesized to prioritize certain developmental systems over others, orchestrating developmental tradeoffs between competing systems. Here, we investigate the influence of maternal effort and maternal glucocorticoids (GCs) on infant play, independence, and growth in wild olive baboons (*Papio anubis*) from Laikipia, Kenya. We collected behavioral data from 41 infants to quantify maternal effort (e.g., nursing and carrying time), infant play, and infant independence (i.e., frequency of infant departures from mother). We paired these behavioral data with maternal glucocorticoid measures analyzed from 864 fecal samples from lactating mothers, and infant growth measures assessed via photogrammetry (N=20 infants). We found that mothers who spent more time nursing and carrying – patterns associated with lower rank and adversity – produced infants who played less (nursing:  $\beta=-0.52$ ; carrying:  $\beta=-0.70$ ), were less independent (nursing:  $\beta=-0.33$ ; carrying:  $\beta=-0.62$ ), but grew faster (nursing:  $\beta=0.22$ ; carrying:  $\beta=0.60$ ) than infants of mothers who nursed and carried less. Sons of mothers with higher GCs played less ( $\beta=-0.23$ ) but grew faster (sex\*GC  $\beta=-1.40$ ) than sons of mothers with lower GCs. Daughters of mothers with higher GCs grew slower than those of mothers with lower GCs (sex\*GC  $\beta=-1.40$ ). These results add to a growing body of literature demonstrating that maternal behavioral and physiological signals shape various components

of infant development in different and sex-specific ways. By creating comprehensive models, we can better understand the complexities of developmental trajectories.

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### An expanded simulation study of past biological structure in the Americas: dental morphology, quantitative genetics, and biodistance "best practices"

KATHLEEN S. PAUL<sup>1</sup>, CHRISTOPHER M. STOJANOWSKI<sup>2</sup> and G. RICHARD SCOTT<sup>3</sup>

<sup>1</sup>Department of Anthropology, University of Arkansas, <sup>2</sup>Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona State University, <sup>3</sup>Department of Anthropology, University of Nevada Reno

Exploring ancient biocultural diversity in the Americas often involves reconstructions of population interaction and microevolutionary processes. Dental morphology features prominently in these initiatives due to the taphonomic durability of dental tissues and the cost-effective, non-destructive nature of phenotypic data collection. While tooth morphology has long been used to approximate underlying genotype, heritability estimates have only recently been reported for several characters. Quantitative genetic approaches have also yielded a suite of analytical "best practices" for dental biodistance research. We previously applied these proscribed practices to simulated analyses of dental morphology data to assess whether reconstructions of population relationships across the Americas are sensitive to trait choice, dichotomization, and weighting. Here, we expand these efforts to a) incorporate data from four additional Archaic North American samples, b) compare simulations that follow distinct missing data treatments (omission versus estimation), and c) compare four simulations that weight traits based on narrow-sense heritability estimates yielded from distinct reference samples. Frequency data were analyzed using proximity measures and hierarchical clustering. Initial results indicate our 19 samples represent three to seven bioregional clusters, with "best fit" varying by data treatment. Simulation dendrograms reveal consistent primary branching of the Archaic Quebec and Archaic California samples; the other Archaic samples are in close proximity on a more inclusive branch. The exceptions are the heritability-weighted simulations, which stray from this pattern depending on the reference estimates applied. These results underscore the sensitivity of dental morphology data to analytical treatment and potential complications arising from broad temporal binning of samples.

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### Making sense of modern human sulcal pattern variation, brain size and temporal lobe boundaries: implications for fossil *Homo*

ALANNAH PEARSON<sup>1</sup>, P. DAVID POLLY<sup>2</sup> and EMILIANO BRUNER<sup>3</sup>

<sup>1</sup>School of Archaeology and Anthropology, The Australian National University, <sup>2</sup>Department of Earth and Atmospheric Sciences, Indiana University, Bloomington, <sup>3</sup>Department of Paleobiology, Centro Nacional de Investigacion sobre la Evolucion Humana

Brain evolution involves changes in processing centres often marked by cerebral folds including sulci and gyri. In the temporal lobe, identification of major cerebral divisions relies on both external and internal sulci especially the superoposterior boundary for the temporoparietal-occipital complexes. Comprehensive quantification of noticeable sulcal variation in extant *Homo sapiens* remains lacking with limitations for paleoneurological inferences of fossil *Homo* endocasts. We examined the association between temporal lobe volume (TLV), left and right hemispheres volume (HV) of the brain (in cm<sup>3</sup>) in T1-weighted *in vivo* Magnetic Resonance Imaging (MRI) of 59 adult humans (male N = 28, female N = 31) generated into three-dimensional virtual models of the brain and identified sulcal variants for the posterior ascending and descending rami of the Sylvian fissure and the ascending and horizontal segments of the superior temporal sulci. Canonical Correspondence Analysis (CCA) examined if the presence or absence of specific sulcal variants was associated with an increase or decrease in TLV or HV. Axis 1 and Axis 2 were associated with TLV and a unique ascending superior sulcal variant, where the presence of this specific variant of the ascending superior temporal sulcus was associated with a smaller left TLV and a larger right TLV. These findings suggest an association between extreme hemispheric asymmetries in modern humans, where absolute brain size, temporal lobe size and the presence of unique sulcal variants at the superoposterior boundary of the temporal lobe offers new possibilities to delimit the temporal lobes in fossil *Homo* endocasts.

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### Detecting signatures of archaic introgression and the not so simple evolutionary history of the major histocompatibility complex

DAVID PEEDE<sup>1</sup>, FEDERICA PIERINI<sup>2</sup>, MARÍA C. ÁVILA-ARCOS<sup>3</sup>, FLORA JAY<sup>2</sup> and EMILIA HUERTA-SÁNCHEZ<sup>1,4</sup>

<sup>1</sup>Ecology and Evolutionary Biology, Brown University, <sup>2</sup>Laboratoire de recherche en informatique, Université Paris-Saclay, CNRS, Inria,

<sup>3</sup>International Laboratory for Human Genome Research, Universidad Nacional Autónoma de México (México), <sup>4</sup>Center for Computational Molecular Biology, Brown University

The major histocompatibility complex (MHC) plays a crucial role in adaptive immunity among vertebrates, and in humans is home to some of the most variable loci in the genome. It is commonly thought that selection favors heterozygous loci that are involved in adaptive immunity as being heterozygous allows for the increased recognition of pathogens. Selection for heterozygous loci will consequently favor introgressed loci since an introgressed locus on a new genetic background is likely to be heterozygous. However, the evolutionary mechanisms that gave rise to the high levels of diversity seen in the MHC region are still hotly debated. Balancing selection—the maintenance of more than one allele in a population—, negative frequency-dependent selection—rare variants having a selective advantage over common variants—, and soft selective sweeps—neutral loci becoming beneficial due to an environmental change— all favor heterozygous loci and are possible explanations for the maintenance of diversity in the MHC region. By analyzing the high-coverage genomes of archaic individuals and the individuals found in the 1000 Genomes Project, we investigate signals of introgression at the MHC region to determine whether introgression has increased levels of heterozygosity which might have facilitated adaptations to distinct pathogens. Furthermore, through coalescent simulations, we show that the levels of diversity found in the MHC region cannot be explained by demography alone suggesting that the MHC region has experienced many different selective pressures throughout its evolutionary history.

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### Forelimb and hind limb duty factor disequilibrium and patterns of limb support in primate locomotion

BERNADETTE A. PERCHALSKI<sup>1</sup> and DANIEL O. SCHMITT<sup>2</sup>

<sup>1</sup>Basic Medical Sciences, University of Arizona College of Medicine Phoenix, <sup>2</sup>Evolutionary Anthropology, Duke University

Primates use higher frequencies of diagonal sequence diagonal couplet (DSDC) gaits, and exhibit greater differences in periods of contact (duty factor, S) of the hind (SH) and forelimbs (SF) during walking compared to non-primates. DSDC gaits mix periods of contralateral and ipsilateral bipedal and tripodal supports in situations when SH is lower than the time between ipsilateral hind and fore footfalls (limb phase, D). We hypothesized that primates can avoid ipsilateral bipods when SH < D by increasing tripodal support via disequilibrium between SF and SH while

walking. We examined 271 bouts of locomotion in primates and felids and compared variation in support patterns with duty factor index (SI = SH/SF). SH and SF were correlated ( $r = 0.56$ ,  $p < 0.001$ ) across the sample. Proportions of bipedal support periods were negatively correlated with SH for walking gaits ( $r = -0.85$ ,  $p < 0.001$ ). 21% of all observed walking gaits used by primates lacked any ipsilateral bipedal support periods, and these bouts were associated with higher differences in SH and SF (average SI = 1.10) compared to bouts with ipsilateral bipedal supports (mean SI = 1.06). These tended to be slower walks, and SI was positively correlated with SH ( $r = 0.41$ ,  $p < 0.001$ ). Primates did not use unequal SH and SF more often when SH < D, possibly because at relatively high walking speeds ipsilateral support periods are not as detrimental to stability as in slower walks, where duty factor disequilibrium may increase tripodal support periods to improve stability.

Funding for this research was provided by the Duke Lemur Center Director's Fund and the National Science Foundation (NSF BSC 1751686).

### Biological anthropology and evolutionary genomics: Transformative opportunities and ethical obligations

GEORGE PERRY<sup>1,2</sup>, MARGARITA HERNANDEZ<sup>1</sup>, SYLVIA KOKUNDA<sup>3</sup> and LEVI BUSINGYE<sup>3</sup>

<sup>1</sup>Anthropology, Pennsylvania State University, <sup>2</sup>Biology, Pennsylvania State University, <sup>3</sup>Batwa Development Program, Uganda

The relationship history of biological anthropology and evolutionary genetics/genomics is complex. At best, genetics is a beautifully integrative part of the discipline. Yet this integration has also been fraught. At worst, evolutionary genomics has been a tool for reinforcing racism and colonialism. We will first present several ethical issues that we believe researchers in this field should take into consideration when designing their studies and disseminating results, including related to the re-use of previously collected samples, the re-analysis of previously published genomic data, risks of developing new hypotheses on the basis of genome-wide selection scan results, and the potential for results to be misappropriated for evil by racial supremacists and other hate groups or otherwise misconstrued. In this context we will also detail processes and learnings from our ongoing evolutionary genomics research with Batwa rainforest hunter-gatherer and Bakiga agriculturalist participant communities in southwest Uganda.

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### Surviving rickets: identifying episodes of childhood rickets in adult individuals from 19th century Hisban, Jordan

MEGAN A. PERRY<sup>1</sup>, COURTNEY OLAH<sup>1</sup>, AKACIA PROPST<sup>2</sup>, LORI D'ORTENZIO<sup>2</sup> and BONNIE KAHLON<sup>2</sup>

<sup>1</sup>Department of Anthropology, East Carolina University, <sup>2</sup>Department of Anthropology, McMaster University

Paleopathological study of a 19<sup>th</sup> century Bedouin group burying their dead near Hisban, Jordan found that over half of the infants (MNI = 24) display skeletal evidence of rickets. The older children and adults represented in the sample, (MNI = 28) do not have rickets or osteomalacia indicative of past or current vitamin D deficiency. Thus, macroscopic skeletal data suggests rickets was primarily a condition of infancy and linked to high infant mortality.

While rickets is unexpected in an agropastoral community living in the UV-rich region of central Jordan, vitamin D deficiency is prevalent among women of childbearing age in modern Jordan and the MENA region, which results in newborns with low serum 25(OH)D levels. Clinical studies link this deficiency to calcium-poor diets, high parity, prolonged breastfeeding, and limited time spent outdoors. Some MENA communities also have a genetic predisposition to hereditary hypophosphatemic rickets (HHR) through mutations involving fibroblast growth factor 23 (FGF23) or vitamin D receptors (VDR). Observing pulp chamber morphology and presence of interglobular dentine (IGD) in 10 first molars and 17 second molars representing adolescents and adults with no skeletal signs of vitamin D deficiency at death indicates that approximately 58% survived at least one episode of vitamin D deficiency, with few differences in terms of severity and timing by sex. Estimated age of occurrence indicates the episodes occurred from just after birth until at least 15 years of age. This indicates rickets at Hisban is not limited to infancy nor tied to an X-linked HHR trait.

### Female Kinda baboon sexual signals are less accurate indicators of fertility

MEGAN PETERSDORF<sup>1,2</sup>, ANNA H. WEYHER<sup>3</sup>, MICHAEL HEISTERMANN<sup>4</sup>, ALISON GOVAERTS<sup>5</sup>, JESSICA L. GUNSON<sup>1,2</sup> and JAMES P. HIGHAM<sup>1,2</sup>

<sup>1</sup>Department of Anthropology, New York University, <sup>2</sup>New York Consortium in Evolutionary Primatology, NYCEP, <sup>3</sup>Department of Anthropology, University of Massachusetts Amherst, <sup>4</sup>Endocrinology Laboratory, German Primate Center, Leibniz Institute for Primate Research, <sup>5</sup>Department for the Ecology of Animal Societies, Max Planck Institute of Animal Behavior

There is variation in the extent to which primate female sexual signals reliably indicate fertility, which may be related to the predominant mechanisms of sexual selection. More accurate

signals are often found in species with stronger direct male-male competition and indirect female mate choice, and less accurate signals in species with stronger indirect male-male competition and direct female mate choice. We tested this hypothesis in a wild population of Kinda baboons in Zambia, combining data on female signals with hormonally-determined fertile-phases. We predicted that Kinda baboons will exhibit less accurate fertility signals as they experience weaker direct and stronger indirect male-male competition. The frequency of copulation calls and proceptive behavior did not differ across the fertile, pre- or post-fertile phases of the cycle. Sexual swellings were largest in the fertile-phase, however, the differences in the mean sexual swelling size across cycle phases were small, raising the question if males can perceive this variation. Additionally, there was high variability in the timing of ovulation relative to the day of sexual swelling detumescence across cycles. Our results suggest that female Kinda baboon signals are less accurate indicators of fertility across signal modalities. These signals may have evolved as a reproductive strategy to reduce male monopolizability, allowing for more female control over reproduction by direct mate choice.

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### Kinship predicts genetic similarity at class II but not class I MHC loci in olive baboons

RACHEL M. PETERSEN<sup>1,2</sup>, CHRISTINA M. BERGEY<sup>3</sup>, CHRISTIAN ROOS<sup>4</sup> and JAMES P. HIGHAM<sup>1,2</sup>

<sup>1</sup>Department of Anthropology, New York University, <sup>2</sup>New York Consortium in Evolutionary Primatology, <sup>3</sup>Department of Genetics, Rutgers University, <sup>4</sup>Primate Genetics Laboratory, German Primate Center

The role of the major histocompatibility complex (MHC) in the process of mate choice is of considerable interest due to its established influence on the immune system, body odor, and potential effects on fitness. Disassortative mating based on MHC composition has been suggested as a means to avoid inbreeding and maximize heterozygosity at this functionally important region. However, empirical studies have found varied support for MHC disassortative mating, and evidence for both assortative mating and 'allele-counting' strategies are apparent in certain study systems. Here, we explore how kinship relates to genetic similarity at the MHC region, as a means to understand how MHC associated mate choice may relate to inbreeding avoidance. We conducted ddRAD sequencing and PCR amplification and sequencing of two class I and two class II MHC loci from the whole blood of 22 captive olive baboons (*Papio anubis*) living at

the CNRS Station de Primatologie in France. We performed a kinship analysis using 26,393 genotyped SNPs and identified 8-13 class I and 2-9 class II MHC alleles per individual. We further identified functionally relevant MHC supertypes based on the physicochemical properties of amino acids involved in antigen binding. Kinship was a significant predictor of shared alleles and supertypes at class II, but not class I loci. These results suggest that the selective pressures maintaining allelic diversity at class I and II loci may differ, and that certain types of MHC driven mate choice have the potential to work independently from mechanisms of inbreeding avoidance.

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### The fall of Meroe: Invasion or decline? The dental evidence

EMMA LW. PHILLIPS<sup>1,2</sup>, JOEL D. IRISH<sup>1</sup> and DANIEL ANTOINE<sup>2</sup>

<sup>1</sup>School of Biological and Environmental Sciences, Liverpool John Moores University, <sup>2</sup>Department of Egypt and Sudan, The British Museum

The Meroitic empire of ancient Nubia ruled over a vast area of the Nile Valley and its hinterlands from ~800BC until 350AD. What caused the empire and its capital Meroe to fall has been widely debated. A popular theory is that Aksumites from northeast Africa were responsible for the demise. How long the Aksumites were in Nubia and whether they permanently settled the region have not been fully explored. This study investigates whether there is biological continuity between the Meroitic and successive regional cultures or if northeast African groups may have contributed to the local gene pool.

Nubian samples from 9 sites across the Nile Valley were compared based on 36 nonmetric dental traits (using the ASUDAS). These specific sites date to the Meroitic (300BC-350AD) through Medieval periods (AD 500-1500). Additional data from Ethiopia and Somalia were used to contextualise the Nubian findings. The mean measure of diverge distance statistic was then applied to calculate inter-sample bio-distances. Multi-dimensional scaling was used to visualize affinities.

Results indicate that there are regional differences in the level of continuity between the Meroitic and successive periods. The post-Meroitic assemblages show the closest affinity to the northeast African samples (MMD=0.04-0.12,  $p \leq 0.05$ ), and the similarity reduces in the medieval period (MMD=0.11-0.17,  $p \leq 0.05$ ). These data suggest a greater genetic influence from northeast

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Africa after the fall of Meroe. This gives credit to the Aksumite involvement in the fall of Meroe, although their presence in Nubia appears to have lasted for only a few centuries.

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### HLA evolutionary trends in admixed Native American populations

FEDERICA PIERINI<sup>1</sup>, DAVID PEEDE<sup>3</sup>, MARÍA C. ÁVILA-ARCOS<sup>2</sup>, EMILIA HUERTA-SANCHEZ<sup>3</sup> and FLORA JAY<sup>1</sup>

<sup>1</sup>Université Paris-Saclay, CNRS, Inria, Laboratoire de recherche en informatique (France), <sup>2</sup>International Laboratory for Human Genome Research, Universidad Nacional Autónoma de México (México), <sup>3</sup>Department of Ecology and Evolutionary Biology, Brown University

The highly polymorphic classical human leukocyte antigen (HLA) genes play a central role in adaptive immunity. Their extensive population polymorphism has been often regarded as a hallmark of past and ongoing pathogen-mediated selection. Owing to their central role in fighting pathogen invasion, HLA genes are also considered prime candidates for studying adaptive admixture. After admixture, specific HLA variants may be beneficial in the recipient population, and thus favored by selection. While various studies have shown signatures of natural selection on the HLA regions in admixed populations, the link between the signal and its functional consequences remain unsolved. In this regard, precise intragenic haplotypes analysis of HLA genes in admixed populations is of great interest for understanding their role in human adaptation to pathogens. Integrating currently available HLA data from different studies and databases we characterize the landscape of haplotypic diversity in various contemporary American admixed populations. We thus depict the HLA evolutionary trends, resulting from both the demographic and selection process, further showing how past admixture has contributed to the actual patterns of genetic diversity, heterozygosity, and haplotypic divergence observed in modern American admixed individuals.

This work was supported by the Human Frontiers Science Program

### Phenotypic plasticity of the *Macaca fascicularis* mandible: a geometric morphometric analysis of wild and biomedical populations

ERIN F. E. PINKSTON<sup>1</sup>, ROBIN L. QUATAERT<sup>2</sup>, BRITTANY KENYON-FLATT<sup>1,3</sup> and NOREEN VON CRAMON-TAUBADEL<sup>1</sup>

<sup>1</sup>Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, SUNY, <sup>2</sup>Comparative Primate Anatomy Laboratory,

Department of Anthropology, University at Buffalo, SUNY, <sup>3</sup>Department of Molecular Biomedical Sciences, North Carolina State University

While the biomechanical effects of varying primate diets have been studied with respect to mandibular shape, the limits of the phenotypic plasticity of the non-human primate jaw are not necessarily well understood. This study examines the resulting morphological variation between the differing diets of two sample populations of crab-eating macaques (wild and biomedical), focusing on medical interventions in the second population. Given that wild individuals consume more biomechanically demanding diets than biomedical individuals, and that biomedical specimens have different mastication patterns after having canines extracted or filed, we expect to find these patterns to result in distinct mandibular morphologies. To test this, landmarks ( $n=31$ ) were collected from 3D scans of mandibles from three populations of adult male *M. fascicularis*: 15 wild specimens and 32 biomedical specimens -16 with altered dentition (e.g., removed or filed canines), and 16 without altered dentition. Landmark configurations were subjected to a Principal Component Analysis (PCA), a Canonical Variates Analysis (CVA), and a Discriminant Function Analysis (DFA). The PCA and CVA highlighted differences in the height of the mandibular ramus, the slope of the gonial angle, and the length of the tooth rows, particularly between the biomedical and wild samples. The altered biomedical sample also displayed a unique morphology potentially related to the resorption of alveolar bone. The DFA results found similar rates of misclassification across all three samples, with the lowest rates of misclassification occurring between wild and altered biomedical populations, highlighting their differing morphologies.

This research is supported by the UB Research Foundation and the Mark Diamond Research Fund (SP-18-13).

### Do people use long-distance relationships to respond to climate variability?

ANNE C. PISOR<sup>1</sup> and JAMES HOLLAND JONES<sup>2</sup>

<sup>1</sup>Department of Anthropology, Washington State University, <sup>2</sup>Department of Earth System Science, Stanford University

At least since the emergence of *Homo*, social relationships spanning distance have been a characteristic feature of human social life. Such long-distance relationships have often been used to manage the risk of resource shortfalls posed by climate variability. However, given these relationships are costly to maintain, we should expect individuals to invest more in them when shortfalls are chronic, temporally positively autocorrelated, and not rare – that is, when shortfalls happen at least occasionally and are somewhat predictable. We evaluate these hypotheses in two communities of Bolivian horticulturalists ( $n=119$ ) where

cash crop production is negatively impacted by precipitation variability but access to long-distance connections is improving. To assess whether precipitation exposure predicts long-distance relationships, we drew on participants' migration histories, social relationships, and demographic data; we also used precipitation data from the US National Center for Atmospheric Research to estimate participants' exposure to unusually dry or wet months. Exposure duration, the temporal proximity of exposures, and exposure frequency was not associated with an individual's number of long-distance relationships. However, males, extraverted individuals, and those who had traveled more had more long-distance relationships. In the human lineage, another function of long-distance relationships is to access patchy resources that are never locally available; ethnographic data suggest that this is their primary function in rural Bolivia, not risk management. We close by refining our predictions about when individuals are likely to use long-distance relationships to manage climate variability and to explain how this can be better studied going forward.

Data collection was funded by the Max Planck Institute for Evolutionary Anthropology Department of Human Behavior, Ecology, & Culture.

### External Energy Exploitation and the Shared Evolutionary Roots of Climate Change and Chronic Disease

HERMAN PONTZER

Evolutionary Anthropology, Duke University

Modernization and industrialization have given rise to two global crises, climate change and non-communicable disease (NCD), which have surpassed infectious disease as the leading global causes of mortality. Here, I examine the shared root cause of climate change and NCD: humans' exploitation of and dependence on external (non-metabolic) energy expenditure (e.g., fire, fossil fuels). The human lineage has been reliant on external energy since the Lower Paleolithic with the use of fire for cooking and other tasks. Dependence on external energy has grown with the advent of agriculture and use of draft animals, the development of wind and water power, and most recently with the exploitation of fossil fuels. Fossil fuel powered mechanization has led to the reduction of physical activity, increased centralization and processing in food production, and greater air pollution (including greenhouse gasses). These changes have, in turn, led to climate change and NCD, which are thus connected to one another and to the hominin lineage's evolved reliance on external energy. Yet despite these connections, solving one crisis is unlikely to meaningfully improve the other. Changes in food production and the built environment needed to address NCD will have minimal effect on global fossil fuel consumption. Moving

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to a carbon-free energy economy is essential in order to avoid the worst potential effects of climate change, but changing energy sources will likely have only modest effects on NCD.

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## Converting Human Evolution Lab Activities to an Online Format

SAMANTHA T. PORTER<sup>1</sup>, TESSA CIOKAK<sup>2</sup>, SAMANTHA GOGOL<sup>2</sup> and KIRSTEN JENKINS<sup>3</sup>

<sup>1</sup>Liberal Arts Technologies and Innovation Services, University of Minnesota, <sup>2</sup>Department of Anthropology, University of Minnesota, <sup>3</sup>Department of Social Sciences, Tacoma Community College

Many concepts in human evolution and related disciplines are traditionally taught using interactive and hands-on methods. These include direct observations of anthropological specimens, such as the examination of fossil casts and skeletal remains, and the modeling of evolutionary processes. Because these activities often use physical objects, it can be difficult to translate these exercises into a remote / virtual learning format.

Here, we discuss lessons learned while preparing remote lab modules for human evolution related courses at the University of Minnesota and Tacoma Community College, which moved to an online format due to the COVID-19 pandemic. These efforts were for college level courses, but our assignments and our core takeaways apply to K-12 education as well.

We describe four specific activities we created to serve as case studies: an interactive natural selection demonstration using the narrative game design tool Twine, a solitaire card game to model genetic drift, the use of 3D renderings to teach skeletal morphology, and original dragon illustrations to teach phylogeny. Through these teaching experiences, we develop recommendations for developing or adopting new online lessons and materials; (1) it is critical to keep exercises simple both technologically and procedurally, (2) we must anticipate technological problems (e.g. poor internet connectivity, computers with limited processing power), and lastly (3) a focus on learning outcomes rather than replicating existing content lead to better student learning. Using these guiding principles, we were able to give students an engaging, interactive, and robust learning experience.

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## Implications of outgroup selection in reconstructing hominin phylogeny

NICHOLAS W. POST<sup>1</sup>, CHRISTOPHER C. GILBERT<sup>2,3,4,5</sup>, KELSEY D. PUGH<sup>4,6</sup> and CARRIE S. MONGLE<sup>6,7</sup>

<sup>1</sup>Department of Anthropology, Stony Brook University, <sup>2</sup>Department of Anthropology, Hunter College of the City University of New York, <sup>3</sup>PHD Program in Anthropology, Graduate Center of the

City University of New York, <sup>4</sup>NYCEP, New York Consortium in Evolutionary Primatology, <sup>5</sup>Division of Paleontology, American Museum of Natural History, <sup>6</sup>Division of Anthropology, American Museum of Natural History, <sup>7</sup>Turkana Basin Institute, Stony Brook University

Understanding the phylogenetic relationships among hominin species is critical to any study of human origins. Of course, the results of such analyses are dependent on both the character data and taxon sampling employed. Many previous studies of hominin phylogenetics have used *Papio* and *Colobus* as outgroups in their analyses. Critically, however, these highly specialized extant monkeys possess derived traits that may confound the character polarity for reconstructing hominin evolutionary relationships. Here, we consider *Victoriapithecus macinnesi* as a more suitable outgroup taxon for hominin and hominoid phylogenetic analyses. This fossil species is anatomically well-known and widely accepted as a stem cercopithecoid, placing it much closer to the crown catarrhine common ancestor than either *Papio* or *Colobus*. Craniodental characters for *Victoriapithecus macinnesi* were scored from published sources and measurements taken on high-quality casts. *Victoriapithecus* was then added to the existing matrix of hominin and hominoid taxa published by Mongle et al. (2019), replacing outgroups *Papio* and *Colobus*. This matrix was analyzed using parsimony and Bayesian methods. Replacing the two extant outgroups with a stem cercopithecoid did not change tree topology in either analysis. Importantly, however, tree-wide consistency indices and bootstrap support values increased in comparison to the previous Mongle et al. (2019) parsimony analysis. This increase in bootstrap values was highest at basal hominin nodes, including the node supporting *Ar. ramidus* as the sister taxon to all later hominins. Our findings suggest that including more appropriate outgroups improves estimation of character polarity, thereby strengthening confidence in the position of basal hominin taxa.

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## Gender and social capital in rural South India: outlining distinct strategies of socialization and support

ELEANOR A. POWER

Methodology, London School of Economics and Political Science

In rural South India, people turn to one another to find work, to get a loan to cover major expenses, and to pass the time in conversation. Importantly, though, men and women appear to be pursuing different strategies in who they form these supportive relationships with. In this talk, I will use two rounds of multiplex social support network data from two villages in Tamil Nadu to sketch out who men and women turn to for different types of support. Overall, men name

more support partners than women, a higher proportion of whom are from outside the village and from other castes. Women's relationships, in contrast, are often stronger, more likely to be reciprocal, and more stable across time. Having first presented these broad comparisons, I will turn to consider how these distinct strategies of socialization shift across the age course. I will pay particular attention to marriage and explore how women's supportive relationships are shaped by post-marital residence and their husband's relations with others. I will conclude by considering how these relationships combine to form a household's social capital, and how this may impact the economic livelihood and material well-being of its members. If both "bridging" and "bonding" social capital are valuable, then the combination of distinct social strategies within a household may be particularly crucial.

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## Multivariate analysis of talar morphology in *Ardipithecus ramidus*

THOMAS C. PRANG<sup>1</sup> and SCOTT A. WILLIAMS<sup>2,3</sup>

<sup>1</sup>Department of Anthropology, Texas A&M University, <sup>2</sup>Center for the Study of Human Origins (CSHO), Department of Anthropology, New York University, <sup>3</sup>New York Consortium in Evolutionary Primatology (NYCEP)

The locomotor behavior of the *Homo-Pan* last common ancestor (LCA) is essential for understanding the evolution of bipedalism. The early hominin *Ardipithecus ramidus* has been argued to possess none of the postcranial features related to African ape-like vertical climbing, implying that hominins evolved from an ancestor unlike any living ape. We test the hypothesis that the *Ar. ramidus* talus (ARA-VP-6/500-023) lacks features indicative of African ape-like vertical climbing. Our dataset includes 11 linear measurements collected on 474 tali representing 70 anthropoid taxa. The fossil sample includes 24 tali representing hominins, hominoids, cercopithecoids, and platyrrhines. Principal Components Analysis (PCA) on geometric mean-standardized distances recovers phylogenetic and locomotor signals among anthropoids. Notably, *Oreopithecus bambolii* is placed in an area of the morphospace containing atelids and orangutans, whereas *Ekembo* tali are more similar to arboreal cercopithecines and colobines. The *Ar. ramidus* talus is most similar to *Pan* and *Gorilla*. Linear Discriminant Analysis (LDA) separates the talar morphology of chimpanzees, bonobos, western gorillas, and eastern gorillas, and classifies *Ar. ramidus* as *G. gorilla* with a high posterior probability. *Ar. ramidus* shares with chimpanzees, gorillas, and atelids a mediolaterally expanded

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anterior talocrural joint linked to the mechanics of vertical climbing. Additionally, we identify talar features potentially indicating a shift in climbing style among later hominins. Our results are consistent with the hypothesis that humans evolved from an ancestor with an African ape-like positional repertoire.

*This research was supported by a Wenner-Gren Foundation Dissertation Fieldwork Grant*

### Stressed to the tooth? A pilot study of cortisol in archaeological tooth structures

LESLIE QUADE<sup>1</sup>, PAUL L. CHAZOT<sup>2</sup> and REBECCA GOWLAND<sup>1</sup>

<sup>1</sup>Archaeology, Durham University, <sup>2</sup>Biosciences, Durham University

Cortisol is a glucocorticoid hormone produced through activation of the hypothalamic-pituitary-adrenal (HPA) axis. It is known as the “stress hormone” for its primary role in the body’s stress response. Although a significant focus in modern clinical research, only a few studies have analyzed cortisol in archaeological human remains and these have been limited to hair. Tooth dentine and enamel preserve well archaeologically and may be possible reservoirs for detectable levels of cortisol in human skeletal remains. To test this hypothesis, 69 teeth from 65 individuals were analyzed via competitive enzyme-linked immunosorbent assay (ELISA) to assess and quantify the cortisol concentrations present within tooth structures. Selected individuals derived from five sites in France dated to between the 1<sup>st</sup> and the 7<sup>th</sup> centuries CE. In both tooth dentine and enamel, detectable concentrations of cortisol were identified in multiple teeth. However, cortisol concentrations were low and not all teeth yielded results that were measurable through cortisol ELISA. Differences in cortisol values between dentine and enamel could suggest different uptake mechanisms or timing. These results indicate that cortisol is incorporated within tooth structures and merits further investigation in both modern and archaeological contexts. Future studies of cortisol in tooth structures would greatly expand the research potential of cortisol in the past and could have implications for studies of human stress across deep time.

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### Chew on this: Dental wear patterns in biomedical and wild *Macaca fascicularis* specimens

ROBIN L. QUATAERT<sup>1</sup>, ERIN F. E. PINKSTON<sup>2</sup>, BRITTANY KENYON-FLATT<sup>2,3</sup> and NOREEN VON CRAMON-TAUBADEL<sup>2</sup>

<sup>1</sup>Comparative Primate Anatomy Laboratory, University at Buffalo, <sup>2</sup>Buffalo Human Evolutionary Morphology Lab, University at Buffalo, <sup>3</sup>Department

of Molecular Biomedical Sciences, North Carolina State University

Previous work has found that the removal or blunting of canines did not alter dental wear patterns in biomedical macaques when compared to dentally unaltered specimens. However, previous work has not compared dental wear patterns with wild specimens, leaving the question: do biomedical and wild macaques exhibit different patterns of dental wear?

We compared maxillary and mandibular dental wear patterns among three groups of male *Macaca fascicularis*: biomedical sample with altered canines ( $n=16$ ), biomedical sample without altered canines ( $n=15$ ), and wild specimens ( $n=16$ ). Wear was scored following Gantt’s (1979) stages for occlusal wear in cercopithecines. The scored stages were then transformed into ranked data for analysis via Kruskal-Wallis and Mann Whitney U-tests.

Statistical tests revealed that the upper M1s in unaltered biomedical specimens had significantly less wear than in the other two groups. The lower M1s in the wild specimens had significantly more wear when compared to the unaltered specimens, but not when compared to the altered specimens. The upper and lower M3s in the wild specimens had significantly more wear than both biomedical groups. These results are consistent with previous work, suggesting that the removal or alteration of canines does not affect wear patterns, but that biomedical and wild specimens experience different degrees and/or patterns of wear. This is likely due to the substantial differences in hardness and variety of foods between biomedical and wild populations. Moreover, dental wear patterns are likely

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### Cranial shape changes with age in male and female adults of *Papio*

ANDREA L. QUINTANILLA<sup>1</sup>, JYHREH A. JOHNSON<sup>1</sup>, EVAN A. SIMONS<sup>2</sup> and STEPHEN R. FROST<sup>1</sup>

<sup>1</sup>Department of Anthropology, University of Oregon, <sup>2</sup>Department of Anthropology, University at Buffalo, The State University of New York

Ontogenetic changes to skull shape from juveniles to adults have been well researched and studied, but those that occur during adulthood are less well known. In this study, we collected 45 3D landmarks with a Microscribe 3DX digitizer of 345 wild-collected baboon (Genus *Papio*) crania representing all six currently recognized subspecies. As a proxy for age, we visually scored maxillary third molars for degree of wear. Landmarks were superimposed with generalized Procrustes analysis using MorphoJ. Procrustes coordinates were regressed against natural log-transformed upper third molar wear stage using multivariate tests

for significance. We used Landmark editor to warp a surface scan to show the shape changes correlated with increased molar wear. Results demonstrated a significant effect of molar wear stage on cranial shape, even after accounting for size, but it is a subtle effect that accounts for approximately 4.5% of shape variance. As the skull ages, the face seems to get longer while the orbitals and zygomatics shift posteriorly. The sexes do not differ in the pattern of shape changes and their regression slopes are parallel, meaning that the sexes do not age differently in their cranial shapes. The degree these shape changes are a consequence of genetics or bone remodeling due to strain experienced during life is unclear. Nonetheless, if this pattern is consistent across papionins, then it may help better to diagnose fossil taxa represented by small samples where it is unclear if differences are taxonomic or due to age.

### Analyzing clinician views on race and genetic ancestry for treating hypertension

CHANTAL RABAY, CAROLINA LOPEZ, SAMANTHA STREULI and AMY L. NON

Department of Anthropology, University of California, San Diego

Despite general consensus that there is no biological basis to race, racial categorization is still used by clinicians to guide diagnosis and treatment plans for certain diseases. In medicine, race is commonly used as a rough proxy for unmeasured social, environmental, and genetic factors that may contribute to disease. The American College of Cardiology’s JNC 8 guidelines in fact provide race-specific treatment plans for hypertension in Black versus non-Black patients, but without genetic evidence for racial differences in drug response. The goal of this ongoing empirical study is to understand how clinicians value and use genetic ancestry data and racial classifications when practicing medicine. We analyzed interview data from 21 clinicians using qualitative analysis of open-ended questions about the use of race-related information and genetic ancestry in clinical decision making, how they defined race, and general perspectives about the role of race and ancestry in medicine. We presented clinicians with video cases of mixed race patients with hypertension symptoms and genetic ancestry results to determine which racial cues were prioritized in designing treatment plans. Preliminary results indicate that clinicians generally did not follow race-specific guidelines, relying instead on personal judgement and experience. Additionally, clinicians’ definitions of race were variable and most did not often prioritize genetic ancestry data over other race related variables in classifying race or treating patients. Understanding how clinicians

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use and value race-based guidelines, genetic ancestry data, and race are important in furthering investigations into the racial disparities in hypertension between Black and White Americans.

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### Serving graduate students during a pandemic and civil rights crisis

JENNIFER A. RAFF

Anthropology, University of Kansas

The global pandemic and civil rights crisis have impacted graduate students particularly hard, causing increased levels of stress, forcing them to adapt to new styles of teaching, preventing or delaying necessary fieldwork or laboratory-based research, and dimming the prospects for academic jobs even further than was the case in a tight job market. How can faculty best mentor graduate students in this uncertain environment, providing a supportive atmosphere while still advancing them through their degree program? This is something that I've been struggling with, particularly as the Director of Graduate Studies for our program. In this talk I will discuss the specific issues that graduate students and their mentors must confront during these two crises. I will share approaches that I and other DGSs have taken in supporting graduate students during this time, such as mechanisms for TAs/ship allocations to accommodate extra work required for maximizing student safety. I will also share areas where we have found ourselves falling short or simply don't have a solution to complex issues. I hope that this will serve as a conversation starter between faculty mentors to share resources and approaches to serving our students.

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### Meroitic childhood diet and weaning at Sai Island, Sudan: A carbon and nitrogen isotopic study of site 8-B-52.B

BRENNA J. RAISOR<sup>1</sup>, TOSHA L. DUPRAS<sup>1</sup>, YANN ARDAGNA<sup>2</sup> and VINCENT FRANCIGNY<sup>3</sup>

<sup>1</sup>Department of Anthropology, University of Central Florida, Orlando, Florida, USA, <sup>2</sup>UMR 7268 Anthropologie bioculturelle Droit Ethique et Santé, AMU-CNRS-EFS, Faculté des Sciences Médicales et Paramédicales de Marseille, France, <sup>3</sup>UMR 8167 Orient & Méditerranée, Sorbonne University, Paris

This research explores the diet and weaning patterns of non-adult individuals from an elite Meroitic (300BCE – 350CE) cemetery (8-B-52.B) located on Sai Island, Sudan. It is notable to mention that this is the first isotopic study conducted on this population, and is one of the first conducted on this time period and region of Sudan. Carbon and nitrogen stable isotopic analyses were conducted on a sample of 54 individuals. These analyses focused on differences in adult and non-adult diet, non-adult weaning patterns, and intra-elite differences between contemporaneous cemeteries at Sai Island to

elucidate patterns of non-adult diet and weaning and the mother-infant dynamic. The isotopic results suggest that both adults and non-adults were consuming a homogeneous diet with the exception of breastfeeding infants, who exhibited enriched  $d^{15}N$  and  $d^{13}C$  values compared to all others in the sample. The isotopic data show that non-adults in this population were likely weaned before 3 years of age as suggested by the assimilation of non-adult  $d^{15}N$  values to those of the adult females. Lastly, no statistically significant differences in non-adult diet and weaning existed between the contemporaneous sites of 8-B-52.B and 8-B-5.A, suggesting homogeneous patterns of diet and weaning between the religious and wealthy elite in this population. This study demonstrates the relationship between social status, age, and dietary patterns during the Meroitic period, but more significantly illustrates the patterns of early life feeding and weaning behaviors that influence the relationship between a mother and her infant.

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### The utility of dental nonmetric ASUDAS traits and trait combinations for inferring human population history

HANNES RATHMANN<sup>1,2</sup> and HUGO REYES-CENTENO<sup>2,3,4</sup>

<sup>1</sup>Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoenvironment, University of Tübingen, <sup>2</sup>DFG Center for Advanced Studies "Words, Bones, Genes, Tools", University of Tübingen, <sup>3</sup>Department of Anthropology, University of Kentucky, <sup>4</sup>William S. Webb Museum of Anthropology, University of Kentucky

Human dental nonmetric traits of the Arizona State University Dental Anthropology System (ASUDAS) are widely used for inferring genetic relationships between populations. However, it remains poorly understood whether certain dental traits or trait combinations preserve genetic signatures to a greater degree than others. We addressed this research gap by testing the utility of 27 ASUDAS traits and all 134,217,700 possible combinations of these traits in reflecting neutral genetic variation in a worldwide sample of modern human populations. Our results show that not all traits are equally well-suited for inferring neutral genetic affinities. As a rule of thumb, dental inferences about neutral genetic affinities based on many traits are more reliable than those based on only a few traits. Trait combinations comprising at least 16 traits, no matter which of the 27 traits are chosen, always capture neutral genetic affinities significantly. Nevertheless, the best performance is achieved when using specific combinations of highly diagnostic traits, and not the full 27-trait set. These high-utility trait combinations consist of batteries ranging from 14 to 20 traits and always comprise the following five traits: mesial ridge (UC), distal accessory ridge (UC), protostylid (LM1), lingual cusp number (LP2), and cusp 6 (LM1). We propose that the high-utility

trait combinations should be prioritized in future research, as they allow for more accurate inferences. Finally, we generated a comprehensive reference table that can be used to validate the utility of a certain dental trait or trait combination employed in previous and future studies.

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### Inuit and the "problem" of climate change: Local perspectives on contemporary challenges

ELSPETH READY<sup>1,2</sup> and PETER COLLINGS<sup>2</sup>

<sup>1</sup>Human Behavior, Ecology and Culture, Max Planck Institute for Evolutionary Anthropology, <sup>2</sup>Department of Anthropology, University of Florida

Human dimensions of climate change research in the Canadian Arctic generally begins with the assumption that the health and well-being of Inuit are threatened by climate change. We examine the relevance of this research framework for Inuit through a thematic analysis of what Inuit in Kangiqsujuq (Nunavik) perceive as challenges to their well-being. As part of a research project focused on the mixed economy in Kangiqsujuq conducted in 2013–2014, 107 Inuit were asked three free-response questions about the major issues facing them and their communities, and about what they liked the most about their community. Climate change rarely appeared in Kangiqsujuarmiut responses to these questions; when mentions of the environment appear, they generally refer to positive aspects of being on the land. In contrast, the problems identified by Kangiqsujuarmiut are strongly focused on a constellation of issues rooted in decades of colonialism and rapid culture change, particularly substance use and the cost of living. The cost of hunting in particular was an important barrier to access to the land and to country food. We conclude that the theoretical framework adopted in Arctic human dimensions of climate change research underestimates Inuit cultural capacity and prevents important economic, political, and social constraints on climate change adaptation from emerging in the context of research. We suggest that more inductive research designs will assist in developing more culturally-appropriate frameworks for examining Inuit responses to climate change.

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### Relative abundance among cercopithecids from Woranso-Mille and other contemporaneous eastern African sites.

HAILAY G. REDA<sup>1</sup>, STEPHEN R. FROST<sup>1</sup> and YOHANNES HAILE-SELASSIE<sup>2</sup>

<sup>1</sup>Anthropology, University of Oregon, <sup>2</sup>Physical Anthropology, Cleveland Museum of Natural History

It was previously assumed that only one hominin species was present in the Afar region 3.6 to 3.0 Ma. However, the discovery of hominins from Woranso-Mille 3.5-3.2 Ma suggests the presence of more taxa. Such diversity of hominins is absent in other contemporaneous Afar sites. This begs the question if Woranso-Mille is distinct in its environment and composition of its fauna 3.5-3.2 Ma. As a result, we have compared the relative abundances of cercopithecoid taxa recovered from Woranso-Mille and other contemporaneous eastern African sites. Due to the fragmentary nature of the fossil record, taphonomic, taxonomic, and other potential biases, we employed a range of methods, considered alternative taxonomic hypotheses from the literature, and used different taxonomic scales, including species, genus, and Delson's dental groups. Similarities or differences between Cercopithecoid faunas were measured using both cord distance and faunal resemblance indices, and analyzed with correspondence and cluster analyses. The correspondence and cluster analyses show that younger sites (3.5-3.2 Ma) are distinct from slightly older sites. It is currently unclear if this temporal change is due to a changing environment, turnover of different taxa, or both. The species level analysis using both cord distance and similarity indices, show that geographically more proximate sites are grouped together. Thus, the Afar localities are more similar to each other than they are to the sites in the Turkana Basin and Laetoli. Further, the preliminary analysis suggests that the 3.5-3.2Ma Woranso-Mille is not significantly distinct from other Afar localities in terms of the cercopithecoid fauna.

### Examining differences among *Australopithecus afarensis* localities: Climate and paleoecology

KAYE E. REED<sup>1</sup>, IRENE E. SMAIL<sup>1</sup>, DENISE F. SU<sup>2</sup>, MARYSE D. BIERNAT<sup>1</sup>, EUNICE F. LALUNIO<sup>1</sup>, KATHERINE WINSLOW<sup>1</sup>, KAILEE BOW<sup>3</sup>, CHLOE CLINE<sup>3</sup>, CHELIE F. GEORGE<sup>3</sup> and MADELEINE ORICCHIO<sup>3</sup>

<sup>1</sup>Institute of Human Origins and School of Human Evolution and Social Change, Arizona State University, <sup>2</sup>Paleobotany and Paleoecology, Cleveland Museum of Natural History, <sup>3</sup>School of Human Evolution and Social Change, Arizona State University

*Australopithecus afarensis* existed from ~3.8 Ma–2.95 Ma across Ethiopia, Kenya, and Tanzania. Since *Au. afarensis* was a long-lived

species, we hypothesized that the species occupied similar environments through time and across space. Environmental variables considered included biotic (vegetation, mammalian community structure, mammalian isotopic signatures) and abiotic (precipitation, seasonality, depositional environments) factors. Published and unpublished data on species presence/absence, body mass, carbon and oxygen isotopes, and mesowear were gathered for fossil assemblages from the sites of Hadar, Woranso-Mille, Kantis, and Laetoli. First, we analyzed the functional traits of the fauna 1) among fossils sites, and 2) among fossil sites with a comparative database of 205 modern African communities (fauna, WorldClim, and vegetation data) with Correspondence Analysis (CA). Vegetation structure as estimated by the CA was similar across fossil localities. We predicted rainfall and seasonality for the fossil localities by regressing CA axis 1 against mean annual precipitation and a metric of seasonality (months of rainfall per year). Fossil site precipitation ranges from 379-700mm per annum. Seasonality differs among sites such that Aralee Issie (Woranso-Mille) had the shortest dry season and Kada Hadar 2 sub-Member (Hadar) had the longest. Dry season lengths generally increase through time, with the youngest assemblages estimated to have extremely long periods without rain. We suggest that while the fossil sites are overall similar in vegetation structure, eventually *Au. afarensis* could not cope with the longer dry seasons, which may have been a factor in its disappearance from the fossil record.

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### A geometric morphometric examination of forelimb skeletal shape and adaptation to leaping in anthropoid primates

THOMAS R. REIN

Department of Anthropology, Central Connecticut State University

Previous research on adaptation to leaping has focused on hind limb skeletal traits associated with the propulsive force needed to perform specialized vertical-clinging and leaping common among strepsirrhine primates. There has been less emphasis, however, on potential skeletal adaptations to the type of leaping performed by many anthropoid primates. Furthermore, forelimb skeletal traits have not been examined as much as those of the hind limb despite the important role of the forelimb during airborne and landing stages of leaping in some species. The objective of this study was to enhance our understanding of how informative different aspects of the forelimb skeleton are regarding leaping behavior across anthropoid primates. Three-dimensional landmark coordinates were collected on the humerus, radius, and ulna of specimens representing 18 anthropoid species including

hominoids, cercopithecoids, and platyrrhines. Taxa were organized into locomotor categories based on published leaping proportion data. Based on canonical variate analysis, shape variation of the distal humerus was most informative, distinguishing species based on the proportion of observed leaping locomotion regardless of taxonomic category. Character states associated with greater proportions of leaping locomotion included a relatively smaller medial epicondyle and a relatively narrow trochlea. Corresponding aspects of proximal ulnar shape variation were informative as well. This exploratory analysis has identified a number of features that correspond to subtle variation in frequency of leaping locomotion across anthropoid primates, suggesting that some aspects of forelimb skeletal shape are informative about this hind limb-dominated movement.

Data collection for this study was funded by the National Science Foundation (Grant number BCS-0849204), L.S.B. Leakey Foundation, and Wenner-Gren Foundation (Grant number 7982).

### Multivariate analysis of soldier diet from the Battles of Himera (480 BCE, 409 BCE)

KATHERINE L. REINBERGER<sup>1</sup>, LAURIE J. REITSEMA<sup>1</sup>, BRITNEY KYLE<sup>2</sup> and STEFANO VASSALLO<sup>3</sup>

<sup>1</sup>Department of Anthropology, University of Georgia, <sup>2</sup>Department of Anthropology, University of Northern Colorado, <sup>3</sup>Archaeological Heritage Section, Superintendency of Palermo, Italy

Diet reflects social practices that illuminate soldiers' interactions with the surrounding communities and circumstances under which they fight. This study offers new dietary information from soldiers who fought in the Battles of Himera through  $\delta^{13}\text{C}$  in enamel apatite which indicates the ratio of C3 and C4 foods in the whole diet. Previous research presented isotope data from soldiers' bone collagen that suggested a diet with C3 plants and animal protein, with possible contributions from fish. Soldiers from both battles had overall higher nitrogen and carbon values than civilians, suggesting a separate diet for soldiers. The addition of apatite  $\delta^{13}\text{C}$  may clarify if increased  $\delta^{13}\text{C}$  values in the soldiers' diet are due to consumption of more C4 plants, historically less likely, or marine consumption, archaeologically and historically supported.

This study presents data from soldiers (n=46) and civilians (n=48) who were analyzed for  $\delta^{13}\text{C}$  in enamel apatite and  $\delta^{15}\text{N}$  and  $\delta^{15}\text{v}$  from bone collagen. The multivariate analysis suggests soldiers from 409 BCE and civilians had diets higher in C3 foods, including terrestrial C3 protein (409 BCE:  $\delta^{13}\text{C}_{\text{ap}}=-12.2\pm 0.3$ ,  $\delta^{13}\text{C}_{\text{col}}=-19.5\pm 0.4$ ,  $\delta^{15}\text{N}=10.9\pm 0.6$ ; Civilians:  $\delta^{13}\text{C}_{\text{ap}}=-12.4\pm 0.5$ ,  $\delta^{13}\text{C}_{\text{col}}=-19.4\pm 0.3$ ,  $\delta^{15}\text{N}=10.4\pm 0.6$ ). Soldiers from 480 BCE had values indicating higher C4 consumption in the whole diet, while still maintaining C3 protein

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sources (480 BCE:  $\delta^{13}\text{C}_{\text{ap}}=-8.6\pm 1.9$ ,  $\delta^{13}\text{C}_{\text{col}}=-17.9\pm 1.1$ ,  $\delta^{15}\text{N}=10.7\pm 0.9$ ). Results suggest there was little consumption of fish. The multivariate isotopic approach allows for nuanced analyses of diet in the Mediterranean region and its armed forces, continuing to challenge ideas of fish consumption in coastal regions and among soldiers who traveled by sea.

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### Effects of physical activity and relatedness on metabolic phenotype in ring-tailed lemurs

REBECCA RIMBACH<sup>1,2</sup> and HERMAN PONTZER<sup>1,3</sup>

<sup>1</sup>Evolutionary Anthropology, Duke University, USA, <sup>2</sup>Animal, Plant and Environmental Sciences, University of the Witwatersrand, Johannesburg, South Africa, <sup>3</sup>Duke Global Health Institute, Duke University, USA

Insufficient physical activity is a major risk factor for cardiometabolic disease (i.e., unhealthy weight gain, heart disease, and diabetes) in humans and may negatively affect health in captive primates. Further, work in humans indicates closely related individuals show correlated metabolic responses after an exercise intervention. Effects of physical activity and genetic relatedness on metabolic phenotype are virtually unstudied in non-human primates. We investigated metabolic responses to changes in physical activity in 16 adult ring-tailed lemurs (*Lemur catta*) at the Duke Lemur Center. We collected data during a period of low activity in indoor enclosures in winter and a period of high activity when individuals were free-ranging in large outdoor enclosures. We compared body mass, physical activity via accelerometry, and blood glucose, triglycerides, HDL- and LDL-cholesterol in winter versus summer. We used husbandry records to approximate relatedness between individuals. We tested whether increases in physical activity were associated with improvements in cardiometabolic profiles, and whether variation in metabolic phenotype was correlated with genetic relatedness. Lemurs had a lower body mass and were more active in summer ( $p<0.01$  paired t-tests). Triglyceride levels decreased in summer ( $p<0.05$  paired t-test), but changes in activity were not associated with changes in other markers of metabolic health. More closely related individuals did not have a more similar metabolic phenotype than unrelated individuals, indicating that genetic relatedness may not explain variation in metabolic response in this species.

*Supported by Duke Lemur Center's Director's Fund for the project "Effects of physical activity and genetics on metabolic phenotype in ring-tailed lemurs"*

### The population history of Indonesia and Melanesia as inferred by Legofit2

ALAN R. ROGERS<sup>1</sup>, HERAWATI SUDOYO<sup>2</sup> and MURRAY COX<sup>3</sup>

<sup>1</sup>Anthropology, University of Utah, <sup>2</sup>Genome Diversity and Diseases Laboratory, Eijkman Institute, <sup>3</sup>Computational Biology, Massey University

We introduce a new statistical method for inferring population history from genetic data and use it to study data from Indonesia and Melanesia. Legofit estimates parameters by minimizing the difference between (a) the observed frequencies with which derived alleles are shared among populations, and (b) the frequencies expected under particular models of history. The new version calculates these expected frequencies using an algorithm with greater speed and accuracy. Preliminary results are based on 70 previously-published genomes from five linguistic families in Papua New Guinea. These results confirm (1) superarchaic admixture into the "neandersovan" ancestors of Neanderthals and Denisovans, and (2) Denisovan admixture into modern Papuans. In addition, they document two pulses of Neanderthal admixture into modern humans: (3) an early pulse into the ancestors of Europeans and Papuans, and (4) a later pulse into Papuans.

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### Modification of chimpanzee diet composition in response to long-term habitat change

SHANNON L. ROIVAS and IAN C. GILBY

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

Habitat change driven by climate fluctuations likely introduced novel selection pressures during hominin evolution. It is not well understood, however, how early hominins may have altered foraging strategies in response to habitat change and variation in the availability of familiar foods. Satellite imagery of Gombe National Park, Tanzania, reveals long-term habitat recovery from a state of anthropogenic disturbance following the park's establishment in 1968; consequently, the chimpanzees of Gombe provide an opportunity to investigate the ramifications of habitat change on diet composition in a large-bodied ape. Utilizing 44 years of observational feeding data from the Kasekela community, we quantified diet quality by the proportion of feeding time spent consuming leaves and pith, a measure previously demonstrated to be negatively correlated with body mass at Gombe. Additionally, we characterized plant diet composition using the proportional contribution of individual plant species to the overall time spent feeding. Preliminary results indicate that after accounting for seasonal variation,

the proportion of time spent feeding on leaves and pith has significantly decreased with time since the park's establishment, suggesting that diet quality has improved. A second preliminary analysis revealed that the relative contribution of the most frequently consumed species has fluctuated, in some instances dramatically, over the past several decades. Overall, these results suggest that chimpanzees respond flexibly to habitat change through alterations in the relative importance of plant foods, and that diet quality increases with habitat improvement.

*Data collection: Jane Goodall Institute, Construction of the long-term database: NSF (DBS-9021946, SBR-9319909, BCS-0452315, IIS-0431141, IOS-LTREB-1052693)*

### Substantial biocultural diversity in the early peopling of the Caribbean as evidenced by Cuban recrod

MIRJANA ROKSANDIC and YADIRA CHINIQUE DE ARMAS

Anthropology, University of Winnipeg

The 'who, when, and how' of the earliest peopling of the Caribbean remain largely unanswered despite the long history of archaeological research in the region. One of the main underlying causes is the reliance on archaeological interpretation rather than on bioanthropological data. Furthermore, the archaeological information was influenced by the dichotomy between the easily recognisable ceramic-bearers from the Orinoco valley and the non-ceramic producing 'Archaic' people. The latter were generally considered to be fisher-hunter-gatherers (FHG) with moderate to high mobility, no ceramics, and no cultivars. We review the results of the last 10 years of bioanthropological research in the Greater Antilles and discuss the variability observed in the mode of subsistence understood through combined starch grain and isotope data, and through the results of ancient DNA analyses. We further combine the evidence of greater than expected variability with the palaeoenvironmental record and 14C dating. Throughout the Caribbean, the palaeoenvironmental record shows human-caused environmental alterations at least two millennia before any recorded archaeological sites, and a further discrepancy between archaeological sites and the age of formal burial sites. The evidence of starch granules of cultivars indicates that even the earliest settlers were small scale food producers rather than FHG, while aDNA demonstrates the presence of more than one lineage among the earliest groups. The peopling of the Americas and the Caribbean should be examined with more openness to incorporating new data in a way that is not biased by the existing archaeological paradigms.

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### Paleopathological reanalysis of an Early Iron Age skeleton from Frankfurt/Main

CAROLIN RÖDING<sup>1</sup> and LIANE GIEMSCH<sup>2</sup>

<sup>1</sup>Paleoanthropology, University of Tuebingen, Germany, <sup>2</sup>Prehistoric Archaeology, Archaeological Museum Frankfurt am Main, Germany

One of Germany's most important prehistoric finds from the Early Iron Age is a chieftain burial from Frankfurt am Main. The burial was excavated in 1966/67 and represents a remarkable discovery, as it yielded an almost complete skeleton of a ~50 year old male together with grave goods in an undisturbed burial mound. The archaeological material was dated to around 700 BCE. Consequently, it is one of the oldest known burials of the Early Iron Age elite in central Europe.

Here, we present a paleopathological reanalysis of the skeleton. We analyzed the virtually reconstructed cranium, axis, and humeri, in order to explore the possible impact of a healed trauma on the left clavicle on other skeletal elements. The new cranial reconstruction allowed the study of several cranial features as well as muscle attachments, linking cranium and postcranium. Linear measurements and surface distance maps between bones and their bilateral counterparts were employed. The trauma was found to have no impact on the muscles involved in head movement. A combination between muscle atrophy in the left arm and muscle hypertrophy in the right arm induced by carrying a sword is the most plausible explanation for the observed postcranial bilateral asymmetries.

All in all, our finds suggest only slight to moderate restrictions in the range of motion caused by the healed trauma. In addition, osteological evidence provides a valuable snapshot in time of a male individual of high status from the Early Iron Age.

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### Interbirth interval and age at first reproduction in populations with disparate energy status

SRISHTI SADHIR<sup>1</sup> and HERMAN PONTZER<sup>1,2</sup>

<sup>1</sup>Evolutionary Anthropology, Duke University, <sup>2</sup>Duke Global Health Institute, Duke University

Female fertility and its determinants, including age at first reproduction and interbirth interval, partly reflect maternal energetic status. Compared to women in natural fertility, small-scale societies, women in post-demographic transition, industrialized populations typically have lower total fertility rates (TFR), reflecting smaller ideal family size, access to contraception, and other socio-economic factors. However, TFR may obscure the role of maternal energetic status, which should favor greater reproductive output in industrialized populations. Here, we compared age at first reproduction and interbirth interval by maternal age for

2,996,423 women in the United States (CDC, year 2018; TFR=1.7) to published data from two natural fertility, subsistence agriculture populations: the Amish (years 1908-1967; N=1,723; TFR=7.5) and the Tsimane (years 2004-2013; N=1,337; TFR=9.0). Mean interbirth interval for multiparous mothers in the U.S. ( $49.2 \pm 36.8$  months), compared with Tsimane ( $39.5 \pm 22.1$  months) and Amish (41.2 months) cohorts, was shorter for women age 15-24 years ( $p < 0.001$ ) but longer for women age 25-50 years ( $p < 0.001$ ). Mean and median age at first reproduction were later for U.S. women ( $26.9 \pm 5.8$  years; 27 years) compared to Tsimane women ( $19.1 \pm 4.9$  years; 18 years;  $p < 0.001$ ). However, 332 (0.03%) first-time mothers in the U.S. sample were younger than the earliest reported age at first birth for Tsimane mothers (14 years). Results are consistent with the hypothesis that energetic status of women in industrialized populations permits greater reproductive output.

### Using museum specimens to assess anthropogenic impacts on nonhuman primate health

SANA T. SAIYED<sup>1</sup>, ANDREA R. ELLER<sup>2</sup>, RITA M. AUSTIN<sup>2,3,4</sup>, STEPHANIE L. CANINGTON<sup>2,5</sup>, SABRINA B. SHOLTS<sup>2</sup> and AGUSTIN FUENTES<sup>6</sup>

<sup>1</sup>Department of Anthropology, University of Notre Dame, <sup>2</sup>Department of Anthropology, Smithsonian Institution, National Museum of Natural History, <sup>3</sup>Department of Anthropology, University of Oklahoma, <sup>4</sup>Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, <sup>5</sup>Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, <sup>6</sup>Department of Anthropology, Princeton University

Anthropogenic pressures on nonhuman primate (NHP) species are wide-ranging and impact multiple aspects of NHP life, including social behavior and diet. As a result, NHP species must be adaptable, yet adaptations may produce specific physiological outcomes. Human foods, constructions, contaminants, and interactions have biological consequences on NHPs that may leave skeletal signatures. Unfortunately, these skeletal health markers are difficult to assess in living populations without invasive methodologies or frequent collection of deceased individuals. Here, we present a novel approach for utilizing museum specimens to attain a macrohistorical perspective on synanthropic NHPs. The EMPHASIS project investigates biological consequences using skeletal remains from 21 NHP genera housed at the Smithsonian Institution's National Museum of Natural History. Of these 21 genera, *Macaca*, *Papio*, and *Chlorocebus* (N=715) were chosen for this study due to their known affiliations with humans. Because museum specimens are rarely categorized based on magnitude of anthropogenic influence, we combined anthrome maps published by Ellis and colleagues (Ellis et al., 2010) from relevant time

horizons with specimen locality data to map each individual using qGIS software. We then assessed individuals for anthrome of origin (rural, suburban, or urban). Preliminary results of "wild" *Macaca* specimens (n=350) revealed that most individuals (n=225) were obtained from anthromes with anthropogenic influence and thus were not wild. Utilizing qGIS mapping capabilities allows for a more accurate exploration of the anthropogenic effects on NHP health across time and geographic locations, as anthrome maps provide a better understanding of anthropogenic land use and, thus, human impacts on NHPs.

### Ontogeny of the distal metacarpal ridge in knuckle-walking apes

LAUREN SARRINGHAUS<sup>1,2</sup>, LAURA MACLATCHY<sup>2</sup> and JOHN MITANI<sup>2</sup>

<sup>1</sup>Evolutionary Anthropology, Duke University, <sup>2</sup>Anthropology, University of Michigan

The distal metacarpal ridge (DMR), a bony ridge on the dorsal metacarpal in African apes, is hypothesized to be a potential knuckle-walking feature. However, this interpretation is complex as the DMR is present to differing degrees of prominence in knuckle-walking African apes and non knuckle-walking species. To test the hypothesis that this feature reflects hand postures adopted during knuckle-walking, comparisons must be made in African apes over the course of locomotor development and between African apes and other genera. We measured the DMR angle of the third metacarpal in 73 *Gorilla*, 173 *Pan*, 16 *Pongo*, 41 *Hylobates*, and 23 *Papio* specimens and compared their distal ridge morphology. We found a difference in ridge angle values among genera (Kruskal-Wallis tests,  $p < 0.05$ ). Post hoc comparisons revealed that adult *Gorilla* and *Pan* do not differ from one another, but both genera have more prominent ridges (i.e. smaller DMR angles) compared to members in the three other genera (all pairwise comparisons,  $p < 0.05$ ). We also found that ridge prominence increased (angle decreased) as individuals age in both *Gorilla* and *Pan*, with the ridge developing only after M1 eruption in both genera, after the onset of knuckle-walking. While some *Papio* had ridges present, ridges in *Papio* and infant African apes were less prominent (larger angle) compared to the adult African apes ( $p < 0.05$ ), possibly reflecting an absence of frequent knuckle usage. Taken together, these findings are consistent with the hypothesis that the DMR is a bony feature indicative of knuckle-walking hand postures.

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## ABSTRACTS

### Geographic Insularity and Locally-Bound Diets: Multi-isotopic Insights into Late Intermediate Period (ca. 1100-1400 CE) Lifeways at Quilcapampa, Sihuas Valley, Peru

BETH SCAFFIDI<sup>1</sup>, JUSTIN JENNINGS<sup>2</sup>, CORINA KELLNER<sup>3</sup>, KELLY KNUDSON<sup>4</sup> and TIFFINY TUNG<sup>5</sup>

<sup>1</sup>Anthropology & Heritage Studies, University of California, Merced, <sup>2</sup>New World Archaeology, Royal Ontario Museum, <sup>3</sup>Anthropology, Northern Arizona University, <sup>4</sup>Center for Bioarchaeological Research, Arizona State University, <sup>5</sup>Anthropology, Vanderbilt University

The Late Intermediate Period ("LIP", ca. 1100-1400 CE) was a time of internecine violence and balkanization in many Andean regions as communities disputed access to resources in the context of dissolution of the Wari and Tiwanaku polities and long-term drought. These dramatic socio-political and climatic changes raise questions about resilience and the diverse ways communities responded to the challenges of the Middle Horizon to LIP transition. Here we use stable and radiogenic isotope analysis to reconstruct dietary and mobility practices in order to understand some of these creative social adaptations.

We reconstruct diet and mobility at the LIP Quilcapampa cemetery from tooth enamel and bone of 24 individuals. Analysis of  $^{87}\text{Sr}/^{86}\text{Sr}_{\text{enamel}}$  carbonates shows one non-local (2SD range = 0.70782 - 0.70814, mean/SD = 0.70798/0.00008), suggesting little immigration to the site. Analysis of  $\delta^{13}\text{C}_{\text{enamel carbonates}}$  shows mean/SD = -8.1 ‰/1.2 ‰, suggesting a mixed  $\text{C}_3/\text{C}_4$  childhood diet. For  $\delta^{18}\text{O}$ , mean/SD = -7.0 ‰/0.6 ‰; this is slightly higher than neighboring groups, suggesting long-term water storage before consumption. There are no outliers, suggesting all sampled individuals consumed local water. For bone collagen, mean/SD  $\delta^{13}\text{C}$  = -14.9 ‰/1.3 ‰; and  $\delta^{15}\text{N}$  = 7.8 ‰/1.4 ‰. For bone apatite, mean/SD  $\delta^{13}\text{C}$  = -9.9 ‰/1 ‰; and  $\delta^{18}\text{O}$  -6.5 ‰/1.4 ‰. This shows a mixed  $\text{C}_3/\text{C}_4$  adult diet, significant inter-individual variation in access to meat, and  $\delta^{18}\text{O}$  is positively correlated with  $\delta^{13}\text{C}$ . One outlier in bone collagen exhibits a diet heavy in  $\text{C}_4$  foods and meat. These multiple data lines support the interpretation of insularity, locally-dependent diets, and limited supra-local interaction in the LIP

*Isotopic analysis was supported by a Pilot grant from the Center for Bioarchaeological Research at Arizona State University, the Royal Ontario Museum, and respective labs.*

### Subsistence harvest diversity, social networks, and adaptive capacity to environmental change in Alaska

SHANE A. SCAGGS<sup>1</sup> and DREW GERKEY<sup>2</sup>

<sup>1</sup>Department of Anthropology, Ohio State University, <sup>2</sup>Department of Anthropology, School of Language, Culture & Society, Oregon State University

As an adaptive strategy and way of life, subsistence economies and social networks in rural Alaska have been shaped by environmental change at multiple spatial and temporal scales. Working together to harvest wild plants and animals and circulating these resources within and between communities, Alaska Natives have been able to survive and thrive for millennia in an environment with patchy spatial distributions of resources, highly seasonal fluctuations in abundance, and long-term climatic and ecological variation. Increasingly, these adaptations to environmental uncertainty must also contend with unprecedented changes driven by anthropogenic climate change and ongoing processes of settler colonialism, globalization, and social change. Despite these challenges, subsistence economies and social networks in Alaska have proven remarkably resilient. This presentation builds on previous research suggesting the resilience of subsistence economies is enhanced by access to diverse resources and the structural patterns of social networks. Using social network analysis of data from 135 households, we investigate the relationship between harvest diversity and network position to better understand the relationship between harvest diversity and productivity and explore the role of harvest diversity in adaptations to environmental change. Our results indicate that both productivity and diversity are positively associated with increased network connections, and that productivity alone provides an incomplete model of the dynamics that shape these networks. We suggest harvest diversity may play a unique role in supporting adaptive capacity and resilience by: (1) maintaining productivity despite environmental change and (2) sustaining network structures that expand access to resources throughout the community.

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### My Heart in Their Hand: Elucidating Psychosocial Stress from Archaeological Hair at a Mass Child Sacrifice at Pampa La Cruz, Perú

BENJAMIN J. SCHAEFER<sup>1,2,3,4</sup>, GABRIEL PRIETO<sup>5</sup> and JOHN W. VERANO<sup>6</sup>

<sup>1</sup>Anthropology, University of Illinois at Chicago, <sup>2</sup>Latin American and Latinx Studies, University of Illinois at Chicago, <sup>3</sup>Gender and Women's Studies, University of Illinois at Chicago, <sup>4</sup>Anthropology, The Field Museum of Natural History, <sup>5</sup>Anthropology, University of Florida, <sup>6</sup>Anthropology, Tulane University

Child sacrifice has been practiced by many ancient societies over time although archaeological evidence is often lacking. Scholars have attempted to investigate the motivations behind intentional state-sanctioned killings; however, the

missing archaeological context leaves these interpretations up for debate. Outside of modern-day Trujillo, recent excavations in Huanchaquito-Las Llamas (HLL) recovered the largest mass sacrifice event in the Americas dated to the terminal Late Intermediate Period (circa 1400 CE). These tributes were drawn from adjacent river valleys and sacrificed during the decline of the Chimú domination of the North Coast. This study draws on data derived from assaying endogenous cortisol in archaeological hair strands from human sacrifices (n=40) at a new sacrificial site north of HLL known as Pampa La Cruz. Hair grows approximately at a rate of 1cm a month and allows for reconstructing monthly patterns of stress leading up to sacrifice. Preliminary results suggest high cortisol levels indicate elevated psychosocial stress that was exacerbated by environmental catastrophe and social instability during the thirteenth and fifteenth centuries CE. This project aims to investigate how various social processes may have played a pivotal role in regulated cortisol production, social inequity, and overall health prior to sacrifice.

*The Massachusetts Cultural Council - Tyngraham*

### Eosinophilia Inhibits Cytokine Responses to Viral and Bacterial Stimulations in a Subsistence Population in Bolivia

INDIA SCHNEIDER-CREASE<sup>1</sup>, AARON D. BLACKWELL<sup>2</sup>, THOMAS S. KRAFT<sup>3</sup>, MELISSA EMERY THOMPSON<sup>4</sup>, IVAN MALDONADO SUAREZ<sup>5</sup>, DANIEL K. CUMMINGS<sup>6</sup>, JONATHAN STIEGLITZ<sup>7</sup>, NOAH SNYDER-MACKLER<sup>1,8</sup>, MICHAEL GURVEN<sup>3</sup>, HILLARD KAPLAN<sup>9</sup> and BENJAMIN C. TRUMBLE<sup>1,8,9</sup>

<sup>1</sup>Center for Evolution and Medicine, Arizona State University, <sup>2</sup>Department of Anthropology, Washington State University, <sup>3</sup>Department of Anthropology, University of California Santa Barbara, <sup>4</sup>Department of Anthropology, University of New Mexico, <sup>5</sup>Biochemistry, Tsimane Health and Life History Project, <sup>6</sup>Economic Science Institute, Chapman University, <sup>7</sup>Anthropology, Institute for Advanced Study in Toulouse, <sup>8</sup>School of Life Sciences, Arizona State University, <sup>9</sup>School of Human Evolution and Social Change, Arizona State University

Exposure to parasites and pathogens over the course of human evolution has shaped the contemporary immune system. Soil-transmitted helminths (STHs) regulate immune function, a property that may guide the host response to downstream infections with viruses and bacteria that elicit strong inflammatory responses. To test whether a multi-parasite and pathogen environment dampens the immune response to viruses and bacteria, we worked with the Tsimane, forager-horticulturalists in the Bolivian Amazon with little market integration and high rates of STH infection. We evaluated how eosinophils, a proxy of both inflammatory response and STH infection, affected cytokine responses to *in vitro* stimulation with H1N1 vaccine and LPS in 179 whole blood

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samples. Eosinophils were associated with lower cytokine responses to H1N1 and LPS, with the strongest effects in women. Eosinophils were significantly ( $p \leq 0.05$ ) associated with lower responses of IFN- $\gamma$ , IL-1 $\beta$ , IL-2, IL-4, IL-7, IL-8 in women and IFN- $\gamma$  and IL-2 in men to H1N1, and with lower responses of IFN- $\gamma$ , IL-4, IL-6, IL-7, IL-8, and GM-CSF in women and IFN- $\gamma$ , IL-1 $\beta$ , IL-6, IL-7, and IL-8 in men to LPS. Eosinophils were variably negatively associated with the responses of Th1- and Th2-cytokine suites to H1N1 and LPS in women and men. Our results suggest that eosinophilia may mitigate host-induced damage related to viral and bacterial immune responses, and suggest that populations that have undergone the epidemiological transition may incur worse outcomes during viral and bacterial infections than populations still living in high parasite and pathogen exposure environments.

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### Mixed-species pairs as a management strategy for gibbons and siamangs: a behavioral comparison of mixed-species and same-species pairs

AMY L. SCHREIER<sup>1,2</sup>, GARRETT REBARCHEK<sup>1</sup>, EVELYN MADDIGAN<sup>1</sup>, KELSEY GREEN<sup>1</sup>, SHARON JOSEPH<sup>2</sup>, YOONJUNG YI<sup>3,4</sup>, SAEIN LEE<sup>3</sup>, HAEUN GE<sup>5</sup>, BAE KEUN LEE<sup>6</sup>, JAE C. CHOE<sup>3</sup> and ANNEKE MORESCO<sup>2</sup>

<sup>1</sup>Biology Department, Regis University, <sup>2</sup>Animal Welfare and Research, Denver Zoo, <sup>3</sup>Laboratory of Behavioral Ecology, Ewha Womans University, <sup>4</sup>College of Biology and the Environment, Nanjing Forestry University, <sup>5</sup>Department of Zoological Research & Management, National Institute Ecology, Korea, <sup>6</sup>Research Center for Endangered Species, National Institute Ecology, Korea

Gibbons and siamangs are known for their monogamous social system, with long-term pairs engaging in social grooming. When a female white-cheeked gibbon (*Nomascus leucogenys*) at Denver Zoo was left without a partner, the zoo paired her with a male red-cheeked gibbon (*Nomascus gabrielle*) so that these social primates would not be alone; similarly, a male red-cheeked gibbon housed alone was introduced to a female siamang (*Symphalangus syndactylus*). The National Institute of Ecology (NIE) in South Korea also housed a mixed-species gibbon pair (female *Hylobates lar* and male *N. gabrielle*). To investigate whether these mixed-species pairs exhibited species-typical social behavior, we compared their activity budgets with those of two wild pairs of Javan gibbons (*Hylobates moloch*) in Gunung Halimun-Salak National Park, Indonesia. We conducted scan sampling of focal animals, recording rest, feed, travel, and social behavior; we collected data from January 2015-February

2016 in Indonesia, June 2018-November 2018 at NIE, and October 2018-December 2019 at Denver Zoo. Our results showed that the wild same-species pairs spent three times as much time feeding and 10% less time resting as the managed mixed-species pairs. However, there were no significant differences in the proportions of time spent socializing, with mixed-species and same-species pairs all spending about 5% of their time engaged in social behavior. These results suggest that being housed as mixed-species pairs - and not alone - can provide positive welfare for managed pairs, allowing them to engage in levels of social behavior typical for wild same-species pairs.

### Old World monkey divergence: adaptive, neutral, or both?

LAUREN SCHROEDER<sup>1,2</sup>, SARAH ELTON<sup>3</sup> and REBECCA R. ACKERMANN<sup>2</sup>

<sup>1</sup>Department of Anthropology, University of Toronto Mississauga, <sup>2</sup>Human Evolution Research Institute, Department of Archaeology, University of Cape Town, <sup>3</sup>Department of Anthropology, Durham University

Molecular and fossil data have provided considerable insight into evolutionary divergence across the family Cercopithecidae, however less is known about the evolutionary processes that underlie these differences. Differentiating between selection and drift is of particular interest, both for understanding the fossil record and evaluating how modern taxa may respond in the future. Here, we apply tests developed from quantitative genetics theory to investigate the evolutionary processes acting at various hierarchical taxonomic levels across Cercopithecidae. Using a large ( $n > 3000$ ) morphometric dataset of matched cranial and mandibular specimens, we test patterns of within- and between-population divergence under a null hypothesis of genetic drift, an approach applied previously to New World monkeys, apes and hominins. Results from analyses of the full skull suggest that natural selection plays a significant role in diversifying the Cercopithecidae as a whole. At a subfamily level, genetic drift was rejected within Cercopithecinae, indicating adaptive divergence within guenons in particular, but not within the Colobinae. However, when crania and mandibles are analyzed separately, there is some indication of selection driving diversification within both African and Asian colobines (but not within Cercopithecinae). Further examination of the data suggests that selection for differences in size may be a large factor driving diversification, and that some individual traits show evidence for selection, even within a more general pattern of neutral evolution. Research on large datasets such as these can provide better

resolution for understanding the complementary roles of selection and drift in driving morphological divergence, and to test correlated evolutionary scenarios.

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### The role of uncoupling protein-1 in cold-induced bone loss: implications for human climatic adaptation

MAISEY SCHULER, REBECCA TUTINO, MIRANDA COSMAN, RACHEL HURWITZ, TAYLOR M. SPENCER, ISABEL HERMSMEYER, ALEXIS STOKEL and MAUREEN J. DEVLIN

Anthropology, University of Michigan

Chronic cold exposure causes elevated sympathetic tone that leads to bone loss, which could increase fracture risk in cold-dwelling humans. Nonshivering thermogenesis (NST) via uncoupling protein (UCP1) in brown adipose tissue may reduce bone loss by maintaining body temperature. To test this hypothesis, we studied the effects of temperature and sympathetic inhibition on bone mineral density (BMD) and body composition in male and female UCP1 knockout (UCP1KO) mice vs. wildtype C57BL/6J (B6) mice. We predicted that cooler temperature would lead to lower BMD in UCP1KO compared to B6 mice, and that sympathetic blockade with propranolol (PRO) would prevent bone loss. Mice were pair-housed from 3-12 weeks of age at 26C (thermoneutrality) or at 22C (cool), with or without PRO in drinking water (5 mg/mL). BMD and body composition were measured by peripheral dual-energy X-ray absorptiometry (Piximus I, GE Lunar). Results indicated no differences in BMD due to temperature or genotype in either sex. In female mice at 22C, BMD was lower in PRO-treated B6 and UCP1KO compared to controls. Unexpectedly, body fat was higher in females of both strains housed at 22C vs. 26C; in female UCP1KO vs. B6 at both temperatures; and in PRO-treated vs. wildtype females in both strains. These preliminary results do not support our hypothesis that UCP1-mediated NST reduces cold-induced bone loss. Microcomputed tomography (pending) will show how NST and sympathetic blockade affect trabecular bone microarchitecture and cortical bone geometry. Understanding how cold affects bone is essential for interpreting ecogeographic patterns of skeletal morphology.

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## ABSTRACTS

### Female choice and sexual coercion in wild orangutans (*Pongo pygmaeus wurmbii*)

AMY M. SCOTT<sup>1</sup>, TRI WAHYU SUSANTO<sup>2</sup> and CHERYL D. KNOTT<sup>1,3</sup>

<sup>1</sup>Anthropology, Boston University, <sup>2</sup>Biology, National University, Indonesia, <sup>3</sup>Biology, Boston University

Due to extreme incongruence in parental investment, the potential for sexual conflict in orangutan reproductive strategies is high. Female orangutans prefer flanged males, but with intense male-male competition and sexual coercion, it is unclear how females are able to exert choice. We hypothesized that female orangutans use initiation and maintenance of associations with preferred males as a mechanism of female choice. We used encounter rates and behavioral measures of proximity maintenance to distinguish between the role of female choice and male coercion in male-female associations in Gunung Palung National Park, West Kalimantan, Indonesia. From May 2018-April 2019, we collected data on initiation, termination, and proximity maintenance during associations between males and cycling females (females without dependent offspring or with offspring over 6 years old). Encounters between cycling females and flanged males were more likely to be female-initiated (83.3%), while encounters with unflanged males were more likely to be male-initiated (80%) (N=16, p=0.035, Fisher's exact test). Additionally, the Brown Index indicates significantly more female proximity maintenance when cycling females associated with flanged males than unflanged males (N=33, W = 198.5, p= 0.012). However, using long-term data on male-female associations, we found that dyads of flanged males and females were less likely to encounter other males compared to dyads of unflanged males and females (N=542, X<sup>2</sup>= 3.3051, df=1, p=0.035). This indicates that flanged males may also use associations to mate guard females. These data indicate that there are behavioral manifestations of both female choice and male coercion in orangutan associations.

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### A new approach to dental diversity in the New World: applying the forensic application rASUDAS2 to a bioarchaeological problem

G RICHARD SCOTT, TATIANA VLEMINCO-MENDIETA and KYRA E. STULL

Anthropology, University of Nevada Reno

Traditionally, the use of metric, morphologic, and genetic variables to evaluate population relationships was accomplished through statistics that use sample means or frequencies to estimate pairwise distances. An alternative to biodistance,

with its emphasis on sample statistics, is a Bayesian application that calculates the probability that an individual is assigned to one of five major geographic groups (East Asia, American Arctic, American Indian, Southeast Asia, Austral-Melanesia) based on crown and root morphology. Drawing on the Christy G. Turner II database, 602 individuals from four major geographic regions in the Americas (i.e., Circumpolar, Northwest Coast, North America, South America) were analyzed using rASUDAS2. Multiple samples were assessed from each region and intra-regional results were consistent. The primary assignments for the Circumpolar samples were: American Arctic (46%) and American Indian (24%); for the Northwest Coast: American Arctic (35%) and American Indian (34%); for North America: American Indian (53%) and American Arctic (27%); and for South America: American Indian (65%) and American Arctic (18%). American Arctic assignments go down from north to south while American Indians assignments go up. Assignments for individuals from the four areas to East Asia were 13%, 15%, 13%, and 11%, supporting the idea that Native Americans differentiated from East Asian ancestors at the same time, consistent with the Beringian Standstill model. Combined assignments to Southeast Asia and Austral-Melanesia were under 10% for the four New World regions, providing no dental evidence for ancestral ties to these areas.

### SACRED Birth: Uncovering Obstetric Racism in the Time of COVID-19 Through Black Birthing Narratives & Medical Illustrations

KAREN A. SCOTT<sup>1</sup> and DANA-AIN DAVIS<sup>2</sup>

<sup>1</sup>Obstetrics, Gynecology, & Reproductive Sciences, and Social Sciences & Humanities, University of California San Francisco, <sup>2</sup>Center for the Study of Women and Society, Graduate Center, City University of New York

**Background:** The unintended consequences of hospital mitigation practices during the COVID-19 pandemic reproduced white patriarchal supremacist norms and narratives about Black bodies and Black births. To date, there is no validated participatory patient reported experience measure (PREM) of obstetric racism to characterize hospital birth experiences of Black mothers and birthing.

**Methods:** We constructed a novel survey instrument containing existing and de novo items for six community identified quality of care domains. The revised list of survey items were then evaluated and revised using the modified Delphi method by an advisory group of Black women content experts in the fields of sexual, perinatal and reproductive health across disciplinary and geographic borders across the U.S. The revised list of items

were then evaluated by community members for validation and review using cognitive interviewing, confirmatory analysis, and hypothesis testing, and psychometric data analysis.

**Results:** Six domains of obstetric racism emerged: (1) Safety; (2) Autonomy; (3) Communication and Information Exchange; (4) Racism; (5) Empathy & Humanity; and (6) Dignity in Blackness. In addition, three domains, Accountability, Social Capital & Kinship, and Holistic Care, emerged as community-informed hospital-based strategies to dismantle and mitigate the harm of obstetric racism.

**Conclusion:** Obstetric racism describes complex social and clinical interactions, communications, counseling, and decision-making that violate the human rights of Black mothers and birthing people across multiple domains. Disrupting theoretical and methodological approaches with, for, and by Black mothers and Black women scholars closed knowledge gaps in existing perinatal PREMs and quality improvement sciences, practice, and research.

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### Looking for Linear Enamel Hypoplasia in Subfossil Lemurs

MELISSA S. SEABOCH<sup>1,2</sup> and LAURIE R. GODFREY<sup>3</sup>

<sup>1</sup>Anthropology, Salt Lake Community College, <sup>2</sup>Anthropology, University of Utah, <sup>3</sup>Anthropology, University of Massachusetts

Linear enamel hypoplasias (LEHs) are linked to stressors, including malnourishment and disease. Prior research reports that LEHs are rare in strepsirrhines, even in known stressed populations. The studies suggested rapid tooth crown formation might preclude the formation of LEH, despite the presence of stressors, because crown formation duration impacts LEH formation. Because crown formation duration is correlated with body size, our research asked whether the larger subfossil lemurs exhibit LEH. Using lighted magnification, we visually examined 292 permanent teeth (38 incisors, 34 canines, 121 premolars, 99 molars; 204 maxillary, 88 mandibular teeth) of subfossil lemurs (*Mesopropithecus* N=1; *Pachylemur* N=109; *Archaeolemur* N=171; *Palaeopropithecus* N=4; *Megaladapis* N=7). We found no surface LEHs, though sample sizes, especially for anterior teeth, were small. LEH is known to be present on all teeth in anthropoids. While LEHs are generally more frequent on anterior teeth, it is not uncommon for premolars to be affected, especially in primates. In a study of 209 lemur teeth, LEHs were limited to the premolars and, more rarely, the molars; incisors and canines were never affected. Factors that may account for the lack of visible LEH in our sample include microstructural prism pattern, enamel thickness, enamel

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secretion rates and duration, enamel extension rates, and timing of crown formation. Further research, (e.g., histological analysis) is needed to understand the low frequency of surface LEH in both extant and extinct lemurs, especially since internal stress lines are present, and the explanation is not likely to be simple.

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### Historical biogeography of hominins inferred using maximum likelihood

YEGANEH SEKHAVATI and DAVID S. STRAIT

Anthropology, Washington University in St. Louis

Phylogenetic biogeography evaluates patterns of vicariance and dispersal in a phylogenetic framework, which may inform scenarios of evolution. Recently, model- and event-based approaches have been developed that examine vicariance and dispersal in a probabilistic framework. This study analyzes hominin biogeography using dispersal vicariance analysis (DIVALIKE) using likelihood-based inference in RASP (Reconstruct Ancestral State in Phylogenies). A recently published cladogram of early hominins was used as a baseline and modified to examine the biogeographic implications of various phylogenetic hypotheses. Hominins originate across eastern and north central Africa. *Sahelanthropus* speciates in north central Africa via vicariance with an eastern African clade, and the ancestor of *Australopithecus afarensis* subsequently expands its range from eastern into north central Africa. An *A. afarensis*-like population expands its range from eastern into southern Africa. *Australopithecus africanus* or its ancestor subsequently speciates via vicariance. *Paranthropus* expands its range into southern Africa and *P. robustus* arises via vicariance with some or all eastern African *Paranthropus*. The ancestors of *Homo habilis* and *H. erectus sensu lato* expand their ranges from eastern into southern Africa. Other biogeographic events depend on the phylogenetic relationships of *A. sediba*. All last common ancestors in the hominin cladogram are found in whole or in part in eastern Africa, highlighting the key role this region plays in early hominin evolution. An ecozone must have periodically existed allowing hominin dispersals between eastern and north central Africa. Most or all southern African hominins are migrants descended ultimately from eastern African ancestors.

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### The effect of an abrasive diet on the pulp volume of the lower second molar in anthropoid primates

KEEGAN R. SELIG<sup>1</sup>, KORNELIUS KUPCZIK<sup>2</sup> and MARY T. SILCOX<sup>1</sup>

<sup>1</sup>Department of Anthropology, University of Toronto Scarborough, <sup>2</sup>Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Dental pulp plays an important role in the maintenance and upkeep of dentine. Under the processes of dental wear, odontoblasts present in the pulp cavity deposit additional dentine to prevent the delicate internal dental tissues becoming exposed and vulnerable to infection. Therefore, we predict that there may be an adaptive advantage for having a higher pulp volume in taxa that consume a more abrasive diet compared to those that eat a less abrasive diet. We studied unworn lower second molars in pairs of extant hominoids, cebids, and pitheciids that vary in the abrasiveness of their diets ( $n = 36$ ). We measured relative pulp volume (RPV) as the ratio of pulp volume to that of the total volume of the tooth (enamel+dentine+pulp) using micro-CT scans. Results of Mann-Whitney tests indicate that taxa with more abrasive diets have significantly higher RPV than closely related taxa with less abrasive diets in all three pairs of taxa (hominoids:  $p = 0.030$ ; cebids:  $p = 0.002$ ; pitheciids:  $p = 0.043$ ). Our results suggest that there may be an adaptive mechanism (i.e. a higher RPV) in the molars of primates to help deal with the challenges of an abrasive diet. Our results provide us with a greater understanding of the relationship between the dental pulp and dietary abrasiveness. Our study also offer insight into the adaptive context of taurodont molars like those of Neanderthals and possible means for testing dietary adaptations in extinct taxa.

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### The effect of reference sample composition and size on dental age interval estimates

VALERIE SGHEIZA<sup>1</sup> and HELEN M. LIVERSIDGE<sup>2</sup>

<sup>1</sup>Anthropology, University of Illinois at Urbana-Champaign, <sup>2</sup>Institute of Dentistry, Barts and the London School of Medicine and Dentistry, Queen Mary University of London

Validation studies in juvenile dental age estimation primarily focus on point estimates. Comparing age interval performance for reference samples of different ancestry group compositions has received minimal attention. There is interest, however, in whether ancestral groups can be combined in one reference sample. We tested the effect of reference sample size and composition by sex and ancestry group on age interval estimates. Model performance was assessed through bias in maximum likelihood estimates, age interval width, and success rate for the estimated 95% age interval capturing true age. The dataset consisted of Moorrees et al. (1963) molar scores from panoramic radiographs of 1120 London children of Bangladeshi and European ancestry and 5-19 years of age. Each reference sample was constructed with a uniform age distribution of 10, 20, 40, or 80 individuals in each year of age with equal numbers by sex and ancestry group if applicable. Type 1 reference samples

contained a single sex and ancestry group, type 2 a single ancestry group, type 3 a single sex, and type 4 both sexes and ancestry groups. Age estimates were performed using full Bayesian multivariate cumulative probit with 5-fold cross-validation. Reference sample size did not consistently affect performance metrics. Types 3 and 4 showed increasing success rates, and all types showed decreasing interval width, with increasing age. Types 1 and 2 showed upward bias below 8 years. Our results show that combining ancestry groups from the same location (London) in a single reference sample does not detrimentally affect age interval estimates.

no funding information to disclose

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### An Analysis of Frontal Sinus Shave Variation Between Population Affinity Groups and Biological Sexes as Seen on Computed Tomography Scans

AUSTIN A. SHAMLOU<sup>1</sup>, SEAN D. TALLMAN<sup>1,2</sup>, OSAMU SAKAI<sup>3</sup> and ARTEM KALIAEV<sup>3</sup>

<sup>1</sup>Anatomy and Neurobiology, Boston University School of Medicine, <sup>2</sup>Anthropology, Boston University, <sup>3</sup>Department of Radiology, Boston Medical Center, Boston University School of Medicine

Frontal sinus variation has been used in forensic anthropology to aid in positive identification since the 1920s; however, little is known about how the sinuses vary by sex or population affiliation. This study utilizes frontal sinus morphology as imaged on hospital acquired computed tomography (CT) scans to test the hypothesis that frontal sinus shape variations will cluster based on population affinity and biological sexes. The CT scans were obtained from 307 individuals representing females ( $n=167$ ) and males ( $n=140$ ) from African ( $n=63$ ), Asian ( $n=74$ ), European ( $n=91$ ), and Latin American ( $n=79$ ) derived groups from Boston Medical Center's Radiology Department. Individual coronal slices of CT scans that represented the overall sinus outline and maximum heights and widths were uploaded into Adobe Photoshop and traced in order to capture the variation in morphology from an anteroposterior perspective. Subsequently, Elliptical Fourier analysis (EFA) was used to evaluate the variation of the frontal sinus outlines, and the EFA coefficients were statistically analyzed using chi-square tests to determine if the differences in coefficients were statistically significant based on population affinity or biological sex. The results indicate that biological sex and population affinity effect the morphological development of the frontal sinus. This study adds to the foundational knowledge about frontal sinus variation and how CT scans can aid in exploring human biological variation.

# ABSTRACTS

## Learning from Captive Gibbons

ALEXANDRA C. SHELDON and THAD Q. BARTLETT  
Anthropology, University of Texas at San Antonio

Gibbons were one of the first taxa to be subject to long-term scientific observations in the wild; nevertheless, field research on gibbon social behavior has lagged compared to some species due to difficulties in conducting detailed observations of these arboreal and swift moving animals. Observations of captive gibbons have the potential to fill knowledge gaps and inform fieldwork. To better understand the breadth and potential of captive research we conducted a systematic survey of the gibbon literature, using traditional search engines combined with citation mining, to identify the most prominent areas of investigation. We limited our survey to primary research on the behavior and biology of all 20 gibbon species. Our analysis focuses on 153 scholarly products (e.g., book chapters, journal articles, theses and dissertations) that fit our criteria. As expected, lar gibbons (appearing in 41.8% of publications) and siamang (32.0%) were the most well represented taxa. But *Nomascus leucogenys* was also well represented (24.8%). The topical focus of research varied, with vocalization (41.2%), social behavior (36.6%), and locomotion (31.4%) most well represented. Gibbon responses to human impacts (e.g. visitor presence) was a small but growing category. The low return rate of literature on some topics, including health and rehabilitation, indicate that gray literature is not well represented and much of the research from theses and dissertations did not result in publication. Finally, most publications were in English, representing a language bias and potential barrier to access for non-English speakers.

University of Texas at San Antonio Dean's Research Fellowship

## A test of the expensive-tissue hypothesis' prediction of tissue competition in humans

MEGHAN K. SHIRLEY<sup>1</sup>, SAMULI HELLE<sup>2</sup>, KIRAN K. SEUNARINE<sup>3</sup>, OWEN J. ARTHURS<sup>3,4</sup>, SIMON EATON<sup>3</sup>, JANE E. WILLIAMS<sup>3</sup>, TIM J. COLE<sup>3</sup>, CHRIS A. CLARK<sup>3</sup> and JONATHAN CK. WELLS<sup>3</sup>

<sup>1</sup>GI, Hepatology and Nutrition, The Children's Hospital of Philadelphia, <sup>2</sup>Department of Social Research, University of Turku, <sup>3</sup>Great Ormond Street Institute of Child Health, University College London, <sup>4</sup>Department of Radiology, Great Ormond Street Hospital

The question of how humans evolved large, metabolically costly brains without a compensatory increase in resting energy expenditure per kilogram body mass commands great interest across disciplines. The expensive-tissue hypothesis (ETH) posited a trade-off between brain and gut tissues. Versions of the ETH (*i.e.*, interrogating gut, or other metabolically expensive tissues) have been tested in non-human animals

with mixed results, however no test had been performed in humans. We filled this gap by collecting high-quality brain and body composition data in 70 healthy young women and using state-of-the-art causal modeling techniques. We applied a model-implied instrumental variable approach within a structural equation modeling framework to test the most likely brain-body trade-off model, given theory and previously published results; namely, a negative, causal relationship between two latent constructs: 'nutritional investment in brain tissues' → 'nutritional investment in body tissues.' The former was indicated by cerebrum, cerebellum, and intracranial volume, and the latter by internal organs, fat, and skeletal muscle. Adjusting for body size, we found a negative causal estimate for the regression of body on brain (-0.41), however estimates ranging from a larger negative association to a small positive association (95% CI -1.08, 0.26) were also compatible with the data under our model. These results suggest a trade-off may exist between energy invested in brain versus body tissues; though inconclusive, they represent an important first step in assessing empirical evidence for the ETH in humans. Analyses using larger datasets are required to build on these findings and expand the evidence base.

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## Examining intra-observer reproducibility of a new data-collection protocol for age estimation based on the auricular surface

ELENA A. SIERRA<sup>1</sup> and JOHN ALBANESE<sup>2</sup>

<sup>1</sup>Archaeology, Simon Fraser University, <sup>2</sup>Sociology, Anthropology and Criminology, University of Windsor

Natural human variation is an unavoidable source of error when estimating age from skeletal remains. There are many factors involved in shaping the morphology of human bone, which tend to increase variation with chronological age. Perhaps because variability is difficult to capture, current methods used in age estimation have been developed with a focus on accuracy rather than reproducibility. To counter this phenomena, we created a new data-collection protocol for age-related features on the auricular surface according to their reproducibility, not accuracy. In order to assess repeatability, we performed a blind intra-observer analysis on 30 individuals. Specimens were chosen using a sampling strategy to obtain a broad range of variation, resulting in individuals being equally distributed by sex and over a wide range of ages. These were selected from the Terry Collection housed at the Smithsonian Institution. Lastly, our methodology divided the possible range of age-related variation into several stages which were given a numerical score. According to our results, over 90% of the time the score given was on the same stage or the

adjacent one. These intra-observer reproducibility results show potential for further investigation into defining a highly reproducible age estimation method.

## Sickle Cell Anemia and Sickle Cell Trait in the State of Pará, Brazil: Prevalence of Clinical Manifestations among Families in the Amazon Region

ARIANA KELLY. SILVA and HILTON P. SILVA  
DEPARTMENT OF ANTHROPOLOGY, UEPA/GEB/UFPA/SEDUC

Sickle Cell Disease (SCD) has a prevalence of about 1% in the population of the State of Pará, Brazilian Amazon, with 4.4% occurrence of Sickle Cell Trait (SCT). Research on the ancestral genomics of people with SCD encompassing 60 individuals with Sickle Cell Anemia (SCA/Hb SS) in the capital, Belém, indicated that 55% of them have first or second-degree relatives with SCA in the family, with confirmed cases of death at birth or during adolescence, severe sequelae of stroke and leg ulcers or other serious clinical manifestations. In this group, 37% of their close relatives have the SCT but are asymptomatic or present mild symptoms such as joint pain, shortness of breath and tiredness, associated with other pre-existing diseases. However, not all family members of people with SCD have access to genetic tests at birth due to the SCT not being considered a significant medical condition in Brazil. Despite their conditions, patients and carriers face difficulties such as lack of resources to travel to the capital for clinical care, lack of information about SCA or SCT, obstacles to obtain consultations with hematologists, and neglect of appropriate care. The high prevalence of both SCA and SCT suggests potential microevolutionary processes taking place among the families, raising concerns as there is no genetic counseling in the region, and the access to the Foot Test, to be performed at birth, is limited in rural areas, indicating neglected to the health of the Black population in the State.

## Patterns of sexual dimorphism in catarrhine cranial morphology

EVAN A. SIMONS<sup>1</sup>, STEPHEN R. FROST<sup>2</sup>, KATERINA HARVATI<sup>3</sup>, KIERAN MCNULTY<sup>4</sup> and MICHELLE SINGLETON<sup>5</sup>

<sup>1</sup>Anthropology, University at Buffalo, <sup>2</sup>Anthropology, University of Oregon, <sup>3</sup>Paleoanthropology, Senckenberg Centre for Human Evolution and Paleoenvironment, Eberhard Karls Universität, Tübingen, Germany, <sup>4</sup>Evolutionary Anthropology Laboratory, University of Minnesota, <sup>5</sup>Anatomy, College of Graduate Studies, Midwestern University

This investigation presents a broad, comparative analysis of patterns of sexual dimorphism in catarrhine cranial shape using geometric morphometrics. Thirty-four 3D landmarks, digitized from 1,665 crania representing 25 catarrhine species,

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were superimposed using generalized Procrustes analysis. Amounts of intraspecific sexual shape dimorphism were quantified as the path distance between males and females, and comparisons of the direction of the sexual dimorphism vector were made using Phenotypic Trajectory Analysis while accounting for a common shape allometry. Averages of the natural log of centroid size for both sexes within each species were also computed and compared with the shape dimorphism data, as were social system categories compiled from the literature.

Across catarrhines, patterns of sexual dimorphism are largely shared. That is, with some exceptions, males and females differ in cranial shape in similar ways. *Homo* has the most distinct pattern of sexual shape dimorphism. Additionally, even after cranial size was accounted for in the model, levels of intraspecific sexual shape dimorphism were related to levels of intraspecific cranial size dimorphism (adj.  $r^2 = 0.6402$ ;  $F_{1,23} = 43.71$ ;  $p < 0.0001$ ). The highest levels of intraspecific sexual shape dimorphism for all catarrhines were found in *Mandrillus*, and the highest levels among hominoids were found in *Gorilla* who also evinced some unique shape dimorphism patterns relative to other species. Species with multimale/multifemale and polygynous social systems had higher levels of sexual shape dimorphism than more monogamous species, with a significant difference among group means ( $F_{2,22} = 3.594$ ,  $p = .045$ ).

### Analysis of language used to describe human variation in forensic anthropology: Race, ancestry, and ethnicity

CASSIE E. SKIPPER<sup>1</sup>, MARIN A. PILLOUD<sup>1</sup>, SAMOURA L. HORSLEY<sup>1</sup>, ALBA E. CRAIG<sup>2</sup>, KRISTA E. LATHAM<sup>2</sup>, KATIE ZEJDLIK<sup>3</sup>, CHAUNESY M.J. CLEMMONS<sup>4</sup>, DEBORAH A. BOEHM<sup>1,5</sup> and CASEY S. PHILBIN<sup>6</sup>

<sup>1</sup>Department of Anthropology, University of Nevada, Reno, <sup>2</sup>Department of Anthropology, University of Indianapolis, <sup>3</sup>Anthropology and Sociology Department, Western Carolina University, <sup>4</sup>Department of Anthropology, Texas State University, <sup>5</sup>Department of Gender, Race, and Identity, University of Nevada, Reno, <sup>6</sup>Department of Chemistry, University of Nevada, Reno

Forensic anthropologists study human skeletal variation to estimate the biological profile of unknown decedents, including estimates of what is typically called "ancestry." This work has been criticized for being typological but is defended as necessary in the identification process. This research aimed to investigate forensic anthropological research and its relevance in missing-persons cases. To achieve this, we evaluated forensic anthropological articles in the *Journal of Forensic Sciences (JFS)* from 1972 to 2020 ( $n=360$ ). Terms were placed into

two categories: classifiers and descriptors. Data were compared with terminology and data kept by the National Missing and Unidentified Persons System (NamUs) and the United States census.

For classifiers, "race" was the most prevalent term (42.4%), followed by "ancestry" (30.6%), "population" (14.6%), "ethnic" (7.6%), and "other" (4.8%). A total of 160 distinct descriptors were identified; the most commonly used ( $\geq 3\%$ ) were "White" (16.0%), "Black" (13.8%), "American Black" (5.5%), "American White" (5.3%), "European" (4.5%), and "Hispanic" (3.0%). The NamUs database does not use this same terminology, illustrating a disconnect between anthropological research and efforts to identify the missing. There is also a bias in terms of race/ethnicity of the missing and unidentified that does not reflect U.S. census data.

This research has identified differences in terminology used in forensic anthropology and in the census and missing-persons reports. It is important for forensic anthropologists to be cognizant of the terms they use in medicolegal contexts, publications, and in public and/or professional spaces to avoid further marginalizing groups and perpetuating oppression rooted in systemic racism.

### Dental morphology and community structure of Plio-Pleistocene cercopithecoid primates from East and South Africa

IRENE E. SMAIL

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

Fossil cercopithecoid primates of the African Plio-Pleistocene are often found together in fossil deposits across East and South Africa. These species may have co-occurred in life and exploited similar types of resources in shared environments, as extant monkeys in Africa and Asia are known to do. Some of these fossil species are represented today by congeneric or descendant species with similar adaptations while others have no modern analogue. This project uses dental morphology to compare community structure across potentially co-occurring fossil and modern cercopithecoid populations (the cercopithecoid taxocene).

Relative enamel thickness, shearing potential, and dental shape ratios from the P4 – M3 tooth row were measured from extant ( $n > 700$ ) and fossil cercopithecoid specimens ( $n > 1000$ ). The latter primarily targeted the Hadar, Shungura, and Koobi Fora Formations of East Africa and the sites of Makapansgat, Sterkfontein, and Swartkrans in South Africa. Principal component analyses were performed separately on the maxillary and mandibular dentitions and resulting component scores were used to reconstruct the taxocene dental morphology at each site.

In general, the African cercopithecoid taxocene is similar across the main fossil sites analyzed. Patterns of overlap between fossil and modern sites may reflect environmental similarities or the adaptability of generalist cercopithecoids. An apparent niche shift from the Plio-Pleistocene to today reflects both taphonomic and ecological factors: a lack of smaller-bodied fossil cercopithecoid and colobine species combined with an expanded dental ecomorphological niche of larger-bodied fossil species.

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### Science on the Alleged Frontiers: Colonialism in the Time of Pandemics

RICK W. A. SMITH

Sociology and Anthropology, George Mason University, Indigenous Science, Technology, and Society Lab, University of Alberta

Public and scientific discourses over the last year have often characterized the intersecting developments of the COVID-19 pandemic, racial violence, and resurgent anti-racist movements as evidence that we are living in unprecedented times. These alleged frontiers have helped galvanize scientific efforts around the world in pursuit of effective treatments and have raised questions about the factors underlying disproportionate deaths along racial lines. The result of these efforts has been the rapid development of multiple potential treatments and vaccine candidates. However, in some instances, treatments and vaccines have moved forward with insufficient testing while in other cases clinical trials have been stalled by the lack of study participants from historically marginalized communities, raising questions about the integrity and efficacy of some medical interventions produced in the urgencies of the COVID-19 era. In spite of discourses regarding the unprecedented nature of these events, the interconnected threats of global pandemics, racial violence, and disproportionate burdens of morbidity and mortality upon marginalized bodies are nothing new. Drawing on case studies from the history of medicine in Baltimore specifically, and multiple histories of pandemics in North America more broadly, this study questions the validity of scientific and political frontierism and examines the conditions that have made it possible. These case studies reveal how scientific and national progress has been forged in moments of sickness and exploitations of marginalized bodies, and can inform more meaningful and historically coherent responses to the multiple intersecting problems we now face.

## ABSTRACTS

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### Elemental evidence for birth in primate tooth enamel

TANYA M. SMITH<sup>1,2</sup>, CHRISTINE AUSTIN<sup>3</sup> and MANISH ARORA<sup>3</sup>

<sup>1</sup>Australian Research Centre for Human Evolution, Griffith University, <sup>2</sup>Griffith Centre for Social and Cultural Research, Griffith University, <sup>3</sup>Department of Environmental Medicine and Public Health, Icahn School of Medicine at Mount Sinai

In 2013 we presented a model for identifying the initiation and cessation of nursing in primate teeth based on changes in the non-essential trace element barium. This drew upon on a study of human physiology; average barium values were seven times higher in colostrum than umbilical cord blood, indicating that barium is enriched in mother's milk relative to fetal supply. Consistent with this, we found that human deciduous teeth ( $n = 22/25$ ) and macaque M1s ( $n = 4/4$ ) showed a marked barium increase in close association with the neonatal line, a microscopic feature formed at birth and visible in sectioned enamel. Here we compare pre- and postnatal trends in barium, lead, lithium, strontium, and zinc, as they can each show developmental patterning in teeth. Barium remains the most consistent biomarker of milk; > 70% of M1 cusps ( $n = 24$ ) show the expected increase from prenatal to postnatal enamel. Exceptions occurred in cusps that had been mineralizing for less than three weeks, showed heavy wear, and/or were derived from bottle-reared monkeys. Only a third of our sample showed postnatal increases in lead and zinc, also reported to be highly enriched in colostrum. In contrast, strontium decreased or remained steady across the neonatal line, as did lithium, suggested limited utility for tracking changes in milk consumption. Research is needed to parse out anthropogenic and natural bioavailable sources of these elements; this would help contextualize substantial variation in absolute values that characterize contemporary humans and nonhuman primates from captive and wild environments.

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### A comparison of diceCT and histology for determination of nasal epithelial type

TIMOTHY D. SMITH<sup>1</sup>, HAYLEY M. CORBIN<sup>2</sup> and VALERIE B. DELEON<sup>3</sup>

<sup>1</sup>School of Physical Therapy, Slippery Rock University, <sup>2</sup>Department of Biology, Slippery Rock University, <sup>3</sup>Department of Anthropology, University of Florida

Diffusible iodine-based contrast-enhanced computed tomography (diceCT) is a potential tool for discriminating soft tissues in serial CT slices, which can then be used for three-dimensional analysis. With increasingly fine scan resolution, diceCT has the potential to supplant histology in some cases as a tool for identification of body

tissues. Here, we studied the head of a fruit bat (*Cynopterus sphinx*) using micro-diceCT. Subsequently, we decalcified, serially sectioned and stained the same head. The diceCT volume was rotated so that the sectional plane of the slice series closely matched that of histological sections. One investigator (HC), blind to the histological sections, examined the diceCT slice series and annotated changes in thickness of epithelium lining the first ethmoturbinal and the roof the nasal fossa and nasal septum. Then, a second investigator (TS) annotated images of matching histological sections based on microscopic observation of epithelial type. Measurements of epithelial perimeter using ImageJ revealed a close match between methods. DiceCT conformed to a gradually increasing perimeter of thicker epithelium as the slice series progresses from rostral to caudal; matching histological sections confirm this to be olfactory epithelium. Only one patch of unusually thick non-olfactory epithelium was annotated in diceCT series. Our results demonstrate that diceCT is, as yet, only a match for histology at low magnifications. However, diceCT slices offer a valuable tool to annotate changes in epithelial thickness. In combination with histology from a representative specimen of the same species, diceCT is highly effective in identifying distribution of olfactory epithelium.

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### Climate change and health among Indigenous Siberians

J. JOSH SNODGRASS<sup>1</sup>, ELLIE THOMAS<sup>1</sup> and TATIANA KLIMOVA<sup>2</sup>

<sup>1</sup>Anthropology, University of Oregon, <sup>2</sup>Medicine, North-Eastern Federal University (Russia)

Arctic and subarctic regions are experiencing profound environmental shifts as the result of global climate change. This has led to long-term shifts in temperature, reductions in permafrost, and glacial and sea ice melting. The present paper systematically reviews the health effects of climate change on contemporary Indigenous Siberian populations, with particular attention to the effects of altered ecology, shifting access to traditional foods, and changes to the burden of infectious/parasitic diseases. Indigenous Siberian populations, like other northern populations, are extremely vulnerable to the effects of climate change as these populations are experiencing rapid economic development and the effects of marginalization and pollution. Furthermore, Indigenous Siberians show overall poor health compared to other Arctic populations, and also pronounced health disparities compared to non-native Russians. Key issues related to climate change in northern Russia include: shifts in weather patterns and ecological conditions; threats to coastal communities from higher sea level; altered access to traditional lands and foods;

disturbances to psychological well-being based on disruption of traditional lifeways; increases in infectious disease burden; and, northern range expansion of parasitic zoonoses. Results of this review indicate that climate change has already altered Indigenous Siberian lifeways and health. Indigenous Siberian populations are serving as bellwethers of global climate change.

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### Using aDNA and Archaeological Data to Explain Migration in the Casas Grandes Region of Northern Mexico

MERADETH SNOW<sup>1</sup> and MICHAEL SEARCY<sup>2</sup>

<sup>1</sup>Anthropology, University of Montana,

<sup>2</sup>Anthropology, Brigham Young University

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. Genetic data must be interpreted through the lens of all available data from the site and surrounding region in order to understand how it fits into the potential for human migration. These ideas will be presented 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 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.

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### Strontium Isotope Analysis Indicates Restricted Mobility among Early Foragers in the High Andes

THOMAS J. SNYDER<sup>1</sup>, BRYNA HULL<sup>1</sup>, EDEN WASHBURN<sup>2</sup>, VICKY OELZE<sup>2</sup> and RANDALL HAAS<sup>1</sup>

<sup>1</sup>Anthropology, University of California, Davis,

<sup>2</sup>Anthropology, University of California, Santa Cruz

Extreme high-altitude environments were some of the final frontiers of human habitation. Recent research shows that the Andean highlands were permanently inhabited beginning around 9000

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years ago. However, it remains unclear whether the specific mobility patterns of these first hunter-gatherers of the Andes were wide-ranging or locally restricted. Recent research at the high-land site of Soro Mik'aya Patjxa (SMP) 8.0–6.5 cal. ka involving light stable isotopes, bioarchaeology, and lithic provenience analysis suggests that mobility patterns were relatively restricted. We present the results of a new study employing strontium isotope ( $^{87}\text{Sr}/^{86}\text{Sr}$ ) analysis of human tooth enamel ( $n=6$ ) from SMP. Strontium isotopes found in biogenic tissue can offer relatively direct and precise measure of land use patterns.  $^{87}\text{Sr}/^{86}\text{Sr}$  values from SMP vary little (0.70695 to 0.70708), indicating that all individuals sampled likely occupied the same home range. A new weighted mixture model approach incorporating published geologic, geographic, and bioavailable  $^{87}\text{Sr}/^{86}\text{Sr}$  data shows that these early hunter-gatherers at the site of SMP were indeed locally restricted in their land use and foraging range. We discuss the implications of these results for the development of social structures and agricultural economies in the region.

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### An ancient coronavirus-like epidemic 25,000 years in ancestral populations from East Asia

YASSINE SOUILMI<sup>1</sup>, ELISE LAUTERBUR<sup>2</sup>, RAY TOBLER<sup>1</sup>, CHRISTIAN HUBER<sup>1</sup>, ANGAD S. JOHAR<sup>1</sup> and DAVID ENARD<sup>2</sup>

<sup>1</sup>Australian Centre for Ancient DNA, University of Adelaide, <sup>2</sup>EEB, University of Arizona

The current SARS-CoV-2 pandemic has emphasized the vulnerability of human populations to novel viral pressures, despite the vast array of epidemiological and biomedical tools now available. Notably, modern human genomes contain evolutionary information tracing back tens of thousands of years, which may help identify the viruses that have impacted our ancestors – pointing to which viruses have future pandemic potential. Here, we apply evolutionary analyses to human genomes to ask if ancient coronavirus epidemics were recorded in the form of genomic adaptation in diverse human populations. Specifically, we use haplotype-based tests of selection such as iHS and nSL on the 1,000 Genomes Project dataset. By using block-randomized genomes to conduct a stringent false discovery rate analysis, we recover selection events involving 42 human genes that interact with coronaviruses (FDR=0.00024). By using ancestral recombination graphs, we estimate that these selection events started synchronously around 25,000 years ago. These adaptive events were limited to ancestral populations from East Asia, the geographical origin of several modern

coronavirus epidemics. Multiple lines of evidence further suggest an ancient viral selective pressure, such as (i) the proximity of the selection signals to lung eQTLs according to iSAFE (proximity test  $P=0.00004$ ) and (ii) the fact that the 42 selected genes are more often antiviral or proviral factors for many viruses (hypergeometric test  $P=0.0006$ ). An arms race with an ancient corona-like virus may thus have taken place in ancestral populations from East Asia. Our study highlights the promise of ancient epidemics to better predict future epidemics.

### Cultural skeletal modifications, stress and lifetime mobility at Ali Kosh, a Pre-Pottery Neolithic site in Iran

ARKADIUSZ SOŁTYSIAK<sup>1</sup> and HOJJAT DARABI<sup>2</sup>

<sup>1</sup>Department of Bioarchaeology, Faculty of Archaeology, University of Warsaw, Poland, <sup>2</sup>Department of Archaeology, Razi University, Kermanshah, Iran

During recent archaeological excavations at Ali Kosh, a Pre-Pottery Neolithic site in Deh Luran plain, SW Iran, a dense assemblage of human remains has been found, with four at least partially articulated skeletons, three separated crania, two mandibles and postcranial elements from three further individuals. All six preserved crania (two males, two females, two subadult individuals) were artificially modified (annular type). In the adult males with preserved crania, avulsion of the upper right central incisor has been noted. Besides these cultural skeletal modifications, severe enamel hypoplasia with a seasonal pattern occurred in three per five individuals with preserved canines.

The patterns of lifetime mobility in 11 individuals from Ali Kosh were assessed using the  $^{87}\text{Sr}/^{86}\text{Sr}$  values in tooth enamel, representing three phases of dental development (approximately 1-3, 4-8 and 10-15 years, multiple measurements available for five individuals). Only two human  $^{87}\text{Sr}/^{86}\text{Sr}$  values were close to the local range (0.70857-0.70861, five modern plant samples), but most individuals fit the range of the upper part of Deh Luran plain (0.70826-0.70848, five modern plant samples). Two individuals migrated from other regions, one likely from the Zagros piedmont in the north of the modern Ilam province, one from the areas closer to the Persian Gulf. Both moved to Deh Luran plain in their childhood. Another individual migrated as a child within Deh Luran plain. Observed distribution of the  $^{87}\text{Sr}/^{86}\text{Sr}$  values in human enamel suggests high degree of mobility, mainly in a regional scale, but with some people migrating from more distant places.

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### Bone Remodeling in the Face of Young Chimpanzees and Humans

JEFFREY K. SPEAR<sup>1,2</sup> and TIMOTHY G. BROMAGE<sup>3</sup>

<sup>1</sup>Center for the Study of Human Origins and Department of Anthropology, New York University, <sup>2</sup>New York Consortium in Evolutionary Primatology, NYCEP, <sup>3</sup>College of Dentistry, New York University

Previous research has shown that modern humans have experienced a shift in the patterns of facial bone remodeling relative to chimpanzees and macaques. Most notably, humans exhibit substantially more bone surfaces characterized by resorption than do those other primates, especially in the maxilla, a pattern presumably related to human orthognathism. However, despite these broad patterns, bone remodeling in humans is highly variable. We used both light and scanning electron microscopy to examine resorptional and depositional surfaces in the face of extant humans and chimpanzees to learn about how variation in bone remodeling patterns may have impacted the evolution of the human face. Six specimens were examined including three *Homo sapiens* and three *Pan troglodytes*. All were of the same dental age, first molar eruption, and the same intraspecific populations. We used light microscopy to identify forming bone surfaces, and scanning electron microscopy to follow up with areas that could not be solidly identified as forming bone surfaces. Each individual had a unique pattern of bone formation and resorption. The most common area of resorption in all species was along the zygomaticomaxillary suture, and many individuals exhibited resorption in the subnasal and infraorbital regions. The human specimens typically had larger and more numerous resorptive areas than the chimpanzees, but there were few truly distinct resorptive areas in humans.

### Where Does Positional Behavior Stand? The Impact of Standardizing Variables

WALKER STANTON<sup>1</sup>, MICHELLE BEZANSON<sup>2</sup>, LIZA J. SHAPIRO<sup>1</sup> and ALLISON MCNAMARA<sup>1</sup>

<sup>1</sup>Anthropology, University of Texas at Austin, <sup>2</sup>Anthropology, Santa Clara University

Field studies of primate positional behavior provide valuable tools for understanding form/function relationships, behavior/environment interactions, and interpreting the fossil record. One challenge in these studies is the ability to make reliable comparisons among species due to the application of different variables in research design. Hunt et al. (1996) provided a detailed list of 74 locomotor and 52 postural modes in order to allow researchers to standardize variables. We reviewed 71 peer reviewed articles published from 1996-2020 to examine how researchers use the standards and the degree to which researchers are presenting data on a given primate's positional repertoire. We found that 61% of the published

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studies used the standardized positional categories or combined the standardized definitions with alternative definitions. Researchers reported an average of 9.3 locomotor and 8.5 postural modes in their results. A total of 66 species were represented and 62% of papers focused on a single species, while 38% papers compared two or more species. Additionally, 59% of the published work focused on locomotion and posture, while 28% limited their ethogram to locomotion, and 13% focused on posture. We also present results on activity budget and substrate variables which further complicate comparisons across species and study sites. Our results indicate that researchers are collecting data on only a subset of primates' diverse positional repertoires which limits our understanding of variability, ecological and morphological influences on movement, and rare behaviors of primates.

### Reciprocity Across Domains Explains Women's Subsistence Cooperation in Boat-Dwelling Shodagor

KATIE STARKWEATHER<sup>1,2</sup> and ADAM REYNOLDS<sup>3</sup>

<sup>1</sup>Anthropology, University of Illinois Chicago,

<sup>2</sup>Behavior, Ecology, and Culture, Max Planck Institute for Evolutionary Anthropology,

<sup>3</sup>Anthropology, University of New Mexico

Cooperative hunting has been suggested as one of the hallmarks of the evolution of human sociality. Much work has been done to understand fitness benefits to men's cooperation in production, though women have been largely overlooked. Given the importance of women's economic production across human societies, and numerous ethnographic accounts of women working in cooperation with others, determining fitness benefits of women's cooperation in production will highlight an important element of the evolution of human sociality. Here, we use social network data collected from one community of traditionally boat-dwelling Shodagor in Bangladesh to characterize women's cooperation in productive tasks. We test hypotheses derived from two theories of the evolution of cooperation – reciprocity and kin selection – among Shodagor women to show how women's reproductive fitness benefits through cooperation in production. Our results show, as predicted, women who cooperate in trading are likely to provide childcare for one another. This suggests that reciprocal cooperation across the domains of work and childcare can provide one explanation for women's cooperation. We also expected kin selection to overlap with reciprocity in that kin who work together should be the most likely alloparents, but our results show the opposite. Kin are important caregivers for all Shodagor women, but kin who trade together are the least likely caregivers for each other's children. We suggest

possible culture-specific and evolutionary explanations for these results and discuss what they might tell us about the evolution of women's cooperation in productive work.

*Data collection was funded by the National Science Foundation (#SMA-1743019) and by the Max Planck Institute for Evolutionary Anthropology's Department of Human Behavior, Ecology, and Culture.*

### Cranial suture fusion does not predict presence of craniodental lesions in cercopithecoids

TYLER STEIN<sup>1</sup>, CLAIRE A. KIRCHHOFF<sup>1</sup>, D. REX MITCHELL<sup>2</sup>, SIOBHÁN B. COOKE<sup>3,4</sup> and CLAIRE E. TERHUNE<sup>5</sup>

<sup>1</sup>Department of Biomedical Sciences, Marquette University, <sup>2</sup>Center for Anatomical Sciences, University of North Texas Health Science Center, <sup>3</sup>Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, <sup>4</sup>New York Consortium in Evolutionary Primatology Morphometrics Group, <sup>5</sup>Department of Anthropology, University of Arkansas

The relationship between age and accumulation of skeletal lesions is well established in humans and chimpanzees but has not been tested in other primate species. We examined this using cranial suture fusion as an age estimate in four cercopithecoids: *Macaca fascicularis* (n=85), *Papio anubis* (n=76), *Nasalis larvatus* (n=53), *Colobus polykomos* (n=58) and *Cercopithecus mitis* (n=35). One of us (TS), scored 20 cranial suture locations from photographs as open, partially fused, or totally fused (0,1,2); intra-observer agreement was 90% or higher for all observations. Mean suture score was calculated by adding the scores of all observed sutures and dividing by the number of observed suture locations; specimens with <19 observations were excluded. The same specimens were also evaluated for skeletal evidence of antemortem tooth loss, pulp cavity exposure, abscesses, periodontal disease, and osteoarthritis of the temporomandibular joint using standard criteria. We then tested for sex differences in suture scores and relationships between suture scores and the presence of craniodental lesions using rank-sum tests in SPSS. There were no significant sex differences in mean suture scores. Mean suture score did not differ according to lesion presence in *Macaca*, *Cercopithecus*, *Nasalis*, or *Colobus*. Mean suture score in *Papio* may be higher in animals without craniodental lesions (p=0.01-0.03). Results may reflect sample size limitations, indicate that the accumulation of skeletal lesions is more closely tied to variables other than age, that suture closure is not an accurate age estimate in these samples, or some combination of these factors.

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### Red-tailed monkeys (*Cercopithecus ascanius*) foraging behavior does not correspond to their energetic condition

RONNIE STEINITZ<sup>1</sup>, MELISSA EMERY THOMPSON<sup>2</sup> and MICHELLE BROWN<sup>1</sup>

<sup>1</sup>Anthropology, University of California, Santa Barbara, <sup>2</sup>Anthropology, 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. Primates have highly diverse diets, and there is a substantial amount of dietary and nutritional variation within primate species, among populations, and within a population over time. Discrepancies between the amount and type of food consumed and an individual's energy balance—energetic input minus energetic expenditure—can reveal environmental constraints, decoupling the connection between foraging and fitness, a common theme in many studies of primate ecology. We examined the relationship between foraging behavior and urinary C-peptide of insulin (UCP), a byproduct of sugar breakdown, collected non-invasively from six groups of free-ranging red-tailed monkeys (*Cercopithecus ascanius*) in Kibale National Park, Uganda. UCP is known to accurately track energy balance in humans and non-human primates. We used information theory to evaluate several models of foraging on particular food items as predictors of energy balance. Interestingly, we found that while the monkeys foraged on high-energy foods, such as ripe fruit, they exhibited low energy balance ( $\beta = -0.53$ ,  $SE = 0.22$ ,  $t = -2.45$ ). These findings illustrate the need to reconsider the suite of environmental pressures that shape primate behavior and ecology, from daily feeding strategies to physiological adaptations to highly variable food availability.

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### Tracing inter-island mobility in the Palauan archipelago: Strontium isotopes from the Chelechol ra Orrak site

JESSICA H. STONE<sup>1</sup>, SCOTT M. FITZPATRICK<sup>1,2</sup>, GEORGE D. KAMENOV<sup>3</sup> and JOHN KRIGBAUM<sup>4</sup>

<sup>1</sup>Anthropology, University of Oregon, <sup>2</sup>Museum of Natural and Cultural History, University of Oregon,

<sup>3</sup>Department of Geological Sciences, University of Florida, <sup>4</sup>Department of Anthropology, University of Florida

The process of initial human settlement has been a major area of research interest in island regions where relatively remote landmasses would have presented unique adaptive challenges. As one of the most recent and widespread population dispersals, settlement of Remote Oceania is a notable case with which to explore the subject. Bioarchaeological evidence has demonstrated that some of the earliest inhabitants of Remote

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Oceania engaged in high levels of inter-island interaction following settlement; however, less is known about early communities in western Micronesia, a comparatively understudied part of the region. An ideal site for exploring these issues is Chelechol ra Orrak in Palau, western Micronesia, which contains one of the oldest and largest cemeteries in Remote Oceania.

For this research we analyzed strontium isotope ratios from tooth enamel and environmental samples collected across Palau to explore human mobility and identify the local origins of individuals from Chelechol ra Orrak. At least two different molars were analyzed for 11 individuals, resulting in a total of 23  $^{87}\text{Sr}/^{86}\text{Sr}$  values. Although background results for the archipelago will be presented based on forthcoming environmental  $^{87}\text{Sr}/^{86}\text{Sr}$  data, present  $^{87}\text{Sr}/^{86}\text{Sr}$  values average 0.70889 ( $\pm 0.000003$ ). Despite low heterogeneity, three enamel samples from two individuals fall outside two standard deviations of the mean  $^{87}\text{Sr}/^{86}\text{Sr}$  value, suggesting the possible presence of non-local people. Trace element analyses indicate low levels of diagenetic alteration in some of the samples, but is not expected to affect Sr isotopic compositions. The addition of environmental baseline data will place individuals within a localized context.

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### Climate Change and forensic anthropology – predictive modelling of projected effects on rates of decomposition

JULIUS B. STRACK and MARTIN J. SMITH

Department of Archaeology and Anthropology, Bournemouth University

Climate Change has long been considered relevant to past trajectories of human development. However, a changing climate in the immediate and foreseeable future might also play an overlooked role in forensic anthropology. Specifically, the changes in temperature and humidity expected from anthropogenic climate change may impact the rate of decomposition, and the estimation of the post-mortem interval.

This presentation argues, that such environmental changes will lead to a reduced accuracy in PMI estimation whilst also increasing the workload of forensic anthropologists, due to faster decomposition.

Using data from four different climate models, each in a "best-case"- (RCP2.6) and a "worst-case"-scenario (RCP8.5), and combining these data with a commonly used formula for PMI estimation, I was able to demonstrate a general

trend of decline for the PMI until skeletonization (PMIS). The analysis covered two seasons and six continents, plus the global average. Changes were calculated as a decadal trend.

Results showed a clear decline in the PMIS for the RCP8.5, and a less prominent decline for the RCP2.6. In the RCP8.5 for a global average the decline is 12.6% in winter and 27.5% in summer. For the RCP2.6 global average the decline is 2.7% in winter and 5.2% in summer.

The decline is more rapid in the northern hemisphere, where the formulae currently used for PMI-estimation are currently considered most accurate. These formulae may lose accuracy in the coming decades. It is important that these issues are considered in advance of these projected changes.

None.

### Impact of COVID-19 on Pregnant and Postpartum Incarcerated People

CAROLYN SUFRIN

Gynecology and Obstetrics, Johns Hopkins University

Institutions of incarceration quickly became hot spots for transmission of COVID-19. Compounding the rapid and large spread of the virus behind bars are the multiple intersecting vulnerabilities incarcerated people have to developing severe disease and their inability to protect themselves from infection and its consequences. COVID has also strained an already strained health care delivery system. This has played out distinctly for pregnant, incarcerated people. It is estimated that there are nearly 60,000 admissions of pregnant people to prisons and jails each year, and at least 1800 who give birth in custody. This presentation will discuss the ways that the pandemic has affected pregnant, incarcerated people—from accessing medical care, to being housed in restrictive housing as a form of infection mitigation, to cessation of supportive pregnancy programs and visitation with children, to ability to provide breast milk, among others. The presentation will use data from several studies that our team has conducted—including prior ethnographic data with pregnant incarcerated people pre-COVID; qualitative interviews with pregnant people in prison who were part of a study that recruited before and during COVID; and survey data from a cross-sectional study done in fall 2020 of 20 carceral facilities about how COVID has affected their pregnancy care services. The empirical data will be grounded in the broader context of mass incarceration and reproductive oppressions that shape incarcerated pregnant

people's experiences. Exploring the intersections between mass incarceration, COVID-19, and pregnancy is essential to be able to improve reproductive well-being for this often overlooked group.

*This presentation is based on prior research that was funded by the Wenner-Gren Foundation, the Society of Family Planning, and the National Institutes of Health.*

### Distinct patterns of early childhood growth represent variation in life history strategy among Daasanach pastoralists living in Northern Kenya

ZANE S. SWANSON<sup>1</sup>, HILARY BETHANCOURT<sup>2</sup>, JESSICA SAUNDERS<sup>1</sup>, ROSEMARY NZUNZA<sup>3</sup>, EMMANUEL NDIEMA<sup>4</sup>, DAVID BRAUN<sup>5,6</sup>, ASHER Y. ROSINGER<sup>2,7</sup> and HERMAN PONTZER<sup>1,8</sup>

<sup>1</sup>Evolutionary Anthropology, Duke University, <sup>2</sup>Department of Biobehavioral Health, Pennsylvania State University, <sup>3</sup>Kenya Medical Research Institute, KEMRI, <sup>4</sup>Department of Earth Sciences, National Museums of Kenya, <sup>5</sup>Center for the Advanced Study of Human Paleobiology, Department of Anthropology, George Washington University, <sup>6</sup>Department of Human Evolution, Max Planck Institute of Evolutionary Anthropology, <sup>7</sup>Department of Anthropology, Pennsylvania State University, <sup>8</sup>Global Health Institute, Duke University

Patterns of somatic growth are important indicators of health and nutritional status in children and have significant consequences for adaptive variation in adult stature. The detection of growth faltering as measured against large multi-national growth standards is common among non-industrialized populations suffering malnutrition and disease. Here we investigate distinct patterns of growth identified among a large ( $n = 4587$ ) group of young children (age = 0-5 years) living in pastoralist Daasanach communities in northern Kenya. Like previous findings from large-scale surveys of non-industrialized populations, Daasanach children demonstrate cross-sectional growth faltering by 3-6 months of age, which continues throughout the first 24 months of life. The prevalence of stunting and underweight peaks between the ages of 18-23 months (stunting: male = 50.5%, female = 28.8% | underweight: male = 70.2%, female = 58.0%). While stunting often persists throughout early childhood in such populations, stunting prevalence in Daasanach children declines after 24 months of age, with polynomial regressions finding that females and males surpass the OSD WHO standard at ~45 and ~47.5 months of age, respectively. Pseudo-velocity curves constructed from Daasanach-specific GAMLSS modeling suggest that linear growth velocity increases after ~20 months of age, with a peak of ~0.98cm/month for males and females aged ~36 months, which is greater than the median WHO velocity standards for children aged

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22-24 months. These results indicate a distinct pattern of growth in both magnitude and timing, with implications for the understanding of human life history variation and public health.

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### The Evolution of Placenta Diversification and Mammalian Reproductive Strategies

MAYA SZAFRANIEC and AMY M. BODDY  
Anthropology, University of California Santa Barbara

Placentas are the original source of nutritional and immunological support from the pregnant body to the fetus. Derived by mostly fetal tissue, the placenta is a shared organ between two genetically distinct individuals. Due to an intense evolutionary arms race during pregnancy, there has been rapid diversification of placental phenotypes, in both form and function, across mammals. The underlying selection pressures that predict placental diversity are not well understood. Previous work on placental evolution focuses on the relationship between degree of placental invasiveness, the level of blood exchange between pregnant body and fetus, and reproductive strategies. Few consider the variation in placenta interdigitation, which represents the surface area exposure between the pregnant body and fetus. Here we test seven life history variables, based on the relationship to mammalian reproductive strategies, to examine the effects of placenta diversification in 648 mammals. We predict a tradeoff between mammalian reproductive strategies and placental intrusiveness. We performed descriptive and multivariate statistics and found placenta interdigitation has a stronger co-evolutionary relationship to life history than invasiveness. All variables tested support the predictions correlating with increased pregnant body investment except for age at first eye opening. We suggest both placenta invasiveness and interdigitation must be considered to understand that evolutionary pressures of placenta diversification. Additionally, we anticipate that this study will provide more context to understand placental evolution and its connection with health, with possible implications with other related phenotypes, including vulnerability to diseases such as cancer.

No funding for this work

### Ecology and opsin variation drives the evolution of hair phenotypes across Indriidae lemurs – implications for human evolution

ELIZABETH TAPANES<sup>1,2</sup>, RACHEL L. JACOBS<sup>1,2</sup>, IAN HARRYMAN<sup>3</sup>, EDWARD E. LOUIS JR.<sup>4</sup>, MITCHELL

T. IRWIN<sup>5</sup>, JASON M. KAMILAR<sup>6</sup> and BRENDA J. BRADLEY<sup>1,2</sup>

<sup>1</sup>Anthropology, The George Washington University, <sup>2</sup>Center for the Advanced Study of Human Paleobiology, The George Washington University, <sup>3</sup>Earth System Science, Stanford University, <sup>4</sup>Conservation Genetics Department, Omaha's Henry Doorly Zoo and Aquarium, <sup>5</sup>Anthropology, Northern Illinois University, <sup>6</sup>Anthropology, University of Massachusetts Amherst

The evolution of pelage (i.e., hair/fur) was arguably one of the most important adaptations underlying mammals' success and diversification. Hair provides organisms with thermoregulation, protection, and a means of camouflage and signaling, and thus is the likely product of both natural and sexual selection. Primates are excellent for understanding these processes since the clade arguably exhibits the greatest hair diversity of any mammal. However, the studies to date that have examined primate pelage evolution have focused largely on the facial region and/or pigmentation. Here, we examine whole-body hair pigmentation and density across Indriidae and test for associations to climate and opsin variation. We collected (1) pigmentation measurements from museum skins and live animals using digital images, (2) pelage density variables using a handheld microscope, (3) climate data from WorldClim, and (4) opsin data. We used principal components analysis (PCA), and the resulting PC values were run against climate variables in phylogenetic generalized linear mixed models (PGLMM) or in simple linear regressions. Across Indriidae, we find significant associations between pigmentation and climate and significant associations between hair density and climate. We also find a positive significant relationship between 'redness' and opsin variation in diurnal genera. Our results support Gloger's rule and provide rare empirical evidence supporting the body cooling hypothesis. Moreover, our results suggest that red hair color and polymorphic trichromacy co-evolved for signaling in some primates. These findings have implications for human hair evolution and illustrate the value of sifakas as a contemporary model to study hair evolution.

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### Population-level variation in later Pleistocene *Cercopithecus* fossil assemblages

CATHERINE E. TAYLOR<sup>1,2</sup>, MARIANNE F. BRASIL<sup>1,3</sup>, TESLA A. MONSON<sup>4</sup>, RYAN M. YOHLER<sup>1,2</sup> and LESLEA J. HLUSKO<sup>1,2</sup>

<sup>1</sup>Human Evolution Research Center, University of California, Berkeley, <sup>2</sup>Department of Integrative Biology, University of California, Berkeley, <sup>3</sup>Berkeley Geochronology Center, University of California, Berkeley, <sup>4</sup>Department of Anthropology, Western Washington University

The guenon (Tribe: Cercopithecini) fossil record is notoriously sparse. Recently, the Middle Awash research project recovered hundreds of cercopithecine fossils from later Pleistocene sediments of the Afar Depression in Ethiopia. Here, we describe  $n=244$  individuals from two different, geographically close, later Pleistocene beds that we assign to *Cercopithecus* sp. (*sensu lato*). These two assemblages are remarkable in their size and preservation, with multiple individuals preserving both craniodental and postcranial material. The fossils from these two beds provided us the uncommon opportunity to assess population-level variation in fossil assemblages by comparing them to extant cercopithecine species. We find that the amount of variation is comparable to that of an extant species of cercopithecine monkey, suggesting the presence of a single species. Both assemblages are within the range of extant cercopithecine species in dental and postcranial metrics. There are a few notable morphological differences in the *Cercopithecus* fossils between the two beds, mostly in postcranial morphology. Since guenons are known to readily hybridize in the wild and have highly generalized postcranial skeletons, determination of locomotor habitus can be difficult, especially in fossils. We explore the implications of such postcranial morphologies, and the limitations that hybridization, postcranial plasticity, and a generalized skeleton impose.

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### The Appropriation of Gender: Relational Ontologies and Diaphyseal Morphology in Late Holocene Hunter-Gatherers from the Far North Coast of Alaska

DANIEL H. TEMPLE and EMILY R. ROSA  
Sociology and Anthropology, George Mason University

Hunter-gatherers engage in reciprocal relationships with nature. Hunters track, kill, process, and spiritually interact with prey to maintain these relational ontologies. Traditional studies of hunter-gatherers emphasize male economic contributions, while erasing female agency over the hunting domain. This study uses long bone diaphyseal properties to explore female contributions to hunting in Late Holocene hunter-gatherers from Far North Coastal (FNC) Alaska. Cross-sectional properties of femora and humeri were collected using CT-scans and compared to Inland/Riverine (I/R), Coastal Bay (CB), and Tigara (TG) cultures of Alaska. FNC femoral properties were consistently greater for males and females across samples. FNC male humeral morphology was comparable between samples. FNC female humeri were similar to FNC males, but significantly larger than I/R females in moments and second moments of area. FNC females had

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greater humeral anterior-posterior/mediolateral bending rigidity, while FNC male and TG female humeral shape ratios approximated circularity. Elevated femoral cross-sectional properties are consistent with intensive hunting across sea-ice and rugged arctic terrain for FNC males and females. However, male humeral shape indicates mechanical adaptation to shear stress, while female humeral morphology is consistent with flexion of *m. biceps* and *triceps*. This may reflect variation in activity patterns such as rowing and throwing among males versus processing and transportation of prey among females. Processing and transportation of prey delivers calorically dense food to communities and maintains relational ontologies between human and animal actors. These findings suggest that female agency over hunting directly contributes to caloric intake and ordains relational ontologies between hunters and nature.

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### Age-related changes in adult chimpanzee social network integration

NICOLE THOMPSON GONZÁLEZ<sup>1</sup>, ZARIN MACHANDA<sup>2</sup>, EMILY OTALI<sup>3</sup>, MARTIN N. MULLER<sup>1,2</sup>, RICHARD WRANGHAM<sup>4</sup> and MELISSA EMERY THOMPSON<sup>1</sup>

<sup>1</sup>Department of Anthropology, UNM, <sup>2</sup>Department of Anthropology, Tufts, <sup>3</sup>Kibale Chimpanzee Project, <sup>4</sup>Department of Human Evolutionary Biology, Harvard

Social isolation is a key risk factor for the onset and progression of age-related cognitive decline in humans, yet older people commonly have narrowing social networks. Human social networks are difficult to describe, and studies have used inconsistent metrics of social aging, hindering attempts to understand these phenomena. However, at least some homologies in social aging may be detectable in our closest relatives, chimpanzees. Chimpanzees have closed social networks but flexible patterns of association, allowing for wide individual variation in sociality. We applied social network analysis to examine how social integration, via grooming and spatial association, changed with age in a longitudinal dataset comprising 38 wild adult chimpanzees in the Kanyawara community in the Kibale National Park, Uganda. Metrics of integration included social attractiveness and effort (network degree and strength), social role (betweenness and local transitivity), and embeddedness (eigenvector centrality). Both males and females decreased their social effort with age, however, males maintained their attractiveness and embeddedness. Older males focused on tighter-knit cliques of grooming partners, while females decreased cliquishness with age. The effects of age were largely independent of rank and reproductive status. Despite age-related changes, both males and females maintained highly repeatable inter-individual differences in

almost all aspects of integration, particularly among mixed-sex partners. As in humans, chimpanzees experience age-related declines in social integration, though not all facets of integration age in the same manner. Individual and sex differences appear to be important mediators of successful social aging.

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### Virtual anthropology available for everyone: the importance of open resources during and beyond COVID-19 pandemic

NICOLE TORRES-TAMAYO and CARLA SAN ROMÁN  
Departamento de Paleobiología, Museo Nacional de Ciencias Naturales

Virtual techniques have become increasingly important in the field of biological anthropology in the last years and are seen as an excellent alternative to classic methods mainly because they reduce the risk of damaging osteological collections and original fossils. The present work emerges in the aftermath of the COVID-19 pandemic that spread across the world in 2020. The subsequent global crisis forced researchers to stay home: museums were closed, visits for data collection were cancelled, and access to institutions that hold software licenses was restricted. This unprecedented situation had a high impact on the scientific performance of many scientists whose research directly depends on access to these infrastructures and materials. This brought the importance of the use of open resources to the fore, as mainly those researchers who were familiar with license-free software and open repositories were capable of keeping up with their investigations during lockdown. The aim of this work is to try to give some answers to the following question: is it possible to conduct entirely virtual anthropological research only using open resources? For this purpose, we briefly summarize the history of virtual anthropology and the workflow (i.e. data collection, data analysis, data sharing), detailing examples of previous virtual anthropology works based on open source software and offering open and free resources for each work step. Lastly, we emphasize the revolution that the rise of the free software R entails for the present and the future in the field of virtual anthropology.

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### STEM outreach initiatives: Integrating biological anthropology within the STEM community

SHARON A. TOTH<sup>1</sup> and ALICIA R. GROSSO<sup>2</sup>

<sup>1</sup>Anthropology, University of Pittsburgh, <sup>2</sup>Physical Therapy, Clarkson University

Science, technology, engineering, and mathematics (STEM) learning is an interdisciplinary approach used to develop critical thinking, hands-on problem solving, and scientific literacy inside and outside the classroom. This year marks 20 years since the National Science Foundation reformatted STEM and 10 years since a sitting president first remarked its importance during the State of the Union address. The STEM curriculum with its primary emphasis on the natural sciences, has excluded the social sciences, including biological anthropology. We argue that biological anthropology has reformed itself with updated scientific methodology and the proposed “biological anthropology” official name change to garner more acceptance within the STEM community. Here, we present how biological anthropology graduate students at the University of Pittsburgh have used anthropological methods to engage in STEM outreach initiatives. Traveling to surrounding schools (K-12) and universities, activities have included cadaver labs, International Archaeology Day, forensic anthropology, continued learning workshops, crime scene investigation day, and diversity teaching lessons. Attendees ranged from children to seniors from an array of educational and socioeconomic backgrounds. We have also utilized anthropological methods to demonstrate STEM principles with at-home kitchen experiments and transportable experiments for military youths at national Yellow Ribbon events. We aim to further normalize the acceptance of biological anthropology into the STEM community, promote women in STEM, create awareness of anthropology to young students prior to attending university; and present the field to non-academic audiences. We also hope to encourage graduate student outreach initiatives for both professional growth and community engagement.

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### Contributions of Evolutionary Anthropology to Understanding Climate-Induced Human Migration

MARY C. TOWNER, ALANNAH TEMPLON and DANIELLE R. KIRSCH

Integrative Biology, Oklahoma State University

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. Climate change has amplified this connection between environment and migration, with the potential to profoundly impact millions of lives. Although climate-induced migration has been at the forefront of other disciplines in the social sciences, evolutionary anthropologists (EAs) have given it little attention. In this paper we draw upon existing literature and contribute our EA perspective to present a framework for

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analyzing climate-induced migration. We focus on three overlapping dimensions—time, space, and severity—relevant to understanding the impact of climate change on human migration. We apply this framework to case studies from North America of people impacted by climate change and extreme weather events, including hurricanes (e.g., Hurricane Katrina), droughts (e.g., Oklahoma dustbowl), rising sea-levels (e.g., Coastal Alaska), and wildfires (e.g., Alberta, Canada). We also consider how access to both economic and social resources influence migration behavior. We highlight insights that an evolutionary anthropological perspective can contribute to existing literature, 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.

### Effect of small sample size on Landmark-Based MNI estimation: A case study from the Lake St. Agnes Mound (16AV26) site

KENNETH G. TREMBLAY and REBECCA SAUNDERS  
Geography and Anthropology, Louisiana State University

Estimating the Minimum Number of Individuals (MNI) in an archaeological sample can be challenging, especially when the remains are fragmentary and commingled. In these cases, the ability to pair-match elements may not be possible. Further, identifying repeating elements is complicated by inventorying standards dividing most bones into three categories of completeness: <25%, 25-75%, and >75%. To address these issues, Herrmann et al. (2014) proposed a method for calculating MNI that involves the use of 344 distinct osteological landmarks on 17 elements to produce more accurate results for these types of samples.

The remains excavated from the Lake St. Agnes Mound (16AV26) site, in central Louisiana, provide an interesting sample to explore the effectiveness of a Landmark-Based MNI estimation. Two burial pits were uncovered during the 1972 excavation by Toth (1979): an early (Marksville/Troyville) pit with secondary, probable bundle burials, and a late (Plaquemine) pit, which also held multiple secondary burials, although these were more complete than the earlier set. On the basis of field observations, Toth estimated an MNI of five for the early pit, and ten for the later one. Traditional methods for MNI calculation have yielded slightly different results for the later pit (MNI=8) which is corroborated by preliminary results for the Landmark Analyses.

This research has the ability to expand upon methods for the estimation of MNI in fragmentary and commingled skeletal samples by exploring their practicality in a small archaeologically derived sample, which would be beneficial due to the regularity of such issues.

### Laryngeal vocals in old world locals: air sacs usage in bonobos

CHELSEA S. TRENBEATH<sup>1</sup> and JARED P. TAGLIALATELA<sup>1,2</sup>

<sup>1</sup>Department of Ecology, Evolution, and Organismal Biology, Kennesaw State University, <sup>2</sup>Department of Research, Ape Cognition and Conservation Initiative

Except for humans, extant great apes have evolutionarily conserved lateral ventricular air sacs extending from laryngeal sacculi. Humans are the only species of Hominidae that lack this anatomical feature attached to the primary vocal apparatus. As we are the only species that produces spoken language, this association has led to hypothesis that the loss of lateral ventricular air sacs was necessary for the evolution of spoken language. However, why these sacs are conserved in all other hominids remains unclear. Computer modeling has indicated that air sacs may increase resonance properties, but there are no data from great apes indicating if vocalizations include the use of air sacs during their production. For this study, we hypothesized that we could use high-frame-rate digital audio/video recordings to determine when bonobos (*Pan paniscus*) inflate their laryngeal air sacs. We identified a region of interest in the air sac area and quantified it using frame-by-frame image analysis. We then compared the difference in areas between resting, swallowing, and vocalizing apes. Preliminary results suggest air sac inflation may be associated with vocal production but not with other states. These methods could be utilized in a variety of settings, enabling data collection to test hypotheses regarding the putative function of laryngeal air sacs in extant great apes. Enhancing our understanding of the conservation of laryngeal air sacs in non-human great apes will strengthen hypotheses related to the loss of these sacs in humans and its relevance for the evolutionary origin of language.

### Estimation of weaning age in a medieval Székely population from the Carpathian Basin

CHRISTINA TRENT<sup>1</sup>, ZSOLT NYARADI<sup>2</sup>, ANDRE GONCIAR<sup>3</sup> and JONATHAN D. BETHARD<sup>1</sup>

<sup>1</sup>Anthropology, University of South Florida, <sup>2</sup>Anthropology, Haáz Rezső Múzeum, <sup>3</sup>Anthropology, ArchaeoTek

Biological anthropologists routinely utilize stable isotope analysis to investigate questions related to breastfeeding and weaning practices in past

communities; however, few studies have examined weaning practices of medieval Transylvanian Székely people who have lived in the Carpathian Basin for centuries. Previous research suggests that women in rural areas wean their children later than women in urban areas; therefore, given the more rural nature of Transylvanian Székely communities, this study hypothesizes that isotopic data used for reconstructing weaning practices will reflect the pattern observed for other rural communities.

This presentation presents novel isotopic data gathered from dental collagen samples of Székely individuals from the archaeological site of Papdomb, located in the rural village of Patakfalva in present-day Romania. The site contains the archaeological footprint of a church and churchyard that served as the cemetery for the villagers of Patakfalva between the 14<sup>th</sup> and 19<sup>th</sup> centuries. A relatively new microsampling protocol was applied to the dentition of non-adults (n=12) in order to establish when the women of Papdomb weaned their children. Given the overall female adult mean  $\delta^{15}N = 11.3$ , it was possible to establish that the approximate age of weaning for the Székely population at Papdomb was between 1.5 and 3.5 years of age. These results are consistent with other studies which suggest that women in rural locations weaned their children later than their more urban counterparts. Further research should be conducted to continue examine weaning practices in other rural Székely communities.

### Primate response to a malaria-like parasite in a natural transmission system

AMBER E. TRUJILLO<sup>1,2</sup> and CHRISTINA M. BERGEY<sup>3</sup>

<sup>1</sup>Department of Anthropology, New York University, <sup>2</sup>New York Consortium in Evolutionary Primatology, NYCEP, <sup>3</sup>Department of Genetics, Rutgers University

Comparative analysis of primate response to malaria and malaria-like parasites may advance our evolutionary understanding of malaria response in humans. However, most research has focused on a single or few loci, typically of the host, and involved experimentally-infected captive primates. We investigated wild red colobus monkey (*Ptilocolobus tephrosceles*) response to the malaria-like parasite *Hepatozoon* using previously published datasets and dual-RNAseq (i.e., parallel investigation of host and parasite transcriptome.) By inferring parasitemia using the ratio of sequencing reads matching the host and parasite reference genomes, we identified colobus genes with expression strongly positively correlated with parasitemia. Such genes included *LSM14A* ( $p = 2.99 \times 10^{-5}$ , adjusted  $p = 0.0449$ ) and *APOBEC2* ( $p = 5.53 \times 10^{-5}$ , adjusted  $p = 0.0454$ ), both implicated in malaria response in humans. The expression of *ACKR1* (alias *DARC*) gene, which has been previously linked to *Hepatozoon*

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parasitemia in primates, was also found to be positively correlated with parasitemia ( $p = 0.0035$ , adjusted  $p = 0.1593$ ). *Hepatocystis*-response genes were enriched for phenotypes, inferred via orthology with human genes, including stomatocytosis, or the production of erythrocytes with an abnormally shaped zone of central pallor (adjusted  $p = 0.0035$ ) and reticulocytosis, or the production of immature erythrocytes which is disrupted during malaria anaemia in humans (adjusted  $p = 0.0256$ ). Such investigations of immune response to malaria-like parasites across non-human primates may identify potential points of intervention that could help alleviate the huge burden that malaria continues to exert on human populations.

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### Cranial injuries as an indicator of socio-cultural changes in the Iranian Central Plateau during the Iron Age

JOANNA TRÁBICKA<sup>1</sup>, ARKADIUSZ SOŁTYSIAK<sup>2</sup> and MOSTAFA DEHPAHLEVAN<sup>3</sup>

<sup>1</sup>The Antiquity of Southeastern Europe Research Center, University of Warsaw, <sup>2</sup>Department of Bioarchaeology, Faculty of Archaeology, University of Warsaw, <sup>3</sup>Institute of Archaeology, University of Tehran

The cemetery of Qareh Tepe, located in the north-western Iranian Central Plateau, is dated back to the Early Iron Age (1200-600 BC), with most burials directly preceding the establishment of the Median state. The excavations conducted in 2018-2019 in the eastern part of the cemetery revealed skeletons of at least 77 individuals, ten of whom showed signs of traumatic lesions.

To verify a possible violent origin of observed injuries, the frequency of trauma to the skull of adolescent and adult individuals was calculated. For 6 out of 36 (16.7%) individuals at least one traumatic lesion was present, including both sharp and blunt force trauma, which is much more than observed at other contemporary Iranian sites (Estark and Gohar Tepe). Most injuries were observed in male individuals, with only one probable perimortem fracture of a female skull. The frequencies of dental caries and skeletal stress markers were relatively low. Carious lesions were noted in 16 per 62 (25.8%) individuals, with only 34 per 723 (4.7%) teeth affected. *Cribra orbitalis* were present in 6 per 42 (14.3%) individuals, while porotic hyperostosis in 5 per 55 (9.1%) individuals.

Taking into account favourable location of the Qareh Tepe, surrounded by area suitable for farming and animal husbandry, as well as rich grave goods, it may be assumed that the skeletal assemblage represented a prosperous population. However, the frequency of cranial injuries,

that has not yet been observed in the region, suggests a significant degree of inter-personal violence during the formation of early Median state.

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### New Harms from Ancient Genomes: Indigenous DNA Extraction in the Next Era of Paleogenomics

KRYSTAL S. TSOSIE

Bioethics and Community Engagement, Native BioData Consortium, Health Psychology, Vanderbilt University

For decades, scientists have collected genomic information from Indigenous peoples and their ancestors with the goal of elucidating human migration events, understanding origins, and identifying ancestral variants contributing to disease. However, such studies may not have offered much benefit to the Indigenous groups who contributed DNA, and many have instead perpetuated stereotypes and other harms. With recent advances in genomic technology facilitating the study of both ancient and present-day DNA, researchers have new opportunities (i.e., through metagenomic soil analysis and other environmentally-derived DNA; through procurement of contemporary genomes from consumer databases and open access datasets) to interrogate these questions. Of concern are the implications to Indigenous descendants, particularly those from groups without recognized sovereignty. While there are increased efforts to ethically engage Indigenous communities globally, more work is still needed as the discipline struggles to absolve itself of the racialized science and extractive biocolonialism that defined its past.

### Stable isotope study of dietary changes in the aftermath of the Black Death in Toulouse, France

JANELLE A. TYLER<sup>1</sup>, ELEANOR CORDINER<sup>1</sup>, SACHA KACKI<sup>1,2</sup>, REBECCA GOWLAND<sup>1</sup>, DARREN R. GRÖCKE<sup>3</sup> and JANET MONTGOMERY<sup>1</sup>

<sup>1</sup>Department of Archaeology, Durham University, <sup>2</sup>CNRS UMR 5199 PACEA, Université de Bordeaux, <sup>3</sup>Department of Earth Sciences, Durham University

The Black Death (A.D.1347-1352) in Europe affected a population already weakened by decades of war and famine and resulted in unprecedented levels of mortality. Some scholars have posited that the resulting population decrease led to dramatic social change and possibly improved diets for the laboring classes.

Carbon ( $\delta^{13}\text{C}$ ) and nitrogen ( $\delta^{15}\text{N}$ ) stable isotopes were utilized to investigate potential temporal dietary changes in medieval Toulouse, France. 172 bone samples were analyzed from a mass grave related to the Black Death (BD) (A.D. 1348,  $n=47$ ), and a pre-BD (A.D. 1330-1334,  $n=69$ ) and

post-BD (A.D.1380-1545,  $n=56$ ) parochial cemetery. No significant differences were observed between the pre-BD and BD groups ( $\delta^{15}\text{N}^{13}\text{C}$   $x = -19.1 \pm 0.3\text{‰}$ ,  $\delta^{15}\text{N}$   $x = 11.3 \pm 0.9\text{‰}$ ;  $\delta^{13}\text{C}$   $x = -19.2 \pm 0.4\text{‰}$ ,  $\delta^{15}\text{N}$   $x = 11.2 \pm 0.7\text{‰}$ ). There was, however, a significant dietary shift in  $\delta^{13}\text{C}$  ( $x = -18.8 \pm 0.3\text{‰}$ ) and  $\delta^{15}\text{N}$  ( $x = 11.7 \pm 0.7\text{‰}$ ) values between the BD and post-BD populations, indicating a more diverse diet after the epidemic. A notable increase in  $\delta^{15}\text{N}$  values between BD and post-BD females ( $x = 11.3 \pm 0.5\text{‰}$ ;  $x = 11.9 \pm 0.8\text{‰}$ ) suggests the Black Death had the biggest effect on the female population of Toulouse for dietary changes.

These results suggest that access to more nutritionally diverse foods, (i.e., animal/marine protein) and possibly  $\text{C}_4$  plants increased after the Black Death. The results also raise interesting questions around gendered access to diet, suggesting reduced social inequalities between males and females in the aftermath of the Black Death.

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### A New Study Assessing the Sexing Technique on the Os Coxa: Observing the Auricular Surface Using Metric and Morphological Variables

ALEXA UGARTE

Anthropology, New York University

Forensic anthropologists and bioarchaeologists establish biological profiles with the remains that they find. The biological profile is used to identify the deceased individual(s). The methodology used to determine sex, age, stature, ancestry, trauma, and pathology are very important for the accuracy of the biological profile. The Phenice method has a 90% accuracy for determining sex and remained high in during these tests; however, the auricular surface can be affected by pathology, ancestry or parturition (Luna et al. 2017; Phenice 1967). The Phenice method focuses on the ischiopubic ramus, the ventral arc, and the subpubic concavity of the pubis bone (Phenice 1967). The auricular surface method has morphological and metric variables such as the overall morphology, apex morphology, elevation, and the length of the auricular surface (Luna et al. 2017; Weaver 1980). Both methods were used in a blind test, of two runs, using 100 adult right os coxae and 12 subadult right os coxae. The length of the auricular surface is a metric variable that shows that adult males in this sample size tended to be longer than 50mm while females tended to be less than 50mm. For subadults, the older the specimen is, the higher the accuracy. The adult success rates in both males and females were not always accurate, however,

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they were more precise in males. Pooled success was not more accurate than the individual runs. Age could have contributed to discrepancies in the methods along with ancestry and illness.

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### Duration of gestational exposure to genocide against the Tutsi in relation to health outcomes in young adulthood

GLORIEUSE UWIZEYE<sup>1</sup>, JULIENNE N. RUTHERFORD<sup>2</sup> and ZANETA M. THAYER<sup>1</sup>

<sup>1</sup>Anthropology, Dartmouth College, <sup>2</sup>Human Development Nursing Science, College of Nursing, University of Illinois at Chicago

Poor health outcomes among Rwandans conceived during the 100-day long 1994 genocide against the Tutsi have been reported. However, the effect of the length of intrauterine exposure to genocide on health outcome is underexplored.

A comparative cross-sectional design was used to examine whether there are differences in health outcomes between those conceived during the first half of the genocide and those conceived in the second half. Measures of multiple adult health characteristics were collected for young adult Rwandans (N = 61) conceived during the genocide period, 30 conceived by genocidal rape and 31 born of genocide survivors not raped.

Being conceived later, and thus experiencing a shorter duration of genocide prenatally, was associated with better outcomes among the exposed to genocide only group. These individuals had lower depression and anxiety (both  $p < 0.047$ ) as well as higher (healthier in this population) subscapular and triceps skinfold thicknesses and BMI (all  $p < 0.019$ ). Except for depression, these differences remained after controlling for participant sex. There were no within group differences among the genocidal rape group.

Those exposed to genocide only who experienced a shorter duration of their gestation during that stressful period had better health outcomes as adults. The fact that there were no differences in the genocidal rape group could be because the stigma, shame, and stress related to rape experienced by pregnant women did not cease with the end of the genocide; thus, the fetus was exposed to stress beyond the genocide duration. Pathways linking exposure and health outcomes should be explored.

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### Testing the pelvic floor hypothesis: patterns of relationship between the canal and gut size

JEANELLE UY<sup>1</sup> and NATALIE M. LAUDICINA<sup>2</sup>

<sup>1</sup>Anthropology, California State University, Long Beach, <sup>2</sup>Biomedical Sciences, Grand Valley State University

The morphology of the human pelvic canal is a compromise between having enough space for parturition (females) and the abdominopelvic

viscera, while also having substantial bony support for the pelvic floor, which supports the abdominopelvic weight. Previous research suggests an expectation that this supportive role results in a narrower pelvic midplane. In this research, we examine how gut size correlates with the size and shape of the true pelvis, which may have implications on how gut size can influence pelvic floor integrity.

Pelves and *in vivo* gut volumes were measured from CT scans of 92 adults (48 female, 44 male). The true pelvis was measured at three obstetrical planes (inlet, midplane, outlet) using 13 3D landmarks. To obtain an individual's gut volume, the sum of the intestine areas (from each image slice) was multiplied by the thickness of the slice. Gut volume was compared to the pelvic planes using bivariate regression to evaluate the relationship between gut size and true pelvis.

Contrary to previous research, we find that, in males, larger gut sizes are associated with wider canal dimensions (inlet, midplane, outlet). In females, we find that larger gut sizes are associated with ischial spines that project more medially and significantly wider pubic symphyses. We hypothesize that the correlation of gut size with canal width in males and pubic symphysis width in females are adaptations to accommodate a larger gut, while more medially projecting ischial spines reduce the risk of pelvic floor disorders in females with heavier abdominal weights.

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### Modeling an Industrialized diet in lab mice shows that vitamin D and diet texture alter mandibular form

ELSA M. VAN ANKUM<sup>1</sup>, KADIN B. MAJCHER<sup>2</sup>, ALLAN T. DOLOVICH<sup>2</sup>, JAMES D. JOHNSTON<sup>2</sup> and JULIA C. BOUGHNER<sup>1</sup>

<sup>1</sup>Anatomy, Physiology, & Pharmacology, University of Saskatchewan, <sup>2</sup>Mechanical Engineering, University of Saskatchewan

Human jaws are shaped by bone remodeling influenced partly by diet: food texture causes stress during chewing, and vitamin D regulates bone cells. After the Industrial Revolution in Britain ca. 1850, a more processed and vitamin D deficient diet became commonplace. How this dietary change affected jaw growth is unclear. Via a mouse model and specialized diets, we tested the effects of dietary texture and vitamin D on mandibular form. We hypothesized that vitamin D is: imperative for normal mandibular growth, and a greater influence on mandibular form than diet texture. C57BL/6J mice weaned at 7 weeks were raised on a soft or hard diet with vitamin D (n=40; n=48), or a soft diet without vitamin D (n=39). Post-sacrifice, adult mice were scanned with a Skyscan1172 micro-CT system and landmarked in Amira. Landmark datasets underwent Principal Component Analysis (PCA) in Morphologika. Mice fed soft diets had shorter mandibles with

diminutive alveolar bone, gentler masseteric crests, a wider angle between dentary bones, and larger bicondylar breadth. Diet groups occupied distinct but overlapping regions of shape space, with texture accounting for 30.8% (PC1) of total shape variance. Presence/absence of vitamin D accounted for 13.8% (PC2) of total shape variance between soft diet groups. Mice fed vitamin D had mandibles with more flaring angular processes, more robust masseteric crests, and elevated alveolar bone. In sum, vitamin D influenced mandible shape less than diet. Mandibular regions' variable response to diet is germane to post-Industrial human jaw changes.

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### Comparison of shoulder functional morphology between *Gorilla* and *Homo*

JULIA VAN BEESEL<sup>1</sup>, JOHN R. HUTCHINSON<sup>2</sup>, JEAN-JACQUES HUBLIN<sup>1,3</sup> and STEPHANIE M. MELILLO<sup>1</sup>

<sup>1</sup>Human Evolution, Max Planck Institute for evolutionary Anthropology, <sup>2</sup>Structure & Motion Laboratory, The Royal Veterinary College, <sup>3</sup>Histoire et archéologie, Collège de France

Arboreal adaptations are traditionally identified by correlating variation in skeletal anatomy with locomotor and positional behavior in living primates. This approach has demonstrated that non-human apes and New World monkeys that share an emphasis on vertical climbing and suspension also share morphological features in the shoulder. Earlier proposed ideas link the cranially oriented scapular spine and glenoid and projecting acromion process to greater arm abduction potential and increased arm-raising performance in non-human apes compared to humans. However, these hypotheses remain largely untested.

Musculoskeletal computer models allow us to quantitatively test how morphological features relate to biomechanical performance. In this study, we developed the first musculoskeletal model of a gorilla shoulder and compared glenohumeral abductor capacity with an existing human shoulder model. We combined standard dissection techniques with virtual anthropology methods to construct the specimen-specific gorilla model.

We infer from our results that differences in musculoskeletal configuration between *Gorilla* and *Homo* have a number of functional consequences. Our model supports a functional enhancement for the *Gorilla* supraspinatus muscle. However, this enhancement is driven by muscle properties and proximal humerus morphology, as opposed to scapular spine orientation. Furthermore, the more cranial orientation of scapular spine and glenoid in *Gorilla* appear to

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alter deltoid muscle paths and thereby enhance its adduction, rather than abduction potential. Contrary to previous assumptions, we found that overall glenohumeral abduction capability is similar between *Gorilla* and *Homo*. These results advance our understanding of adaptation in living apes and can improve functional interpretations of the hominin fossil record.

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### Sex- and gender-based tuberculosis mortality in early 20<sup>th</sup> century Newfoundland: Future considerations for demographic anthropology and epidemiology

TAYLOR P. VAN DOREN and LISA SATTENSPIEL  
Anthropology, University of Missouri

The selective mortality hypothesis suggests that acute exposure or pre-existing infection with tuberculosis (TB) increased the probability of pneumonia and influenza (P&I) mortality during the 1918 influenza pandemic, leading to a hastened decline of TB mortality in post-pandemic years. This study addresses sex-based differences in TB mortality in Newfoundland to assess if there is evidence to support this hypothesis, and to investigate gendered determinants of these differences. Death records and census data from the Provincial Archives of Newfoundland & Labrador were used to calculate age-standardized island-wide TB mortality for the years 1900-1939. The Joinpoint Regression Program (version 4.8.0.1) was used to estimate significant changes in mortality rates throughout the study period, and maximum likelihood estimates between yearly sex-based mortality rates were calculated to identify significant differences. Regression analyses did not predict significant decline for males or females that can confidently be associated with 1918 influenza pandemic mortality, and female mortality was consistently higher than that of males. This result challenges the generalization that male TB mortality was higher in the early 20<sup>th</sup> century. TB was known to spread primarily in crowded dwellings, in which women fulfilled primary domestic roles and may have been in close contact with infected individuals. Further, female nurses were burdened with the responsibilities of providing long-term care, education, and familial support for tuberculous patients. These results suggest that observed sex-based differences are more driven more by gendered determinants, and therefore results highlight the importance of more thorough anthropological, demographic, and epidemiologic investigations of gender-based respiratory mortality.

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### Investigation of covariation in the morphology of different carpals, and the link with locomotion, in different primate taxa

MARIE J.M. VANHOOF<sup>1</sup>, TIMO VAN LEEUWEN<sup>1</sup>, LORENZO GALLETTA<sup>2</sup> and EVIE E. VEREECKE<sup>1</sup>

<sup>1</sup>Development and Regeneration, KU Leuven - campus Kulak - Belgium, <sup>2</sup>School of Life and Environmental Sciences, Deakin University - Waurn Ponds, Victoria - Australia

Carpal morphology varies greatly across primate taxa, and although adaptive signals in hand bone morphology have been studied extensively, it is not clear how the morphology of the carpal bones covaries between carpals or with locomotion. In our study, we focus on the carpals of the ulnar column and investigate (1) if there is covariation between hamate and triquetral morphology, and (2) the covariation with locomotion. We performed a 3D Geometric Morphometrics (GM) analysis using 3D bone models of 310 specimens (12 different genera). The carpal shape is defined using fixed landmarks, and a principal component analysis is carried out on the aligned shape coordinates to quantify shape variation. Afterwards, analysis of variance was used to test for significant differences across groups and a TukeyHSD to perform pairwise post-hoc comparisons. A 2 Block Partial Least Squares (2B-PLS) analysis was used to investigate covariation between hamate and triquetral morphology. The 2B-PLS analysis indicates a significant covariation ( $p=0.001$ ) between hamate and triquetral morphology, in which (semi-)terrestrial taxa, like macaques and baboon, have a hamate with a wide body and a small hamulus in combination with a robust triquetrum, while arboreal taxa, like gibbons and orangutans, have a more narrow hamate with a large hamulus and a cylindrically-shaped triquetrum. These results suggest a clear link between carpal morphology and locomotion, as primates with a similar locomotor behaviour show a similar carpal bone morphology, yet we will investigate this further by using locomotion data in the 2B-PLS analysis in future research.

### Comparisons of Paleoepidemiological Profiles for Four Prehistoric Northern California Populations

JANE VANNAHEUANG<sup>1</sup>, GENEVIEVE HAN<sup>2</sup>, KAREN LI<sup>2</sup>, JESSICA M. CRONIN<sup>2</sup>, ANNABEL T. DAVIS<sup>3</sup>, REBECCA S. JABBOUR<sup>4</sup> and GARY D. RICHARDS<sup>5</sup>

<sup>1</sup>Department of Public Health, University of California, Berkeley, <sup>2</sup>Department of Integrative Biology, University of California, Berkeley, <sup>3</sup>Cognitive Neuroscience Program, University of California, Berkeley, <sup>4</sup>Department of Biology, Saint Mary's College of California, <sup>5</sup>Department of Biomedical Sciences, A.A. Dugoni School of Dentistry, University of the Pacific

Understanding the types and frequency of occurrence of various diseases and developmental anomalies in prehistoric California requires population-level assessments. To date, such assessments have not been available. Preliminary data has, however, been collected during curation of the skeletal collections held by the Phoebe Hearst Museum of Anthropology, UCB. Data is available for 2,570 of 7,250 individuals. We employ these data to develop and compare paleoepidemiological profiles for four prehistoric Northern California populations.

We compiled data from five localities with large populations ( $N=2,299$ ). Sites represent the Early (Windmill Sites; Ala-307,  $\approx 4750-2200y$ ), Middle (Ala-328/329,  $\approx 2500-300y$ ), and Late Horizons (CCo-138, 1300-1500y). Diseases and anomalies were classified following Ortner and Putschar (1981) into 13 major groups, each with a variable number of subgroups. Data on affected elements and individual age and sex were also assessed.

The percent of the population impacted by diseases/anomalies varied from  $\approx 5\%$  to  $\approx 20\%$ . The Windmill and Ala-328 populations have the highest percentages at 19.5% and 12.8%, respectively. Major disease categories observed include (most/least): Lesions of the joints, jaws, and teeth; traumas, infectious diseases, skeletal malformation, tumors, and reticuloendothelial/hemopoietic disorders. Beyond the expected high frequency of joint lesions, infections and traumatic conditions, which are generally related, occur at relatively high frequencies. Tumors occur at low frequencies, being absent in the Windmill and Ala-329 samples, but reach a high of 7% in the Ala-328 population.

These results represent the first delineation of the frequency of occurrence of diseases and anomalies at a geographic, temporal, and population level in California.

### High energy expenditure causes shifts in the gut microbiota that buffer host energy balance

EMILY M. VENABLE<sup>1</sup>, ANDREW S. BOLZE<sup>1</sup>, BRYCE A. CARLSON<sup>2</sup> and RACHEL N. CARMODY<sup>1</sup>

<sup>1</sup>Human Evolutionary Biology, Harvard University, <sup>2</sup>Department of Anthropology, Purdue University

Recent research suggests that the gut microbiome plays a central role in host energy homeostasis. However, the contributions of the gut microbiome to host energy balance during periods of high energy expenditure remain unclear, as most studies to date of gut microbial responses to changes in energy balance have manipulated energy intake rather than expenditure. Previously, we reported significant differences in gut microbial community structure between high-running cohorts of humans and mice and their limited-running conspecific controls. Here, we report that inoculation of

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germ-free mice with gut microbial communities harvested from human ultramarathoners (n=6) led to significant increases in adiposity (p=0.0086) and decreases in lean mass (p=0.0019) relative to germ-free controls (n=6). Critically, these phenotypic differences did not emerge in gnotobiotic mice harboring gut microbial communities harvested from human non-runners/low-runners (n=6). Further, gnotobiotic recipients of ultramarathoner gut microbial communities gained more weight per gram of food consumed than did recipients of non/low-runner gut microbial communities (p=0.0008). 16S rDNA sequencing of fecal samples confirmed high-fidelity transmission of the gut microbiota between donor and recipient, with significant differences in gut microbial community structure observed between recipients of ultramarathoner versus non/low-runner inocula (p<0.001) that paralleled differences previously reported for the human donors. Our results underscore the possibility that gut microbial responses to high energy expenditure may help buffer host energy balance. We speculate that similar buffering by the ancestral human gut microbiome could have reduced early barriers for the hominin adoption of energetically expensive behaviors such as endurance running.

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### The delto-fulcral angle as measure of the 3D configuration of the primate shoulder joint complex

EVIE E. VEREECKE<sup>1</sup>, VALERIE VERMEULEN<sup>2</sup>, MARIE VANHOOF<sup>1</sup>, ALEXANDER VAN TONGEL<sup>2</sup>, PIETER CORNILLIE<sup>3</sup>, LIEVEN DE WILDE<sup>2</sup> and ELAINE KOZMA<sup>1</sup>

<sup>1</sup>Development & Regeneration, KU Leuven, <sup>2</sup>Human Structure & Repair, Ghent University Hospital, <sup>3</sup>Veterinary Sciences, UGhent

The shoulder girdle is a complex joint system that varies widely within primates. In humans, where the forelimbs have lost their locomotor function, morphological changes are pronounced. Previous studies have identified morphologies that may predispose humans to shoulder pathologies. In the current study, we apply a medical image-based methodology to non-human primates and explore differences in 3D configuration of the shoulder complex and its relation to forelimb function and pathology. Through a collaboration with European zoos, we obtained CT scans of complete shoulder girdles of primate cadavers, and data from online repositories were also included. Here, we focus on the hominoids (non-human primates, n=47; humans, n=60). We created 3D models of the shoulder complex, and measured the delto-fulcral triangle, a proxy for the supraspinatus outlet. The models indicate substantial variation in this parameter between hominoid primates. The average alpha angle ranged from

30°±8° in Asian apes to 41°±8° in African apes, with humans falling in between (33°±4°). For the roof, Asian apes and humans fall at the higher end with 103°±6° and 102°±5°, respectively, while African apes are at the lower end with 88°±5°. The difference between the African and Asian apes in delto-fulcral triangle suggests it reflects functional differences. No conclusions could be drawn regarding shoulder pathologies, though values for the roof in omarthrosis patients fall at the high end of that measured for hominoid primates. We plan to expand our dataset with other primate taxa and include additional measures of 3D configuration.

*The research was funded by KU Leuven, UGhent and BAEF.*

### Children and Childhood in the Avars and Gepids of Migration Period Hungary

KIRSTEN A. VEROSTICK

Anthropology, University of South Florida

This presentation discusses children and childhood through an extended life history and life course framework, focusing on Avar and Gepid populations of the Great Hungarian Plain during the Migration Period (4<sup>th</sup>-8<sup>th</sup> century AD). This research investigated the hypothesis that breastfeeding and weaning practices (BWPs) differed between these populations due to variation in their overall subsistence practices and general cultural practices. Analyses of stable isotopes were applied to 131 individuals from four cemetery sites, two Avar sites and two Gepidic sites. Bulk stable isotopic analysis of bone collagen indicated no significant differences between adults and non-adults at each of the sites analyzed, with the exception of non-adults who were still breastfeeding and in the process of weaning. Weaning time using bulk nitrogen isotope data and the WARN program did not reveal any specific patterning between sites or populations. Microsampling of first permanent molars from a subsample of both non-adults and adults suggests no specific patterns of BWPs within populations, as each site analyzed revealed different BWPs. Isotopic life history profiles were created for the subsampled individuals to analyze BWPs on an individual level and included the microsampling isotopic data, bulk element isotopic data, grave goods and paleopathological data. As there were no clear BWPs within the populations and a generally similar diet, it is suggested that cultural practices, generational cohort differences and agency are responsible for variations in BWPs within the sites and populations. Additionally, some individuals indicated relationships between BWPs and either increased or decreased mortality.

### Deep bioarchaeology: settlement of the Americas under a Big Data and Data Science approach

DANILO VICENSOTTO BERNARDO<sup>1,2</sup> and TATIANA FERREIRA DE ALMEIDA<sup>1,3</sup>

<sup>1</sup>Laboratório de Estudos em Antropologia Biológica, Bioarqueologia e Evolução Humana, Instituto de Ciências Humanas e da Informação, Universidade Federal do Rio Grande, <sup>2</sup>Programa de Pós-Graduação em Antropologia - PPGAnt, Instituto de Ciências Humanas. Universidade Federal de Pelotas, <sup>3</sup>Laboratório Clínico, Hospital Israelita Albert Einstein

Bioarchaeology, as a discipline based on the investigation of the biocultural interactions of populations, has been crucial for investigating the occupation of the New World, allowing the proposition of models discussing the origin, dispersion, and chronologies of Native Americans. However, different models have been proposed as the most credible for explaining how the settlement occurred. Such discrepancies are due to the diversity and specificity of different markers, leading scholars of the subject to, for an operational reason, work with small data cuttings. Currently, the amount and diversity of data on the subject is enormous and mathematical approaches, such as those used in Big Data and Data Science analyzes, can offer the opportunity to fill gaps and reduce divergences from different sources of information. Here we present a study based on a Big Data approach to jointly evaluate different markers classically used in Bioarchaeological studies, such as biological affinities, frequency and prevalence of traumas and violent events, style and quality of life and data of archaeological context of diverse native populations distributed in the Americas. The different sets of data were submitted to Decision Tree Analysis and Machine Learning algorithms and compared with models of settlement commonly found in specialized literature. Our results, still preliminary, demonstrated that we are still far from confidently predicting which of the tested models best fits the set of data used, probably due to the extreme complexity of the scenario, with multiple adaptive possibilities, on which the emergence of the human being occurred in the Americas.

### Twenty-twenty Hindsight: Ethical Reform and the Reshaping of Genetic Anthropology

MIGUEL G. VILAR

Anthropology, University of Maryland, Science and Exploration, National Geographic Society

Last year shook the world like no other in recent history. COVID-19 handed the globe a collective pause, blurred immediate futures, and forced me and millions others to change jobs. As a researcher, I canceled field and lab work, and as a grants officer I pulled and delayed grants; all teaching and knowledge-sharing went virtual.

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Concurrently, social movements nationwide forced me to question myself as a PI, self-trusted with studying "others." Yet 2020 also gave me time to evaluate my choices, and ultimately grow deeper as a genetic anthropologist in a field fraught with missteps.

Genetic anthropology is a young anthropology, as it requires recent DNA technology. However, it is that tool that allows us, with some authority, to advance century-old discussions. In the eighties I witnessed DNA hijack the *Out of Africa* hypothesis and in the nineties reshape the story around peopling of the Americas. The 2000s brought the first human genome, hominin admixture, and me to consumer genetics; and by the 2010s paleogenomics was front, center, and unrestrained.

In 2020, however, circumstances forced me to take stock and rebrand as bridge-builder and mixed-methods researcher. It's no longer about what DNA can do, but what should we anthropologist do better. COVID-19 helped impress ethics and equitability in my anthropology. Further, as an upshot of social movements such as BLM, we must now require collaborative inclusion of people we once considered "samples." The field must have mutually-intellectual and cross-experiential contributions, and not simply the suffixed acknowledgement of others' biological samples.

### Adaptive Introgression of the Denisovan variant of the gene *MUC19* in American populations

FERNANDO A. VILLANEVA<sup>1,2</sup>, KELSEY E. WITT<sup>2</sup>, RATCHANON PORNMONGKOLSUK<sup>2</sup> and EMILIA HUERTA-SÁNCHEZ<sup>2</sup>

<sup>1</sup>Anthropology, University of Colorado Boulder, <sup>2</sup>Ecology and Evolutionary Biology, Brown University

The gene *MUC19* encodes a member of the gel-forming mucin protein family, which is related to lacrimal and salivary gland function in humans. *MUC19* has been previously proposed as a top candidate for positive selection in Indigenous American populations. *MUC19* is also archaically introgressed, where modern humans carry the Denisovan variant. Although all humans carry a small fraction of archaic ancestry across the genome, there are few examples of adaptive introgression cases of Denisovan variants, and in particular, the contribution of archaic introgression in how Indigenous Americans have adapted to their environments remains underexplored. Here, we find the Denisovan *MUC19* at low frequency in Europeans (0.5-3.3%), East Asians (2.4-11%), and Southeast Asians (5.2-12.8%), but find it at higher frequencies in admixed Americans (5.9-30.5%). Furthermore, when we filter the version of *MUC19* in admixed American individuals based on the ancestry identity of that portion of the genome, the Denisovan *MUC19* is found at extraordinarily high frequencies in the Indigenous American

ancestry tracks (Colombia: 14.5%, Peru: 27.5%, Puerto Rico: 32.4%, Mexico: 48.7%). The high frequency of the Denisovan *MUC19* in Indigenous Americans is surprising, as genes are often depleted for archaic ancestry due to past strong purifying selection. Taken together, our results suggest that the Denisovan *MUC19* is driving the signature of positive selection previously discovered at this locus, although the functional benefits in Indigenous individuals are as-of-yet unclear. It is likely that the Denisovan version served as the raw material for positive selection as American populations adapted to novel environments.

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### Characterization of the inhabitants of South America using nonmetric dental data

TATIANA VLEMINCQ-MENIETA and G. RICHARD SCOTT

Anthropology, University of Nevada, Reno

The peopling of the Americas has been widely studied since European colonization beginning in the 15-16<sup>th</sup> centuries. While focus has been on the timing and routes of entry into North America, less attention has been devoted to South America. The present study investigates a dental characterization of South American populations, focusing on diversification through time. The dental traits in this analysis were scored by C. G. Turner and represent 54 samples and seven South American countries spanning from 11,000 to 500 BP: Argentina (n=23), Bolivia (n=74), Brazil (n=559), Chile (n=222), Ecuador (n=332), Panama (n=141), and Peru (n=917). Thirty-two key traits were initially selected using the manual outlined by Scott and Irish (2017), but due to small sample sizes and data editing, final biodistance analyses were run on 13 traits and 17 samples. Results show a clustering of Peruvian assemblages around an old Ecuadorian site (Santa Elena, 10,800-6,500 BP), while the rest do not follow any clear geo-chronological patterns. These findings suggest that other South American populations may have been more mobile than Peruvian groups for the time frame examined. The complex population history of South America is evident in the lack of East to West and old (Late Pleistocene) to recent (Holocene) trends. Future studies will increase sample sizes and geo-chronological variation and account for external factors (e.g., environment) that may affect the phenotypic expression of dental traits.

### The impact of scurvy mortality during the transition of agriculture in northern Vietnam

MELANDRI VLOK<sup>1</sup>, MARC F. OXENHAM<sup>2</sup>, KATE DOMETT<sup>3</sup>, HIROFUMI MATSUMURA<sup>4</sup>, HOANG T.

HIEP<sup>5</sup>, TRAN T. MINH<sup>5</sup>, NGUYEN T. MAI HUONG<sup>5</sup>, NGHIA T. HUU<sup>5</sup> and HALLIE R. BUCKLEY<sup>1</sup>

<sup>1</sup>Department of Anatomy, University of Otago, <sup>2</sup>School of Archaeology and Anthropology, Australian National University, <sup>3</sup>College of Medicine and Dentistry, James Cook University, <sup>4</sup>School of Health Sciences, Sapporo Medical University, <sup>5</sup>Department of Prehistoric Archaeology, Vietnam Institute of Archaeology

The agricultural transition in Mainland Southeast Asia (from 4500BP) was unique in that mixed foraging and farming practices continued until the Iron Age (1500-500BP). This slow transition has been argued by some bioarchaeologists to have minimized the detrimental health impacts of cereal agriculture on human groups. However, as is the case in agricultural transitions in other regions of the world, early Neolithic (agriculture) sites present with significant evidence of high fertility rates suggesting possible increase in population density which is known to have a negative impact on population health. We aimed to investigate the evidence of Vitamin C deficiency (scurvy) at the early Neolithic site of Man Bac in northern Vietnam (4000-3500BP) to determine whether the agricultural transition significantly influenced nutrition and whether malnutrition was associated with a decrease in survivorship during this period. Seventy individuals (adults and nonadults) were differentially diagnosed following the Snoddy et al. (2018) criteria. Cox proportional hazard models were used to test whether the skeletal presence of scurvy was associated with decreased survivorship. Eighty percent (35/44) of nonadults and 35% (9/26) of adults presented with probable scurvy. The Cox proportional hazard models demonstrated no significant differences in survival amongst nonadult ages with or without probable scurvy (n=44, OR=0.981, p=0.961), but a decreased survival of adults with probable scurvy was observed (n=29, OR=0.545, df=1, p=0.123). Our outcomes suggest high levels of micronutrient deficiency, which also increased risk of death during the early agricultural transition in Mainland Southeast Asia indicating a detrimental effect to health.

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### The evolution of the human chin: a quantitative genetic analysis of hominoid craniomandibular form

NOREEN VON CRAMON-TAUBADEL<sup>1</sup>, JILL E. SCOTT<sup>2</sup>, CHRIS A. ROBINSON<sup>3,4,5</sup> and LAUREN SCHROEDER<sup>1,6,7</sup>

<sup>1</sup>Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, <sup>2</sup>Department of Sociology and Anthropology, Metropolitan State University of Denver, <sup>3</sup>Department of Biological Sciences, Bronx Community College (CUNY), <sup>4</sup>Doctoral Program in Anthropology, City University of New York

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Graduate Center,<sup>5</sup>The New York Consortium in Evolutionary Primatology (NYCEP),<sup>6</sup>Department of Anthropology, University of Toronto Mississauga,<sup>7</sup>Human Evolution Research Institute, University of Cape Town

It is currently unclear whether the human chin is the product of direct selection or a by-product of evolutionary pressures on other cranial regions. Here, we apply a quantitative genetic approach to hominoid craniomandibular traits to assess the latter hypothesis. 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 masticatory and basicranial traits. Second, where directional selection was identified, we reconstructed the pattern of selection acting on specific traits. Overall, results indicate that much of the diversity in extant hominoid mandibular form is explained by strong stabilizing selection; however, a rapid evolutionary rate (suggestive of directional selection) was detected along the human branch. Reconstructed selection gradients indicate strong selection along the human lineage acting to decrease palatal, basicranial, and alveolar length (for both the mandible and maxilla), as well as anterior dental arcade width and anterior corpus height, and to increase posterior dental arcade width, consistent with selection for a parabolic dental arcade. However, for the majority of the 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. The correlated responses were all negative, indicating that they were under the influence of strong negative selection coefficients acting elsewhere, likely related to facial retraction. Thus, our results provide evidence that the distinct human chin could be an evolutionary by-product of direct selection on other aspects of skull form.

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## Advancing Data Justice: A Need for Anthropologists to Address Data Disparities and Dataveillance

JENNIFER K. WAGNER

Center for Translational Bioethics & Health Care Policy, Geisinger

Data justice is a principle essential to the fulfillment of the international human right to participate in science and share in its benefits (UDHR, Art. 27; ICESCR, Art. 15.1.b). In the United States, precision health initiatives and learning healthcare system models have gained momentum. Meanwhile complex ethical, legal, and policy matters—including the meaning of the human right to science and guidance for effective data stewardship—have remained unresolved and under-prioritized. Furthermore, legal mechanisms intended to ensure fairness are blurred by

public-private partnerships and data repurposing. Generous interpretations of “quality improvement” and “public health” combined with datafication simplified by widespread mobile health technologies create conditions that seemingly clash with concurrent efforts to advance participant-centered approaches to research. Participation in science is seemingly inescapable for the “data rich” and unattainable for the “data poor,” creating counterintuitive data exposure and dataveillance risks. Without adequate ethical principles directing equitable research practices, such data disparities become runaway processes that undermine trust in science, impede scientific advancement, and reduce potential benefits for everyone. An examination of relevant domestic law (e.g., statutory authority of the Federal Trade Commission and state Attorneys General), international human rights law (e.g., General Comment No. 25 to ICESCR, Art. 15.1.b and the Universal Declaration of Bioethics and Human Rights), and diverse stakeholder efforts (e.g., CARIN Alliance Code of Conduct) reveals the possibility for new synergies to mitigate emerging data disparities and develop meaningful guidance to curb harms associated with discriminatory dataveillance. Anthropologists are needed to advance data justice.

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## It's not just mass: Load position matters for speed and cost

CARA M. WALL-SCHEFFLER

Biology, Seattle Pacific University, Anthropology, University of Washington

The energetic cost of walking has clearly been shown to vary with mass and speed; however, among humans, the metabolic cost of carrying loads has not consistently increased proportionally to the mass carried. In fact, the cost of carrying mass, and the speed at which human walkers carry this mass, has been shown to vary with load mass, load position, and load description (e.g. child versus groceries). Here, we investigate the energetic cost and speed changes of people (N=15) walking through the woods carrying their own babies (mean=10.6kg) in three different positions—on their front, side, and back using the same Ergo fabric baby sling. People carrying their babies on their backs are able to maintain their unloaded walking speed (1.4m/s), and show the lowest increase in metabolic cost (joules/meter, 17.4%). Conversely, carrying babies on the front and on the side show a decrease in speed (p=0.1, 2.2% decrease) and a significant increase in metabolic cost (p<0.001, 21.1% increase). Kinematic data show that walkers decreased their contact time (p=0.029) and swing time (p=0.004)

during side and front loading but not during back loading. This provides energetic and kinematic evidence for the preponderance of back carrying cross-culturally.

## Comparative morphological variation of rotation and weight-bearing points in the shoulder girdle of extant Cercopithecidae

CORINNE G. WALTERS<sup>1</sup>, LISA M. DAY<sup>1</sup>, MARIE VERGAMINI<sup>2</sup> and AMY L. RECTOR<sup>1</sup>

<sup>1</sup>Anthropology, School of World Studies, Virginia Commonwealth University, <sup>2</sup>Integrative Life Sciences, Virginia Commonwealth University

Variation in joint structures in extant arboreal and terrestrial quadrupedal Cercopithecidae correlates with substrate preference and locomotive type. Previous elbow joint studies suggest that locomotor repertoires of Cercopithecidae can be differentiated through distal humerus and the proximal ulna shape analysis (Rector et al., 2018). Exploring morphological variation in the shoulder girdle could provide another way to identify locomotor repertoires in extant and fossil Cercopithecidae.

Scapular outlines were collected from a sample of 180 extant specimens using a MicroScribe point digitizer. Species were assigned a primary traveling locomotor category. Colobines were categorized as arm-swing branch quadrupeds and remaining species were categorized as ground quadrupeds, branch quadrupeds, or branch and ground quadrupeds. Variation in scapular shape was analyzed using MorphoJ 3D geometric morphometric PCA, PGLs, and phylogenetic ANOVAs. The analyses tested whether locomotive pattern can be established from the shape and variation of Cercopithecidae scapula.

Results suggest that morphology of the scapula differs between all four locomotive groups as well as within certain African and Asian groups. Furthermore, weight-bearing points are variable across groups and can be used to identify main locomotor strategies. Rotation points may not be as varied between locomotive types as range of motion in the shoulder is not considerably different between Cercopithecidae arm-swing brachiators and quadrupeds. This study contributes ecological information about niche differentiation, resource competition, and community organization in living primates. Further exploration of locomotor variation within African and Asian Cercopithecidae, especially Colobines, could provide more information on the timing and adaptive contexts of Cercopithecidae locomotor evolution.

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## Naiyena Epul, a new Pleistocene hominin site in the Nachakui Formation, West Turkana, Kenya

CAROL V. WARD<sup>1</sup>, FRANCIS H. BROWN<sup>2</sup>, J. MICHAEL PLAVCAN<sup>3</sup> and FREDRICK K. MANTHI<sup>4</sup>

<sup>1</sup>Pathology and Anatomical Sciences, University of Missouri, <sup>2</sup>Geology and Geophysics, University of Utah, <sup>3</sup>Anthropology, University of Arkansas, <sup>4</sup>Earth Sciences, National Museums of Kenya

The West Turkana Paleo Project conducted fieldwork led by one of us (FKM) at the new fossil-bearing locality Naiyena Epul in northern Turkana County, Kenya. Although comprising an area of less than 12 km<sup>2</sup>, the fluvial deposits at Naiyena Epul have yielded 75 vertebrate fossils, including bovinds, monkeys, carnivores, suids, and three hominins. The fossil-bearing exposures contain a number of tuffs that are compositionally most similar to those of the Okote and Ileret Tuff complexes of the Koobi Fora Formation, with ages ranging from ~1.48 and ~1.3 Ma. The most secure correlation is the Lokapetamoi Tuff, with an age of 1.43 Ma, that immediately underlies the fossil-bearing strata, suggesting that these deposits date to 1.42 Ma and represent the Nattoo Member of the Nachakui Formation. Of the hominins, two are attributable to *Homo erectus* and one to *Paranthropus boisei*, so Naiyena Epul represents one of the most recent contemporaneous occurrences of these taxa and of *P. boisei* in West Turkana. The *Homo* specimens consist of two partial mandibles with tall, narrow corpora. One displays a heavily worn M<sub>2</sub> with a clear toothpick groove along its distal cervical margin. The third hominin fossil is fragment of juvenile maxilla preserving little morphology but containing complete crowns of I<sup>1</sup>-P<sup>3</sup>. The size and morphology of the P<sup>3</sup> is consistent only with *P. boisei*, so this specimen provides new data on the maxillary dentition of this species. Naiyena Epul provides novel information about the morphology of *P. boisei* and biogeography of both hominin taxa.

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## Global Bony Labyrinth Shape Variation with Climate and Subsistence Strategy

DEVIN L. WARD<sup>1</sup>, LAUREN SCHROEDER<sup>2</sup>, JOCELYN E. ROY<sup>1,3</sup>, MADELYN HERTZ<sup>1,4</sup>, ALEXANDRA UHL<sup>5</sup>, EMMA POMEROY<sup>6</sup>, JAY T. STOCK<sup>4,7</sup>, LYNN E. COPE<sup>8</sup>, KAREN L. BAAB<sup>9</sup>, T. BENICE VIOLA<sup>1,10</sup> and MARY T. SILCOX<sup>11</sup>

<sup>1</sup>Department of Anthropology, University of Toronto, <sup>2</sup>Department of Anthropology, University of Toronto, Mississauga, <sup>3</sup>Faculty of Computer Science, University of Strathclyde, <sup>4</sup>Department of Anthropology, Western University, <sup>5</sup>Department of Cultural, Environmental, and Global Studies, Salve Regina University, <sup>6</sup>Department of Archaeology, University of Cambridge, <sup>7</sup>Department of Archaeology, Max Planck Institute for the Science of Human History, <sup>8</sup>Department of

Medical Sciences, Frank H. Netter, MD School of Medicine, Quinnipiac University, <sup>9</sup>Department of Anatomy, Midwestern University, <sup>10</sup>Institute for Archaeology and Ethnography, Siberian Branch, Russian Academy of Sciences, <sup>11</sup>Department of Anthropology, University of Toronto Scarborough

Variation in human cranial shape has long been investigated for associations with global climate and subsistence strategy. The bony labyrinth surrounds vital sensory organs, governing balance and motion. It has been the subject of intraspecific analyses focusing on sexual dimorphism, body size, and population level differences, but apart from early work with small sample sizes, this part of the cranium has not been investigated for intraspecific variation associated with environmental variables.

Here, we investigate the influence of climate and subsistence strategy on the bony labyrinths of 270 humans from 15 different groups. These groups are associated with climates ranging from arid to humid, and tropical to arctic across North America, Europe, Africa, and southeast Asia, as well as terrestrial hunter forager, marine hunter forager, agricultural, and industrial subsistence strategies spanning the past 8000 years.

We collected semilandmarks across the three semicircular canals and the common crus on computed tomographic data, using a protocol designed to eliminate the effect of differences in scan resolution. After sliding the semilandmarks and performing a generalized Procrustes analysis, limited intra- or inter-observer error was identified and there was no significant directional asymmetry. Subsequent unilateral analysis was unable to identify differences between individuals related to climatic or subsistence variables. These results suggest that labyrinthine shape variation among humans is not shaped by subsistence strategy or climate, and point to a possible protective mechanism for inhibiting plasticity during life. This mechanism would prevent shape changes which could influence function and warrants further, microstructural exploration.

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## Biological responses to permanent occupation and tuber domestication in the Andean Altiplano

JAMES T. WATSON<sup>1,2</sup>, RANDALL HAAS<sup>3</sup> and CAITLIN MCPHERSON<sup>1,2</sup>

<sup>1</sup>Arizona State Museum, University of Arizona, <sup>2</sup>School of Anthropology, University of Arizona, <sup>3</sup>Department of Anthropology, University of California, Davis

Permanent human occupation of the high-altitude Andean *Altiplano* by 9ka presented unique challenges for human adaptation, which resulted in both biological and cultural responses. Greater

investment in wild plant resources between 5-7ka (cultivation and increased consumption) likely played a significant role in domestication of starchy tubers. Previous research identified that significant investment in tuber processing and consumption led to positive selection at genetic loci related to improved starch digestion. In addition, stature and body size estimated from long bones of individuals recovered from the Middle/Late Archaic site of Soro Mik'aya Patjxa (SMP) in the southern Titicaca Basin identify that early farmers were smaller (male stature = 152.3 ± 4.8 cm and body mass = 55.9 ± 2.5cm; female stature = 146.2 ± 2.1 cm and body mass = 54.1 ± 1.3 cm) than populations living at lower altitudes (male stature = 159.1 ± 3.8 cm and body mass = 60.3 ± 1.8 cm; female stature = 149.8 ± 3.7 cm and body mass = 52.2 ± 1.1 cm), but similar to modern indigenous groups living on the Altiplano. We argue that these patterns reflect developmental constraint, which are plastic (non-genetic) responses to stress associated with development at high-altitude. In contrast to plastic developmental responses to environmental stress, we argue that niche construction related to tuber consumption drove positive genetic selection for changes to the internal human metabolic environment. This case study provides an example of mosaic biological responses to human adaptations within both natural and human-mediated environments.

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## Do chimpanzees really have a spacious birth canal? A reanalysis of cephalopelvic proportions and implications for the obstetrical dilemma in humans

NICOLE M. WEBB<sup>1,2</sup>, CINZIA FORNAI<sup>1,3</sup>, VIKTORIA A. KRENN<sup>1,3</sup> and MARTIN HAEUSLER<sup>1</sup>

<sup>1</sup>Institute of Evolutionary Medicine, University of Zurich, <sup>2</sup>Department of Palaeoanthropology, Senckenberg Research Institute and Natural History Museum Frankfurt, <sup>3</sup>Department of Evolutionary Anthropology, University of Vienna

The tight fit between the neonate skull and the female pelvis characteristic of human birth is believed to be exceptional in its magnitude, especially relative to the great apes. This long-held assumption that great apes possess a capacious birth canal, free of significant obstetric constraint, has been imperative to research focused on elucidating the complex birth mechanism in modern humans. It derives from an observed ratio in *Pan* of 0.57 for the pelvic inlet's anteroposterior diameter to maximum fetal head length. It is therefore perplexing that female chimpanzees, being slightly smaller in body size than males, have absolutely larger birth canal dimensions. However, direct observations of chimpanzee birth showed that

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the fetal head is usually fully extended or flexed during delivery. Moreover, the anteroposterior diameter of the pelvic inlet is not actually obstetrically relevant, as it is obliquely oriented to the axis of the birth trajectory. Here, we virtually quantify the true fit between the fetal skull and the female pelvis using CT-based 3D models. We show that the ratio of the submentobregmatic diameter of the fetal head to the anteroposterior diameter of the pelvic midplane (perpendicular to the axis of the birth canal) is 0.85, reserving only a 15 mm space between the bony pelvis and the fetal skull for soft tissue. This tighter cephalopelvic fit compared to previous analyses may indicate that birth-related selective pressures played a role in the evolution of pelvic sexual dimorphism in chimpanzees, thereby informing critical assumptions of the obstetrical dilemma hypothesis in humans.

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### Activity budget and gut microbiome fluctuations among and within reproductive states in wild primates indicate fine-scale host flexibility

SHASTA E. WEBB<sup>1</sup>, JOSEPH D. ORKIN<sup>2</sup>, RACHEL E. WILLIAMSON<sup>1</sup> and AMANDA D. MELIN<sup>1,3,4</sup>

<sup>1</sup>Anthropology & Archaeology, University of Calgary, <sup>2</sup>Institut de Biologia Evolutiva, Universitat Pompeu Fabra-CSIC, <sup>3</sup>Maternal and Child Health, Alberta Children's Hospital Research Institute, <sup>4</sup>Department of Medical Genetics, Cumming School of Medicine, University of Calgary

Pregnancy and lactation increase energy demands of primates and other mammals. To mitigate these demands, females selectively eat energy-dense foods, decrease physical activity, and/or undergo physiological changes. The gastrointestinal microbiome, which influences host metabolism 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 in free-ranging animal populations. Studies that examine behavioral and/or gut microbiota fluctuations across the reproductive cycle typically identify three reproductive states—pregnancy, lactation, and cycling. Here, we sought to examine behavior and gut microbiota not only among but also within these states by splitting states each into 3 stages. We analyzed activity budgets ( $n=13,750$  scans) and 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 in 2014–2018. To analyze gut bacteria, we sequenced the V4 region of the 16S rRNA gene from fecal DNA. Activity did not differ significantly among reproductive states. However, we found significant changes in activity budget within reproductive states—specifically during mid-lactation—suggesting behavioral flexibility at

a fine scale. Traditional indicators of increased energy harvest in gut microbiota did not differ significantly among or within reproductive states, but several bacterial taxa were significantly differentially abundant during late pregnancy and early lactation. Investigating reproductive microbial ecology in wild primates among and within reproductive states contributes to deeper understanding of behavioral flexibility, roles microbes play in the reproductive cycle, and maternal fitness.

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### Survivorship at Medieval St. Gregory's Priory and Cemetery, Canterbury, England

SINA D. WHITE, PATRICK MAHONEY and CHRIS A. DETER

School of Anthropology and Conservation, Skeletal Biology Research Centre, University of Kent

Throughout the 11th to 15th century AD, Canterbury was a major theological center that educated clergy and influenced pilgrimages. During this period, the city expanded as people migrated from nearby towns to start businesses and sell at markets to provide for pilgrims and travelers. As Canterbury transformed into an urban environment, it led to adverse living conditions that affected the health of the population. This study examines the differences in survivorship for individuals living in medieval Canterbury. Age-at-death and biological sex were reconstructed for individuals ( $n=498$ ) recovered from St. Gregory's Priory and Cemetery (1084–1537). Kaplan Meier survival analysis is used to assess possible differences in survivorship between adult males and females. The survival curve suggest that adult males experienced increased survivorship relative to females (Log Rank  $p < 0.001$ ). This difference in survival is explored within the context of social status, mobility, and settlement patterns.

### Factors shaping the gut microbiomes of *Eulemur rubriventer*

TABOR WHITNEY<sup>1</sup>, LAURA O. DIAKIWI<sup>6</sup>, DIANA M. CHRISTIE<sup>7,8</sup>, NELSON TING<sup>7,8</sup>, KATHERINE R. AMATO<sup>1</sup>, ANDREA BADEN<sup>3,4,5</sup> and STACEY TECOT<sup>2</sup>

<sup>1</sup>Department of Anthropology, Northwestern University, <sup>2</sup>School of Anthropology and Laboratory for the Evolutionary Endocrinology of Primates, University of Arizona, <sup>3</sup>Department of Anthropology, Hunter College, CUNY, <sup>4</sup>New York Consortium in Evolutionary Primatology (NYCEP), <sup>5</sup>Department of Anthropology, The Graduate Center, CUNY, <sup>6</sup>Department of Ecology, University of Wyoming, <sup>7</sup>Department of Anthropology, University of Oregon, <sup>8</sup>Institute of Ecology and Evolution, University of Oregon

The gut microbiome consists of microbial communities that reside in the gastro-intestinal tract of living organisms. Variation in this system has been linked to health outcomes in humans and animals by affecting digestion, immune system development, and pathogen invasion. However, we still lack a complete understanding of the factors that shape gut microbiome variation, particularly in wild primates. The central objective of this research is to determine which factors are predicting inter-individual variation in the gut microbiome of red-bellied lemurs (*Eulemur rubriventer*). We sequenced the 16S rRNA hypervariable V-4 region to characterize the gut microbiome from 26 genotyped individuals across eleven pair-bonded social groups residing in Ranomafana National Park. This research estimates to what degree genetic relatedness, social group membership, diet, sex, and geographical distance drive inter-individual variation in the microbial communities residing in red-bellied lemurs. Other than sex, all factors play a significant role in predicting gut microbiome composition. However, our model has high levels of variance inflation inhibiting our ability to determine which factors are more predictive of gut microbial composition. This is one of few studies that analyzes environmental, genetic, and biological factors' impact on variation in the gut microbiome. Our results provide evidence that there is a need for more research that considers various sources of influence on gut microbial variation. For endangered species as a whole, understanding how such factors shape variation is critical in recognizing the consequences this variation has on host nutrition, health, and its overall effect on host ecology and conservation.

### Childhood obesity's influence on the oral microbiome and oral health

PAMELA S. WHYMS<sup>1</sup>, AFSAR NAQVI<sup>2</sup>, DERIC TRUSKOSKI<sup>3</sup>, ARACELI VALVERDE ESTEPA<sup>2</sup>, SAHAR ALRAYYES<sup>3</sup>, SLOAN WILLIAMS<sup>1</sup>, CHAD SILVER<sup>3</sup>, SARIA AWADALLA<sup>4</sup> and CHRISTINA L. NICHOLAS<sup>1,5</sup>

<sup>1</sup>Anthropology, University of Illinois at Chicago, <sup>2</sup>Periodontics, University of Illinois at Chicago, <sup>3</sup>Pediatric Dentistry, University of Illinois at Chicago, <sup>4</sup>Epidemiology and Biostatistics, University of Illinois at Chicago, <sup>5</sup>Orthodontics, University of Illinois at Chicago

Childhood obesity leads to an increased risk for many negative health outcomes, like diabetes, asthma, high cholesterol, high blood pressure, low self-esteem, and depression, and the influence of obesity and its negative outcomes disproportionately affects socioeconomically disadvantaged groups. In 2014, approximately 20.4% of U.S. sixth graders were obese, while 29.2% of Chicago sixth graders were obese, with disparities among racial/ethnic groups. Obesity has also been suggested to be associated with oral inflammation, periodontal disease, and variation in the oral microbiome. This project aims to examine the association between

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childhood obesity, oral microbiome diversity, and oral health. We recruited a diverse group of participants (n=35; aged 10-12) from a US urban setting through UIC's Pediatric Dentistry Clinic in Chicago, collecting demographic information, detailed dietary data, height, weight, and salivary samples. Saliva samples were sent to LC Sciences for whole genome sequencing, and results indicated that 34 out of 2,510 species showed differences ( $p \leq 0.05$ ) in abundance between obese and non-obese subjects. We also found positive associations between BMI and gingival (gum) bleeding during dental treatment ( $p = 0.012$ ) and between BMI and dental plaque scores ( $p < 0.001$ ). These results indicate an association between obesity and oral health, which may be mediated by dysbiosis of the oral microbiome. Future *in vitro* work will investigate the function of oral biota that showed increased/decreased abundance in obese children to ascertain whether these species may be a causal factor for the recorded poorer oral health outcomes.

Center for Clinical and Translational Sciences Pilot Grant, University of Illinois at Chicago; Biomedical Research Award American Association of Orthodontists Foundation

### Rethinking how anthropologist analyze burned human remains: The need for a more quantitative approach

AMANDA WILLIAMS

Anthropology, Truckee Meadows Community College

Fatal fires produce a range of physical alterations to the body that can be studied and analyzed to interpret perimortem events. Currently, the anthropological community lacks a consistent, objective, and detailed method for describing burn injuries or patterns in a variety of settings and conditions. Previous models were constructed from specific fire environments, and therefore are not widely applicable today. There is a need to create a scale based on quantitative experimental data (e.g. duration and temperature of fire) that provides insight into the nature of the fire and cause of injuries contributing to the condition of the remains.

Observations from four main fire environments were used in developing a new quantitative method for analyzing heat related damage. This model assesses burned remains by applying a total body score (TBS) based on the affected body region (i.e., skull, upper and lower limbs, thorax, and hands/feet). This study found notable differences in total body scores between fire environments. Outdoor and confined space contexts exhibited some of the highest total body scores (TBS 28 to 33) compared to structure and vehicle fires (TBS 16 to 25). The results demonstrate there is a pattern between fire environments and bodily conditions, making it possible to model heat related damage. This research also lays

the foundation for applying a more quantitative approach to analyzing and interpreting burned human remains. More importantly, it enhances our understanding of the underlying processes that affect thermal alterations.

This research was partially funded by the Mountain Desert and Coastal Forensic Anthropologists, the University of Montana Foundation, and the Toelle-Bekken families at UM.

### These farmers weren't doing much farming: A dietary reconstruction of Late Neolithic cave burials of Belgium using dental microwear texture analysis

FRANK L. WILLIAMS<sup>1</sup>, CHRISTOPHER W. SCHMIDT<sup>2</sup> and JESSICA L. DROKE<sup>3</sup>

<sup>1</sup>Anthropology, Georgia State University, <sup>2</sup>Anthropology, University of Indianapolis, <sup>3</sup>Anthropology, University of Wyoming

The Late Neolithic cave burials from the Belgian Meuse Basin represent one of the final dietary records of early farmers prior to the onset of the northern European Bronze Age. To reconstruct the dietary profiles of these Late Neolithic farmers, dental microwear texture analysis was conducted on deciduous and permanent molars from three well-studied caves, radiocarbon dated to ~4,635 to ~3,830 years before present, including Bois Madame (n=18), Maurenne Caverne de la Cave (n=24) and Sclaigneaux (n=25). Epoxy resin dental casts of the original dental impressions were created; these were scanned by a white-light confocal profiler and the resulting point cloud subjected to scale-sensitive fractal analysis. A comparative sample of foragers and food producers (n=645) contextualized the results. The three caves do not differ from one another in enamel textural complexity (*Asfc*) or anisotropy (*epLsar*), and both deciduous and permanent molar comparisons provide the same signal of overlapping dietary regimes. Regardless of chronology or geography, the individuals from these cave burials consumed a variety of coarse or poorly processed foods, resulting in elevated complexity (*Asfc* mean=1.928; standard deviation=0.539). The elevated anisotropy (*epLsar* mean=0.00231; standard deviation =0.00054) of the Belgian cave burials indicates a reliance on poor processing technology and/or wild foods that required considerable heterogeneous jaw movements to effectively process. The diets of Late Neolithic farmers of Belgium resemble those of paleoforagers of Lagoa Santa, Brazil and Archaic Indiana forager/farmers, and are dissimilar to a worldwide assemblage of farmers as well as agriculturalists of Early Bronze Age England.

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### Best Practice Guidelines for Gibbon Tourism: learnings from Cambodia and China

JESSICA L. WILLIAMS<sup>1</sup>, PENG-FEI FAN<sup>2</sup> and ALISON M. BEHIE<sup>1</sup>

<sup>1</sup>Biological Anthropology, Australian National University, <sup>2</sup>Life Sciences, Sun Yat-sen University

Nature-based tourism can be a useful conservation tool in regions of high biodiversity value if based in scientific research. Despite the existence of several gibbon focused programmes, there has been little investigation into the impact of tourist presence on the behaviour and/or stress of the gibbons. We collected data on the northern yellow-cheeked crested gibbon (*Nomascus annamensis*) at Veun Sai-Siem Pang National Park (VSSPNP) and the Skywalker hoolock gibbon (*Hoolock tianxing*) at Mt. Gaoligong National Nature Reserve (GNNR), China with the aim of extending the IUCN's best practice guidelines for great ape tourism to include gibbons. We also surveyed tourists who participated in both tourism programmes. The observed gibbons spent significantly less time resting and more time scanning and *N. annamensis* gibbons were more likely to self-groom when in the presence of tourists. Faecal cortisol levels were not found to respond to tourism. Surveys of tourists revealed that only international tourists participated in the program at VSSPNP, while the program at GNNR attracted mostly domestic travellers. Using these two case studies, we present the first best practice guidelines for gibbon tourism, helping both existing and new gibbon tourism programmes to balance animal welfare with increasing tourist demand and stakeholder expectations.

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### Inferred lifestyle better explains variation in lumbar wedging than inherent population differences

SCOTT A. WILLIAMS<sup>1,2</sup> and IRIS ZENG<sup>1,3</sup>

<sup>1</sup>Center for the Study of Human Origins, Department of Anthropology, New York University, <sup>2</sup>New York Consortium in Evolutionary Primatology, <sup>3</sup>Department of Architecture, MIT

Clinical studies on modern human spinal curvature are abundant, and several techniques for quantifying lordosis using medical images of living people have been formalized. However, the fragmentary nature of the human osteological and hominin fossil records does not allow the direct application of these methods; therefore, researchers have relied on the wedging of lumbar vertebrae and other osteological correlates of lordosis to extrapolate the degree of lumbar lordosis in the archaeological and paleo-anthropological contexts. Previous research on lumbar wedging suggested that modern human

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populations vary in degree of lumbar lordosis. Cunningham (1886) argued that Europeans have more lordotic lower backs than various populations of “savages,” which he argued retain a primitively less lordotic lumbar column. Cunningham also argued that vertebral wedging is not affected by mechanical influence during one’s lifetime. Here, we examine bony wedging of lumbar vertebrae and test for differences between recent cadaveric humans and a global sample of non-urban, pre-industrial people represented in archaeological samples. We find significant differences between both sexes of these two groups but no significant differences between geographically-defined groups within each larger category. Therefore, we argue that lifestyle (e.g., postural traditions, furniture use, and activity) plays a significant role in the plasticity of lumbar vertebral body shape, especially during development. Potentially, recent European and American populations demonstrate greater lordosis on average than non-urban, pre-industrial archaeological populations not because they are better adapted to upright posture but rather due to poor posture and inadequate core muscular support, requiring exaggerated bony contribution to lordosis.

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### Evaluating the stress of malarial infection and other environmental factors in a 5th century CE Umbrian community through the mother-infant dyad

JORDAN A. WILSON<sup>1</sup>, DAVID G. PICKEL<sup>2</sup> and TIMOTHY NEWFIELD<sup>3</sup>

<sup>1</sup>Anthropology, The University of Arizona, <sup>2</sup>Classics, Stanford University, <sup>3</sup>Biology/History, Georgetown University

Because of the special metabolic and immunological relationship that exists between a mother and a developing infant, fetal and neonatal health can provide unique information about the external environmental conditions that existed during gestation and lactation. This poster presents updated research on 59 fetal, infant, and child remains from the ongoing excavation of the late antique (5th century CE) infant and child cemetery at Poggio Gramignano, located near the Umbrian town of Lugnano in Teverina, Italy. This cemetery is the largest known Roman infant cemetery and thus highly unique. Past research centered on these infant remains has provided some of the most robust evidence of *Plasmodium falciparum* malaria in the premodern world, a parasitic disease which poses increased risk to pregnant women and infants. Comparing fetal individuals to neonates, our skeletal analysis shows the emergence of pathological lesions indicative of hematopoietic disease and nutritional deficiencies in the very early postpartum period (before eight weeks). These results suggest high rates of maternal infection in the second and third

trimester of pregnancy, resulting both in preterm delivery and nutritional stress in infants before and after birth. Our findings are interpreted within a biocultural framework that considers how a rural context, which contrasted sharply with urban Rome, impacted infant and maternal health, especially in terms of sanitation, diet and nutrition, disease ecologies, and female parity. This study demonstrates the utility of using fetal and neonatal remains as a proxy for maternal health and, by extension, community health.

### Applying a holistic body of evolutionary theory to the practice of forensic anthropology

ALLYSHA P. WINBURN<sup>1</sup> and MICHALA K. STOCK<sup>1,2</sup>

<sup>1</sup>Anthropology, University of West Florida,

<sup>2</sup>Sociology and Anthropology, Metropolitan State University of Denver

The discipline of forensic anthropology has been critiqued for its lack of a theoretical basis. In response, practitioners often assert that their analyses are implicitly grounded in evolutionary theory. However, the nature of this theoretical grounding is little discussed in the forensic anthropology literature, beyond, for example, statements indicating that sex-based pelvic differences have evolved in response to increasing encephalization within the genus *Homo*, or that clinal variation in features like nose form have evolved within our species due to environmental pressures that differ on a gradient. As evidenced by a PubMed review of publications between 1970-present in the *Journal of Forensic Sciences* (JFS) and the *American Journal of Physical Anthropology* (AJPA), of 2,055 articles discussing biological profile analysis, 46/497 (9.3%) in the JFS and 483/1558 (31.0%) in the AJPA contain reference to evolutionary theory, adaptation, or selection. The role of natural selection in shaping the morphologies analyzed in biological profile estimation is undeniable. Yet, adaptation in response to environmental pressures does not explain all variation within our species. Further, evolutionary theory is not monolithic; different perspectives on the primacy of functional adaptation versus structural constraint can lead to differences in interpretation of human skeletal morphology and lead researchers to novel approaches in creating new or improving current methodologies. Various theoretical perspectives underpin forensic anthropological analyses, and in order for forensic anthropology to be truly grounded in evolutionary theory, these theoretical perspectives must be not only made explicit but also interrogated in terms of how they inform forensic anthropological interpretations.

### Bioethics as a dynamic issue: Holistic approaches to understanding and applying ethics to study design

TAIYE WINFUL

Department of Anthropology, Genetic Anthropology and Biocultural Studies Laboratory, Vanderbilt University, Nashville, TN

Anthropologists have challenged bioethicists to incorporate more holistic approaches to applying ethics in ‘real world’ situations. Where bioethicists tend to use systematic philosophical approaches to moral dilemmas, anthropologists apply malleable approaches designed to be responsive to variable cultural contexts. For example, anthropologists emphasize the importance of community and the effects of social issues, political economy, and cultural tradition in decision-making. This difference in approach contributes to the contentious relationship between anthropologists and bioethicists. Despite nuanced perspectives, anthropologists have not enjoyed a durable role in shaping contemporary bioethics.

The lack of nuance becomes problematic when researchers attempt to reconcile ethical issues against a standard of morality rather than what Patricia Marshalls defines as a “culturally constituted and continually evolving” process. Reflecting on the IRB review of my work with African descendants in the United States and Nigeria, I will discuss the importance of conceptualizing bioethics as a dynamic issue, especially when working with communities abroad. Comparing these review processes is instructive about the organizational structures, influenced by culture and society, that impact decision-making in respective communities. In this presentation, I suggest that a focus on the way that IRB reviews are done can also offer insights and contextualization into community decision-making. Within a cross-cultural setting, considerations of the IRB review processes can lead to more informed conversations on bioethics and can aid researchers in applying more holistic approaches to study design.

### The lasting impact of pandemics – changing demography of 1918 Influenza survivors

AMANDA WISSLER

School of Human Evolution and Social Change, Arizona State University

Epidemics have substantial power to alter human biology, demography, and culture. Previous studies of the Black Death have shown that the post-Black Death populations had increased survivorship for almost two centuries, likely due to a combination of factors including a “culling effect” on the weakest members of society. Though not as deadly as the Black Death, the 1918 Influenza Pandemic killed an estimated 50 million people globally. Demographic studies using historical records data show that average

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US life expectancy decreased by as many as 10 years in the period immediately following the pandemic. Despite the enormous impact of this event, it is unclear if and how population health and survivorship changed for those who survived the pandemic. This study tests whether the 1918 Influenza Pandemic had a lasting impact on survivorship after 1918. Demographic data were collected on a sample of individuals (N=663) who died before and after the 1918 pandemic from the Hamann-Todd documented skeletal collection. The data were analyzed using Kaplan-Meier survival curves and logistic regression. Results demonstrate that post-pandemic individuals have a statistically significant increase in survivorship compared to pre-pandemic individuals with post-pandemic individuals living, on average, about 5 years longer. These results build on previous anthropological studies of epidemics, enhancing our understanding of the long-term impacts of epidemic events on human biology and society. Furthermore, these results are broadly applicable to the current COVID-19 pandemic, informing predictions of how the SARS-CoV-2 virus may shape population health and demography in years to come.

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### Accounting for Neanderthal ancestry differences in Eurasians using archaic SNP identification and simulations

KELSEY E. WITT<sup>1,2</sup>, FERNANDO VILLANEVA<sup>1,2,3</sup> and EMILIA HUERTA-SANCHEZ<sup>1,2</sup>

<sup>1</sup>Center for Computational and Molecular Biology, Brown University, <sup>2</sup>Department of Ecology and Evolutionary Biology, Brown University, <sup>3</sup>Department of Anthropology, University of Colorado - Boulder

Neanderthal ancestry is found in all modern Eurasian populations, although it is distributed unevenly – East Asians have more Neanderthal ancestry than Europeans. Multiple demographic models have been suggested to explain this difference, including additional archaic gene flow from Neanderthals into the ancestors of modern East Asians and “dilution” of Neanderthal ancestry in Europeans due to gene flow from an unadmixed modern human population. To attempt to understand this difference, we identified archaic SNPs in modern Eurasian human populations (sequenced by the 1000 Genomes Project) and compared patterns of individual- and population-specific archaic coverage between the European (EUR) and East Asian (EAS) populations. While East Asians and Europeans carry approximately the same number of archaic alleles across the population, East Asians have a higher rate of allele sharing between individuals and therefore a larger number of Neanderthal variants per individual than Europeans. We then ran simulations

using demographic models consistent with the “additional archaic gene flow” and “dilution” hypotheses to test which demographic scenario was most consistent with a larger per-individual allele count but similar per-population allele count in East Asians as compared to Europeans. While neither demographic model individually replicates the empirical results, combining these models results in an allele distribution across individuals and populations that is similar to that found in modern Eurasians. Therefore, the distribution of Neanderthal alleles across modern Eurasians is the result of multiple interactions between Neanderthals and modern humans, and gene flow between modern humans with archaic ancestry and unadmixed populations.

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### Intra-individual variation in the cross-sectional geometry of the first metatarsal, femur, and tibia

JESSICA WOLLMANN and MICHELLE CAMERON  
Department of Anthropology, University of Toronto

Cross-sectional geometric properties (CSGP) of leg bones can inform about levels of terrestrial mobility. Typically, these analyses focus on the femur and tibia, but it is questioned if metatarsals are equally informative. This study examines femora, tibiae, and first metatarsals to evaluate variation in the CSGP between groups with different mobility patterns and the relationship between CSGP of bones within the lower limb. The sample consists of protohistoric Andaman Islanders (n=28) and Holocene (10,000 – 2,000 BP) Later Stone Age (LSA) Southern Africans (n=36). Data were acquired from past studies of these groups. Mann Whitney U-tests and multivariate statistics evaluated variation between groups. Ordinary least squares regression evaluated the intra-individual relationships between CSGP of the femur, tibia, and first metatarsal. LSA Southern Africans had significantly more robust femora and tibiae, but not first metatarsals, than Andaman Islanders. LSA Southern Africans also had a much broader range of variation in CSGP. The strength of relationships between the CSGP in the leg is dependent upon loading pattern. Additionally, while the femur and tibia are always closely related, the relationships to the first metatarsal are variable. LSA Southern Africans are more terrestrially mobile than Andaman Islanders and have a wider range of variation in their CSGP, but these differences are not reflected in first metatarsals. The femur and tibia experience similar patterns of loading, specifically in compression and tension, but this loading pattern is different in the first metatarsal. First metatarsals do not reflect the same biomechanical patterns as seen in the leg.

### Histological changes in midline basicranial synchondroses across age in *Saguinus*

BRODY WOOD<sup>1</sup>, HALEY CORBIN<sup>2</sup>, JANE TAYLOR<sup>2</sup>, CHRISTOPHER VINYARD<sup>4</sup>, JAMES CRAY JR.<sup>2</sup>, VALERIE B. DELEON<sup>5</sup> and TIMOTHY SMITH<sup>1</sup>

<sup>1</sup>School of Physical Therapy, Slippery Rock University, <sup>2</sup>Department of Biomedical Education and Anatomy, The Ohio State College of Medicine, <sup>3</sup>Department of Biology, Slippery Rock University, <sup>4</sup>Department of Anatomy and Neurobiology, Northeast Ohio Medical University, <sup>5</sup>Department of Anthropology, University of Florida

Previously, the timing at which basicranial synchondroses cease growth activity has been implicated in development of basicranial angulation in anthropoids, especially humans. However, few primate species have been studied histologically. Here, we examine microanatomy of the spheno-occipital synchondrosis (SOS) and intrasphenoidal synchondrosis (ISS) at three post-natal stages in a tamarin (*Saguinus oedipus*). We serially sectioned and stained heads of newborn, one-month-old, and juvenile cadaveric tamarins. The zone of proliferating chondrocytes (ZPC) at each age was then assessed for the presence of proliferating nuclear cell antigen (PCNA), using immunohistochemistry. Both synchondroses remain patent in all specimens from birth to juvenile stages. PCNA reactivity is detected in the ZPC of both synchondroses at all ages. At the early ages, SOS had better organization than ISS, with more numerous chondrocytes organized into longitudinal rows. The most notable change across age is a marked reduction in cross-sectional area of the ZPC relative to the total cross-sectional area of both synchondroses, especially in the juvenile compared to the younger aged specimens. Furthermore, in the juvenile the longitudinal rows of proliferating chondrocytes was reduced to only two to four cells in both synchondroses. Our findings imply synchondroses are of greatest importance for promoting longitudinal growth in tamarins during infancy. Our findings also reveal ISS patency is prolonged in at least one New World primate. In contrast, previous work has demonstrated early (perinatal) fusion of the ISS in humans. Further work should determine whether early ISS fusion is a human, or hominoid characteristic.

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### Evolution of hominin pelvic sexual dimorphism

MIRELLA A. WOODERT<sup>1</sup>, VIKTORIA A. KRENN<sup>1,2</sup>, CINZIA FORNAI<sup>1,2</sup>, NICOLE M. WEBB<sup>1,3</sup> and MARTIN HAEUSLER<sup>1</sup>

<sup>1</sup>Institute of Evolutionary Medicine, University of Zurich, <sup>2</sup>Department of Evolutionary Anthropology, University of Vienna, <sup>3</sup>Department of Palaeoanthropology, Senckenberg Research Institute and Natural History Museum Frankfurt

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The marked sexual dimorphism in pelvic shape of modern humans is traditionally attributed to a tradeoff between adaptation to bipedal locomotion and obstetric sufficiency. Accordingly, sexual dimorphism is assumed to be minor in great apes and in small-brained *Australopithecus*. We therefore hypothesize that pelvic sexual dimorphism correlates with birth difficulty and a tighter cephalopelvic fit during hominin evolution. As the central portion of the hipbone is best preserved in fossils, we focused our analysis on two sexually diagnostic characteristics of modern humans, the greater sciatic notch and the arc composé. Our sample comprised multiple reconstructions of A.L. 288-1 and KSD-VP-1/1 (*Australopithecus afarensis*), Sts 14, Sts 65 and StW 431 (*A. africanus*), MH1 and MH2 (*A. sediba*), KNM-WT 15000, KNM-ER 3228 and OH 28 (*Homo erectus*), the Neanderthals from La Chapelle-aux-Saints and Kebara, modern humans (n=130), and *Pan*, *Gorilla*, and *Pongo* (n=40). The shape of the greater sciatic notch and the arc composé was quantified on surface models using 3D geometric morphometric methods and 6 fixed and 5 sliding landmarks. The principal component analysis of Procrustes shape coordinates showed a clear separation of the sexes in modern humans driven by greater sciatic notch shape and the presence of an arc composé in females, and also the fossil hominins plotted according to their presumed sex. The results were independent of the reconstructions of the fossil remains. In contrast, the great apes showed extensive overlap of the sexes. This might suggest that obstetric selection was already present in early hominins including australopithecines.

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### Identifying the timing of puberty in a modern skeletal sample from the United States

JORDAN T. WRIGHT and JONATHAN D. BETHARD  
Anthropology, University of South Florida

Biological anthropologists investigate the onset and progression of puberty in order to gain insight into marked social changes surrounding the transition to adulthood in both contemporary and past populations. It is well known that numerous factors influence the pubertal growth spurt and the implication of this reality is important for biological anthropologists interested in contemporary human skeletal biology, as well as for those researchers interested in understanding how pubertal growth has changed over time. Recent work by Henderson and Padez (2017) examined pubertal timing in the Coimbra Identified Skeletal collection and demonstrated that females matured faster than males. In this study, skeletal markers of puberty described by Lewis et al. (2015) were recorded from CT scans drawn from the New Mexico Decedent Image Database

(n=400). The average age of the female cohort (n=197) was 16.72 years and the average age of the male cohort (n=203) was 15.39 years. As expected, females' progression of puberty was, on average, earlier than that of males in the sample. Menarche was found to have been achieved by an average age of 16.17 years and males reached deceleration at a mean age of 16.27 years. This study demonstrates that pubertal growth can be assessed from CT scans in order to understand adolescent growth in contemporary populations. Detrimental factors known to be associated with membership of marginalized groups such as low socioeconomic status and food insecurity may have delayed skeletal development and the onset of puberty of some individuals in the study sample.

### Longitudinal body mass variation of individuals from 20 strepsirrhine populations at the Duke Lemur Center

GABRIEL S. YAPUNCICH  
Evolutionary Anthropology, Duke University

Body mass is an important biometric that covaries with many other ecological variables in primates. Although there have been some efforts to quantify body mass variation within primate populations, the degree to which body mass varies within an individual over their adult lifespan has received little attention. Here, using historical data, longitudinal variation in body mass is calculated for 357 adult individuals representing 20 captive strepsirrhine populations at the Duke Lemur Center. All recorded body masses of an individual were binned into biannual "seasons" and the time intervals with the densest representation within a population (a minimum of eight seasonal observations of eight individuals) were identified for analysis. Body masses measured during known illnesses or pregnancies were excluded. In most populations (n=17), mean individual coefficients of variation (CVs) were constrained between 4.96 and 8.26. Cheirogaleids, which experience large fluctuations of body mass associated with seasonal torpor, exhibited substantially larger individual longitudinal CVs (*Cheirogaleus medius*: 12.49; *Microcebus murinus*: 14.01). *Daubentonia* individuals showed less longitudinal variation (2.49) than other strepsirrhines. There were no significant correlations between individual CVs and individual body mass. Across all populations, females exhibited significantly greater longitudinal variation (median CV=7.17) than males (median CV=5.84). On average, individual CVs were 63% as large as CVs calculated across the population, so that throughout their adult life, individuals achieved approximately two thirds of the variation observed across a population at any one time. Overall, these results highlight the dynamic nature of body mass in adult strepsirrhines.

### The second epidemiological transition: Survivorship and industrialization in London

SAMANTHA L. YAUSSEY<sup>1</sup>, SHARON N. DEWITTE<sup>2</sup> and GAIL HUGHES-MOREY<sup>3</sup>

<sup>1</sup>Department of Sociology, Social Work, and Anthropology, Utah State University, <sup>2</sup>Department of Anthropology, University of South Carolina, <sup>3</sup>Department of Biology, Russell Sage College

The second epidemiological transition describes a shift in the most common causes of death in human populations from infectious diseases to degenerative (non-communicable) diseases. In England, the transition began in the mid-1800s, and though there is relatively reliable historical data on age at death and cause of death following the transition, there is less information available regarding age at death in the periods prior to the transition. Previous bioarchaeological work examined mortality patterns prior to the transition in London but relied on conventional age estimates that are biased and not informative about demographic patterns at later adult ages (>45 years). In this study, we examine the relationship between adult age at death and time period in individuals from four sites in London (New Churchyard, New Bunhill Fields, St. Bride's Lower Churchyard, and St. Bride's Church Fleet Street) prior to and during the period of industrialization (c. 1569-1853 CE) using Kaplan-Meier survival analysis. Adult (>15 years) age-at-death was estimated using the method of transition analysis (second edition). Survival analysis results indicate significantly lower survivorship among individuals prior to industrialization (c. 1569-1670 and 1670-1739 CE) compared to individuals in the industrial period (c. 1740-1853 CE) ( $p < 0.001$ ). These results suggest that, in London, survivorship was improving in the mid- or late 18<sup>th</sup> century, prior to the recognized beginning of the second epidemiological transition itself and resulting in older mean ages at death for individuals in the industrial period compared to previous centuries.

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### Leveraging the Language of Modern Video Creation in Science Engagement

KATRINA E. YEZZI-WOODLEY<sup>1</sup> and SAMANTHA T. PORTER<sup>2</sup>

<sup>1</sup>Anthropology, University of Minnesota, <sup>2</sup>Liberal Arts Technologies and Innovation Services, University of Minnesota

All forms of media, from academic journal articles, to television and film have their own "language." This language is the unique way words and visuals are used to convey meaning. Regular consumers of these media become versed in these languages, even if they are not consciously aware. Thus, if a piece of media breaks from the

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expected language the reader / viewer can find it jarring, perplexing, or simply uninteresting. For example, bad film editing and cinematography can produce a viscerally negative or derisively humorous reaction in viewers.

Like the forms of media mentioned above, modern social media content platforms have their languages and tropes. In order to effectively leverage these platforms for science communication, one must also become fluent in these languages. In this poster, we synthesize common elements of the language of YouTube. Specifically, we list and provide examples of common elements of popular vlog style videos, for example, cut-aways, pop-ups, animations, editor commentary, and reaction videos. We demonstrate how these elements can be leveraged to create videos on human evolution that are engaging to modern viewers, particularly youth, by creating a video using an example from paleoanthropology.

By providing a starting lexicon of this language, we hope to aid science communicators in creating engaging content for a younger social media savvy audience.

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### Javan gibbons select their sleeping trees to avoid predation and not because of intraspecific competition based on long-term data

YOONJUNG YI<sup>1,2</sup>, AHYUN CHOI<sup>2</sup>, RAHAYU OKTAVIANI<sup>3</sup>, SAEIN LEE<sup>2</sup>, HYEIN JO<sup>3</sup> and JAE C. CHOE<sup>3</sup>

<sup>1</sup>College of biology and environment, Nanjing Forestry University, <sup>2</sup>Interdisciplinary Program of EcoCreative, Ewha Womans University, <sup>3</sup>Division of EcoScience, Ewha Womans University

Sleeping related behaviors are critical for individual fitness in relation to predation and/or intraspecific competition. We conducted a long-term study to investigate characteristics of sleeping trees in a diurnal primate, the Javan gibbon (*Hylobates moloch*) in Gunung Halimun-Salak National Park, Indonesia. We collected data on sleeping trees from three habituated gibbon groups over 392 days (n = 910 data points) from 2014 to 2020. During the study period, gibbons used 35 tree species and preferred relatively tall and thick trees (i.e. *Altingia excelsa*:62%, *Lithocarpus sundaicus*: 12%). Adult females and males from the same group slept on different trees in 84% of cases. Even though the gibbons reused 27% of sleeping trees more than once, 70% of reused trees were reused only once, suggesting that they have relatively numerous sleeping trees. They also reused sleeping trees at least several months later. Moreover, as in other *Hylobates* species, the Javan gibbons did not move once they sat on the sleeping trees, suggesting that their sleeping tree selection and sleeping related behaviors are

potentially related to anti-predator strategies. We observed two sleeping tree individuals used by different gibbon groups during the study period, indicating the likely absence of strong competition over sleeping trees. Our results indicate that sleeping trees might be a limited resource, although not limited enough to be a subject of severe competition in Javan gibbons.

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### Toward the understanding of dietary adaptation of *Gigantopithecus blacki*: A bite force analysis on lower postcanine dentition

ZHIXING YI

School of Earth Sciences, China University of Geosciences (Wuhan)

**Objective:** Bite force (BF) is an important indicator in dietary reconstruction. The bite force was systematically analyzed for mandibular cheek teeth of *Gigantopithecus blacki*.

**Methods and Materials:** Sixteen permanent mandibular teeth (Chui Feng cave and Mohui Cave, Guangxi, China) were scanned by micro-computerized tomography, followed by routine processes to generate virtual mesial sections. Two parameters, cuspal enamel thickness (CET) and dentine horn angle (DHA), were measured on the functional cusp of mesial sections. A recent study, using both fracture experiments and Finite Element Analysis, demonstrated that bite force can be estimated on tooth cusp and a corresponding equation, linking BF to CET and DHA, was proposed. This method was adopted to assess BF.

**Results:** The average molar BF is 1512N, which is larger than taxonomically broad primate taxa. Besides, *G. blacki* shows a distal-ward reduction in BF, with the average BF of premolar (2217N) being approximately 1.5 times that of molar. This distal-ward BF reduction is mainly attributed to the distal-ward DHA increment, but not to the slight distal-ward CET increment.

**Discussion:** In a new way, the great BF strengthened previous consensus that *G. blacki* is capable of consuming food that hard to crush/abrade. The significant BF difference between premolar and molar suggests their different roles in feeding processes. A possible scenario is that hard food is crushed into small particles by premolars owing to larger BF and the subsequent grinding process is mainly performed by molars due to larger occlusal surface area.

### Changing patterns of variability in human lower limb skeleton during growth and the implications for human evolution

AN-DI YIM<sup>1</sup> and CHARLES C. ROSEMAN<sup>2</sup>

<sup>1</sup>Department of Anthropology, University of Illinois at Urbana-Champaign, <sup>2</sup>Department of Evolution, Ecology, and Behavior, University of Illinois at Urbana-Champaign

A population's response to natural selection is dependent on the variational properties of its phenotype. While the variational properties of human limb skeleton are well-studied in adults, it is currently unknown whether or how variation changes during ontogeny (growth and development) within or among different groups. This study compares the cross-sectional variance-covariance (VCV) matrices of femur and tibia linear measurements across different age stages in a sample of two contemporary groups of different geographic origins (n = 650 for South African children aged 0-15 years; n = 791 for American children aged 0-18 years). We found that VCV matrices of the two groups are highly correlated in corresponding age stages (r ranges for femur: 0.912-0.999; for tibia: 0.973-0.996) except for the juvenile period (7-11 years of age, r = 0.750 for femur, 0.713 for tibia), this is consistent with juvenile growth period being more variable, both in timing and growth rate. Additionally, we found the VCV matrices change drastically during growth for both groups. Using relative eigenanalysis to visualize the change of VCV matrix in covariance space, we found that VCV matrices of the two samples move through covariance space differently in both breakdown by age stage and breakdown by year comparison. The results show that the covariance structure of human limb skeleton is not constant during growth, and that each group has its unique patterns of change. This indicates natural selection will have differing effects across different age stages and in different groups.

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### Investigating the relationship between the mental and mandibular foramina, tooth root surface areas, and diet

CAITLIN B. YOAKUM and CLAIRE E. TERHUNE

Anthropology, University of Arkansas

The inferior alveolar nerve (IAN) enters the mandible via the mandibular foramen, supplies nervous sensation to the mandibular teeth, and exits via the mental foramen to supply all sensation to the lower lips and gums. While some research has examined the relationship between mental foramen diameter and diet, little work has examined the relationship between diet, tooth root surface area, and the cross-sectional area (CSA)

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of both the mental and mandibular foramina. While the enamel surface of teeth is the primary interaction point with food items, the tooth roots are the anchors within the mandible that provide support and nerve/vessel pathways. This study aims to examine the relationship between the mental and mandibular foramina and root surface area, and the relationship between the root surface area and diet in 49 species of primates ( $n = 126$ ). PGLS regressions for all tooth classes ( $M_1$ ,  $P_4$ ,  $C_1$ ,  $I_1$ ) found significant relationships between root surface area and mandibular length ( $p < 0.001$ ,  $R^2 = M_1:0.88$ ,  $P_4:0.83$ ;  $C_1:0.91$ ;  $I_1:0.89$ ). A PGLS for root surface area and foramen CSA showed significant relationships for both the mandibular foramen ( $p < 0.005$ ;  $R^2 = M_1:0.91$ ,  $P_4:0.89$ ,  $C_1:0.73$ ,  $I_1:0.80$ ) and mental foramen ( $p < 0.001$ ,  $R^2 = M_1:0.63$ ,  $P_4:0.63$ ;  $C_1:0.68$ ;  $I_1:0.60$ ). No significant relationships were found between root surface area and primary diet, though results hinted at a relationship between molar and incisor root surface area and frugivorous and folivorous secondary diets. This study provides a framework for future work examining the relationship between the above hard-tissues, the surrounding soft-tissues, and the IAN.

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### Assessing the migration of early farmers in the American Southwest through biological and cultural markers

AARON J. YOUNG<sup>1,2</sup> and JAMES T. WATSON<sup>1,2</sup>

<sup>1</sup>School of Anthropology, University of Arizona,

<sup>2</sup>Arizona State Museum, University of Arizona

The biological consequences of migration increase the genetic and phenotypic diversity and resilience among small-scale communities. Differences in the presence of projectile point type during the Early Agricultural period (EAP) (2100 BC-AD 50) in the American Southwest indicate that migration likely occurred from northern Mexico into the Tucson Basin. A projectile point, endemic to northern Mexico, appeared in the Tucson Basin during the early San Pedro phase of the EAP and disappeared from the Basin during the following phases. The authors test this migration hypothesis by comparing mortuary patterns among sites in the Tucson Basin and northern Sonora. Our comparison indicates that groups at both geographic locations practiced a unique mortuary pattern. Mortuary patterns for individuals postdating the early San Pedro phase in the Tucson Basin are dominated by flexed body position (89%) and north-south orientation (64%). These patterns are not present among individuals from northern Sonora or individuals in the Tucson Basin dating to the early San Pedro phase. These findings support that migration into the Tucson Basin during the early part of the EAP likely occurred, which resulted in the display of a distinct social identity that then disappeared due to the assimilation of groups into the dominant local

identity. This assimilation was likely concomitant with genetic admixture that assured the biological viability of these small-scale communities and contributed to successful adaptation and, eventually, population growth.

### Assessing Asymmetry in the Platyrrhine Postcrania

LIAM M. ZACHARY and LESLEY H. EASON

Anthropology, University of Arkansas

Postcranial skeletons are rare in the primate fossil record. In this context, determining whether left and right specimens of the same skeletal element belong to the same individual is important for accurate paleobiological reconstructions of taxa. A better understanding of the degree of postcranial asymmetry in extant primate clades can aid in these determinations. Here, asymmetry was assessed in paired (left and right) postcranial elements of platyrrhines using three-dimensional geometric morphometrics (3DGM). Paired skeletal elements belonging to the same individual were predicted to be morphologically more similar to each other than to elements belonging to different individuals. Homologous landmarks were collected on the left and right talus and distal humerus of four atelid species ( $n=4$ ). Landmark sets were collected twice, and both trials were included in subsequent analyses to assess the impact of intraobserver error. Trials on the same specimen cluster together in the PCA plot of the GPA-aligned coordinates, and the left and right specimen pairs are clearly separated along the PCA axes. The results suggest that for platyrrhine tali and distal humeri, left and right pairs can be matched using 3DGM. Results also support the use of samples with both left and right tali and distal humeri for comparative morphological analyses. However, homologous landmarks may not be the best method for evaluating postcranial asymmetry because there were instances where error on the same specimen exceeded differences between left and right specimens. Further study is needed to assess postcranial asymmetry in other primate clades and skeletal elements.

### Upper and lower ribcage covariation across ontogeny in human males and females

SARAH M. ZALESKI

Anthropology, University of Florida

Previous research has shown that sexual dimorphism in human adult thoracic morphology relates to divergent growth trajectories between males and females. Other research demonstrates that the upper and lower thoracic regions differ in ontogenetic shape change. The current study tests for sex differences in upper and lower ribcage covariation across ontogeny using decedent computed tomography data from the Center

for Forensic Imaging at the University of New Mexico. The sample includes 44 females and 48 males, aged 0-21 years. I collected three-dimensional landmark coordinate data representing thoracic shape in SlicerMorph and completed geometric morphometric analyses in R Geomorph and Morpho. Results from a two-block partial least squares analysis indicate significant covariation ( $p=.001$ ) between the upper and lower ribcage across ontogeny, with both regions most prominently showing mediolateral expansion, increased rib curvature, and rib lowering with age increase. The first latent variable explains 95.9% of the total covariation. A comparison of slopes between males and females shows similar patterns of upper and lower ribcage covariation. The magnitudes of this covariation in sex-specific two-block partial least squares analyses are also similar. These results suggest that the observed thoracic dimorphism in adults does not stem from sex differences in upper and lower ribcage covariation across ontogeny. A common relationship between thoracic size and shape in males and females of this sample suggests that allometry plays a key role in adult sex differences in thoracic shape.

### A reassessment of the variability of *Homo erectus*: the case of analyzing different cranial regions

CHI ZHANG

Anthropology, University of Pittsburgh

Most previous geometric morphometric analyses (GMAs) have consistently shown that *Homo erectus* is less variable than *Homo sapiens* or various non-human primate species based on analyzing variations in overall cranial shapes. Less attention has been paid to individual cranial bones. Therefore, this study examines whether GMAs focusing on different cranial regions can yield differential variabilities of *Homo erectus*. For this purpose, semilandmark and landmark datasets that cover the entire cranium, the posterior cranium, the temporal region, and the frontal region were collected from 3D models of fossil and extant hominin crania (including 35 *Homo sapiens* crania). Variability within a group is calculated as the sum of pairwise Procrustes distances (SSD) between specimens. To determine whether *Homo erectus* is significantly more variable than *Homo sapiens*, the SSD of *Homo erectus* is compared with 10,000 SSDs of *Homo sapiens* randomly generated by the bootstrap method. Principal component analysis (PCA) was used to visualize patterns and degree of overall variations among individual specimens. Results show that the temporal and frontal bones of *Homo erectus* are significantly more variable than *Homo sapiens*, whereas the entire and posterior cranial shapes are not. This incompatibility is likely because the analyses of individual bones place more weight on small-scale, localized variations

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than do the analyses of the entire and posterior cranium, as demonstrated by PCA. Overall, this study suggests that future GMAs should also analyze individual cranial bones and localized variations to provide a comprehensive understanding of *Homo erectus* variability.

### Intraspecific Shape Variation in the Primate Cranium and Mandible: a Quantitative Genetics Approach

JULIA M. ZICHELLO<sup>1,2,3</sup>, CHRIS ROBINSON<sup>3,4,5</sup> and CHARLES ROSEMAN<sup>6</sup>

<sup>1</sup>Department of Natural Sciences, College of Mount Saint Vincent, <sup>2</sup>Division of Anthropology, American Museum of Natural History, <sup>3</sup>New York Consortium in Evolutionary Primatology, CUNY, <sup>4</sup>Department of Biological Sciences, Bronx Community College, <sup>5</sup>Doctoral Program in Anthropology, The Graduate Center, CUNY, <sup>6</sup>Department of Evolution, Ecology and Behavior, University of Illinois at Urbana-Champaign

Identifying patterns of crano-mandibular shape variation *within* extant primate species is central to understanding the processes that influence morphological evolution. Here we use a quantitative genetics approach which brings together population genetic data with intraspecific crano-mandibular shape data. The central aim is to determine if taxa with more shape variation in the skull are also those that are more genetically diverse at neutral loci. We quantified intraspecific shape variation in the primate cranium, and the mandible, in 11 extant hominoid taxa using 3D geometric morphometrics. Two major objectives of this study are: 1) determine if the magnitude of intraspecific shape variation in the mandible is congruent with neutral genetic diversity ( $\pi$ ) for each taxon. 2) Compare results from the cranium to those from the mandible. Previous work has shown that cranial vault shape variation within hominoids is consistent with neutral genetic diversity. Surprisingly, our results here show that the magnitude of shape variation in the hominoid mandible is also largely congruent with neutral genetic diversity. This is unexpected given the selective and developmental pressures on the mandible related to mastication. Importantly though, humans are the exception and do not follow this pattern. Mandibular shape variation in humans exceeds the expectations of neutrality. We hypothesize that greater shape variation in the human mandible compared to other primates is driven by human dietary heterogeneity. This quantitative approach can further decipher how evolutionary processes have shaped the extant primate skull and provide a new lens for understanding shape variation within extinct hominin species.

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### Determinants and influences of infant spatial relationships with adult males in a wild primate: a mechanism for intergenerational transmission of early adversity?

MATTHEW N. ZIPPLE<sup>1</sup>, CHELSEA A. SOUTHWORTH<sup>2</sup>, STEFANIE P. CLINTON<sup>1</sup>, ELIZABETH A. ARCHIE<sup>2,3</sup> and SUSAN C. ALBERTS<sup>1,3,4</sup>

<sup>1</sup>Biology, Duke University, <sup>2</sup>Biology, University of Notre Dame, <sup>3</sup>Institute of Primate Research, National Museums of Kenya, <sup>4</sup>Evolutionary Anthropology, Duke University

A primate infant's experience during early life is heavily influenced by characteristics of its biotic environment, including characteristics of its mother and its broader social environment. For example, infant baboons are more likely to die if their mothers experienced high levels of early life adversity. These intergenerational effects may be mediated by differences in the social environment experienced by infants born to mothers that experienced high levels of early adversity. Adult males play an especially important role in infants' experience by providing protection and a zone of relative safety in which an infant can develop. Here we present the most detailed analysis to date of the determinants of the immediate adult male social environment that infants experience and the influences of adult males on a wide range of infant behaviors. We show that the average number of adult males within 5m of infant baboons is significantly repeatable over time ( $R = 0.15$ ) and that this repeatability is partially explained by the levels of early life adversity experienced by the infant's mother. We also show that the number of adult males in close proximity to an infant predicts a wide range of fundamental infant behavioral traits, including the mother-infant spatial relationship, infant activity budgets, and the frequency of both positive and negative social interactions with non-mothers. Our results are consistent with the possibility that the effects of maternal early life adversity can be transmitted, in part, via differences in the early life social environments that infants of high-adversity mothers experience.

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