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diet and sedentary lifestyle, we predicted greater age-related dysregulation in laboratories. But if costs of a wild lifestyle accelerate aging, we expected greater age-related dysregulation at the sanctuary, whose environment better approximates the wild. We found that semi-free-ranging chimpanzees exhibited lower overall dysregulation ($x_2=70.67$, $p<0.001$) and lower age-related change in dysregulation ($x_2=6.25$, $p=0.01$). Age slopes in sanctuary chimpanzees (0.06) were lower than laboratory chimpanzees (0.22), as well as previously published slopes for industrialized humans (0.14) and forager-horticulturalists (0.17). We further found that although neither population show significant differences in dysregulation by sex, they exhibit distinct aging profiles across different body systems ($p<0.001$): while sanctuary chimpanzees showed fastest dysregulation in immune system biomarkers, laboratories dysregulated fastest in circulatory and liver/renal markers. This provides some insights into the specific ways that different lifestyles impact aging outcomes.

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Modularity and mosaic evolution in the macaque skull: A study of multivariate shape variation in phylogenetic context

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Mosaic evolution of the primate skull is expected to be facilitated by the skull's modular organization, where relatively-autonomous anatomical modules are determined by genetic, developmental, and functional factors. In this preliminary study, we used craniometric data to explore patterns of modularity and mosaic evolution in the skulls of 14 living species of the genus *Macaca*.

We analyzed 66 linear skull measurements, collected from one representative adult male specimen for each species. The measurements were transformed to dimensionless log-shape variables (where a specimen's "size" was defined as the log-transformed geometric mean of its measurements) and then standardized to z-scores. Our working phylogeny for *Macaca* was drawn from published molecular studies. To explore the data for evidence of modularity and mosaic evolution, we employed the Parins-Fukuchi clustering procedure, using the program *greedo*. In addition to identifying evolutionary modules, *greedo* can estimate relative rates of shape change across a phylogeny.

Surprisingly, the Parins-Fukuchi algorithm only finds a single, well-delineated module (essentially, the entire skull) in our best-fitting model. This result suggests that modular autonomy within the

Macaca skull is not as clear-cut and pronounced as we might expect from theory or from published studies that have been carried out at higher taxonomic levels. Our examination of relative rates of shape change revealed that rates were highest within the *fascicularis-arctoides* species groups, while rates in the *silenus* species group (including Sulawesi taxa) were considerably lower.

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Microstructure and Homology in the Human Upper and Lower Limb

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Whether the fore- and hindlimbs of tetrapods are serially homologous elements or developmentally and evolutionarily distinct remains a point of contention among researchers. Additionally, organisms that display functional divergence between the fore- and hindlimbs, such as humans, show less integration of morphological traits. This study analyzes the microstructure of long bones from the upper and lower limbs of humans to establish any relationships in vascularization and bone proportion in paired elements (ulna/fibula and humerus/femur). We predicted that due to functional divergence of the upper and lower limbs in humans compared to quadrupedal organisms and the different developmental trajectories of fore- and hindlimbs, there will not be a similarity between the paired elements, but that fore- and hindlimb elements will show differences in microstructure. A modern American cadaveric sample of 9 females and 10 males (15–105 y.o. (sd=29.87)) was evaluated using histologic samples from the midshaft of the ulna, humerus, fibula, and femur. Osteon population density, porosity area percentage, and bone area percentage were collected. Data were analyzed using an ANOVA and Tukey's HSD to evaluate the cross-sectional microstructure relationship between paired and unpaired elements. Results from both tests indicate that there is no significant difference in tested variables among any of the elements since paired "homologous" elements were as similar to each other as they are to other unpaired counterparts. While homology may be contributing to the similarities between appendages, microstructural features do not support any divergence due to functional differences.

Birthing Across the Diaspora: Making Sense of Embodiment through Black Parenting and Pregnancy

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Low birthweight (LBW) is tied to a wide range of both long- and short-term adverse health outcomes including increased risk of infant mortality, and cardiovascular diseases and metabolic diseases in adulthood. Currently, about 13% of Black infants are born LBW annually, compared to the national average of 8.5%, with the overall LBW rate increasing steadily over the last decade. While it is hypothesized that exposure to systemic and cultural racism have made Black women and their infants especially vulnerable to adverse outcomes in pregnancy and birth, the particular biocultural mechanisms that drive the high rates of LBW have yet to be fully elucidated. Using cohort data from the National Longitudinal Study of Adolescent to Adult Health study, we find that Black women experienced statistically significant rates of LBW ($P<0.001$), and that they were significantly likely to have been diagnosed with high blood pressure ($p<0.001$) and diabetes ($p<0.001$), as well as reporting recent experiences of "feeling blue" ($p=.026$). Notably, these self-diagnoses of poor mental health are not accompanied by increased formal diagnoses of depression, anxiety, or PTSD. Black feminist theory reimagines the relationship between Black women's bodies, subjectivities, and experiences of oppression and resistance—a useful framework for further theorizing biocultural embodiment for biological anthropologists working with Black women. This presentation engages Black feminist scholarship to contextualize the subjective experiences of Black women navigating pregnancy amidst disproportionately high experiences of poor mental and physical health, highlighting the social contexts and political stakes of LBW outcomes.

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An analysis of cranial and pelvic covariation, with implications for the evolution of cephalopelvic disproportion in non-human primates

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Cephalopelvic disproportion and its potential impact on human pelvic evolution has been a focus of anthropological research for over 70 years. Recent research on anthropoid primate sexual dimorphism has indicated that obstetric selection may affect multiple primate lineages rather than being a hallmark of the hominin lineage



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alone. Additionally, the proposed method of selection, mismatch between the size of the cranium and the size of the pelvic canal, implies that the cranium and pelvis may be coevolving and that traits in these two skeletal regions may therefore covary. While covariation between the adult cranium and pelvis has been shown in humans, this has yet to be explored in many non-human primate lineages. Here, we test patterns of covariation between the cranium and pelvis of four genera with different hypothesized levels of cephalopelvic disproportion: *Hylobates* and *Cebus* (high cephalopelvic disproportion), *Alouatta* (low cephalopelvic disproportion), and *Lophocebus* (expected average cephalopelvic disproportion) using two-block partial least squares analysis. Results indicate high rates of covariation between the cranium and pelvis ($r\text{-PLS} > 0.9$, $p = 0.0001$) across all taxa, with bigger pairwise differences among taxa when genera with high cephalopelvic disproportion (*Hylobates*, *Cebus*) are compared to genera with low (*Alouatta*) or average (*Lophocebus*) cephalopelvic disproportion. This supports the idea that the cranium and pelvis covary and that this relationship may be stronger in lineages with high levels of reported cephalopelvic disproportion. Our results have implications for the role that obstetric selection may have played in shaping cephalopelvic disproportion across multiple anthropoid lineages.

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An archaeogenetic and paleopathological evaluation of an early medieval Iberian community at La Olmeda (Spain, 6th – 11th c. CE)

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The period spanning Late Antiquity and the Early Middle Ages in the Iberian Peninsula was characterized by social, political, and economic shifts. Urbanization and widespread migration are thought to have altered the genetic landscape of the local post-Roman population. While mobility

can be closely tied to the spread of infectious disease, limited historical sources from this period in Iberia hinder the reconstruction of the epidemiological landscape.

Here we present molecular and morphological analyses of human remains from the Roman Villa at La Olmeda (Palencia, 6th – 11th c. CE). We studied 49 individuals spanning 500 years and evaluated them for 1) changes in genetic ancestries over time, 2) ancient pathogen DNA, and 3) skeletal evidence of infectious disease. Our results contribute to the debate on the timing of the introduction of African ancestry into NW Iberia, with genetic data indicating that North African ancestry was already present in this area before the arrival of Islamic peoples, alongside an individual with a genetic profile similar to modern-day Basques. Despite an absence of contemporary written references, tuberculosis, brucellosis and malaria were identified in this population. All of these diseases may offer insight into the mysterious fevers mentioned in contemporary historical sources from this region. Additionally, the genetic identification of malaria disproves a published hypothesis that malaria was absent in early medieval Iberia.

This interdisciplinary study offers a new perspective on the timing of the introduction of African ancestry into Iberia and challenges previous understandings of the epidemiological landscape in early medieval Iberia.

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Cultural World Heritage Sites: An imbalance of conservation techniques and funding between the global north and global south using Laetoli, Tanzania, East Africa animal and human trackways as a case study

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A critique of UNESCO's Global Strategy for a Balanced, Representative, and Credible World Heritage List is given, representing the disproportion of sites in the global north and the global south. The global north currently holds the majority of sites on the World Heritage List, with a substantial proportion of funding being fueled into maintenance and conservation of these sites. This leaves sites in the global south highly neglected and at a higher risk for damage and/or destruction due to inadequate funding and unsubstantial conservation efforts. In order to scrutinize this problem, a case study of the animal and human trackways in Tanzania, East Africa will be employed. The current state of the Laetoli footprints show signs of weathering, erosion, and anthropogenic

damage. Locality 7, Site A presently exhibits severe cracking and water runoff depreciation. This is irreparably damaging both hominin and animal footprints. Hominin footprints from 3.6 million years ago are incredibly important since they assist paleoanthropologists in answering one of the fundamental questions in anthropology – the evolution of bipedal locomotion. Animal trackways are significant because they assist anthropologists in constructing paleoecologies and assess evolutionary pressures. Encouraging conservation techniques could be implemented at Laetoli that would address the degradation of the trackways, while benefitting the locals and economy.

The variation of maternal and fetal energy requirements and their role in birth timing

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The traditional view that bipedalism-related pelvic constraints and larger brain size are the primary cause of human birth difficulties has been challenged numerous times in recent years. As an alternative, the "Energetics of Gestation and Growth" (EGG) hypothesis proposes that maternal metabolic limitations and fetal energy requirements play a central role in the neurological immaturity and secondary altriciality observed in human neonates. According to the EGG hypothesis, labour is initiated when exponentially increasing fetal energy requirements surpass the maximum maternal metabolic capacity, suggested at around 2.0–2.1×basic metabolic rate (BMR). However, our analysis of 11 additional studies on pregnant females with varying geographic and socioeconomic backgrounds revealed an enormous variability in maternal metabolic scope that also partly exceeded the 2.1×BMR threshold. Further, recent data from athletes indicate a sustained metabolic ceiling of about 2.5×BMR that cannot realistically be crossed by fetal energy demands. Via calculating fetal energy requirements during pregnancy based on weight data of over 25 million livebirths, we found rapid growth until week 35 with substantial tapering thereafter. This finding contradicts the exponential growth pattern of fetal energy requirements towards the end of pregnancy and the starvation of the fetus immediately before birth posited by the EGG hypothesis. Rather, it supports recent research indicating a more intricate interplay of factors affecting birth timing, e.g., fetal membrane senescence and decidual inflammation. Birth timing thereby requires more