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Sex differences exist across a range of human diseases, that to date have been understudied and largely unexplained. For example, females in industrialized populations exhibit a higher prevalence of most autoimmune diseases than do males. By contrast, females have a lower risk of developing cancer, with nearly all cancers showing a higher incidence in males. Here we present the Pregnancy Compensation Hypothesis (PCH), which explains both the proximate and ultimate (evolutionary) mechanisms responsible for sexual dimorphism observed in human disease, as mediated by selection on the immune system due to pregnancy and placentation. We suggest that because evolution has shaped the human immune system differently in females and males, dramatic shifts in our reproductive ecology and environment have led to sex differences in diseases to be more pronounced in urban, industrialized contexts. Under the PCH, we propose that the evolution of eutherian placentation exerted sex-specific selection on female immune function to tolerate fetal antigens while still defending the pregnant individual against pathogens. We theorize that this process is regulated proximately via hormones and mediated genetically by dosage on sex chromosomes, and that today, the mismatch between an ancestral environment and urban industrial environment interacts with this evolved compensatory immune regulation and results in the observed sex differences in disease risk. Finally, a sedentary lifestyle that affects reproductive hormone levels exacerbate these differences. We unpack the interrelated components of the PCH related to shifting reproductive states, parasite loads, and energetic availability, which are particularly relevant for sex differences in human disease.

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Observing Similarities of Pre and Post-Contact Cranial and Dental Modification in Two Sites from Western Mexico (1350-1580 AD)

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Barra de Navidad, Jalisco (1580±90 AD) and Amapa, Nayarit (1350±60 AD) are two sites located in modern day Western Mexico. These sites were settled by agricultural communities similar to those in central and southern Mesoamerica. This region widely practiced cranial and dental modification throughout both the Pre-Columbian and Post-Contact periods. A total of 7 individuals from Barra de Navidad (6) and Amapa (1) were analyzed for such cultural modifications. At Barra de Navidad (2) and Amapa (1), 43% of the sample population presented tabular oblique cranial deformation. Whereas 29% of the

sample population had dental modification in the form of filed teeth - 1 young adult male from Barra de Navidad and 1 young adult female from Amapa. The male from Barra de Navidad had filed central and lateral maxillary incisors. The female from Amapa also displays tooth filing, but unfortunately only the left central maxillary incisor was present for analysis. Patterns of tabular oblique cranial deformation fit a pattern observed through Western Mexico and Southern Mesoamerica that relate to social status and identity. In contrast, patterns of dental filing may be representative of different clan lineages, or performed as a rite of passage into adolescence. Considering the distance between both sites and the different time periods, it is interesting that the same patterns of dental modification are found in both sites. We suggest that although the pattern of dental filing is the same, it is not indicative of clan lineage but rather, may represent a rite of passage.

Dengue susceptibility and resistance in a Guatemalan cohort: incorporating an evolutionary perspective using signatures of natural selection

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Evolutionary medicine seeks to incorporate perspectives from medicine, public health, and anthropology to understand how our evolutionary past affects our overall health in the present. We implement this approach to understand how past selection shapes modern genetic susceptibility to Dengue Virus. DENV is a mosquito-borne RNA virus belonging to the family Flaviviridae. It is widespread in subtropic and tropic environments, with up to 390 million infections each year. We leveraged indigenous American genomic signatures of selection to identify resistance and/or susceptibility loci to this modern pathogen in a Guatemalan cohort. We recruited dengue infected (60) and uninfected (120) participants from health centers throughout Guatemala. Infection was confirmed using the InBios DENV Detect IgG and IgM Capture ELISA method. Exome sequence data were generated using the IDT xGen Exome Research Panel. SNPs showing significant associations with DENV-infection were identified with logistic regression that used an additive model of inheritance. Covariates including control for population stratification were

included in the model. Functional impact of the significant SNPs was assessed using the Encode track of UCSC Genome Browser. This determined if significant SNPs lie in regions characterized by H3K27Ac marks, DNase I hypersensitivity, or ChIP-seq transcription factor binding and/or in regions characterized by miRNAs, snoRNAs, or lincRNAs. Furthermore, gene ontology analysis was conducted to reconstruct potential pathways affected by DENV-infection. Our results demonstrate the effect of past selection on modern infectious disease risk, bridging the gap between the medicine and anthropology—directions to which anthropology can steer the conversation towards an evolutionary framing.

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Did *Pierolapithecus* have an ape-like thorax? 3D shape analysis of the *Pierolapithecus catalaunicus* lower rib IPS21350.58 and its implications for understating its bauplan

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Pierolapithecus catalaunicus (12 Ma; Vallès-Penedès Basin, Spain) is a middle Miocene ape from NE Iberian Peninsula considered a stem hominid (i.e., early member of the great-ape-and-human clade). Even though there are signals of monkey-like features in its pelvis, other evidences point to a modern ape-like orthograde bauplan. This is partly based on the ribs morphology, indicating an ape-like wide and shallow ribcage, different from the narrow and deep monkey ribcage. However, the information about its ribs is based on qualitative comparisons, so an accurate 3D quantification is necessary to confirm this assessment. Here we use 3D geometric morphometrics of 8 landmarks and 44 semilandmarks per rib to explore if the best-preserved rib of *P. catalaunicus* (IPS21350.58) had an ape-like or monkey-like morphology. To explore that, we compared it with a sample of central-lower ribs (N=376) from extant monkeys (*Macaca*,

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Ateles, *Alouatta*), apes (*Pan*, *Pongo*, *Hylobates* and *Symphalangus*) and humans (*Homo*). PC1 clearly separates monkeys (negative scores) from apes and humans (positive scores), IPS21350.58 clearly plotting in the positive scores, close to the ribs 7-8 from *Pan* and *Pongo*. The negative values of PC1 are linked with elongated ribs dorsoventrally with no torsion, whereas the positive values are linked with curved ribs dorsoventrally with some torsion. Therefore, assuming individual rib/ribcage covariation, it is highly likely that *P. cata-launicus* ribcage was ape-like, confirming previous results. Finally, the fact that monkey-like features have been found in its pelvis, along with the modern ape-like ribcage morphology, suggests a mosaic evolution of the hominid torso.

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Elemental signatures and growth defects in teeth show differential morbidity and mortality tied to variable weaning and dietary practices among missionized Guale on the Georgia coast (ca 17th century).

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The DOHaD hypothesis represents an important theoretical shift in bioarchaeology regarding how we interpret indicators of early life stress, adult health, and age-at-death. Considerations of cultural context, however, are necessary for more meaningful interpretations of links between childhood stress and subsequent mortality risk. This paper explores the implications of weaning age and diet for childhood stress and mortality risk among indigenous Guale interred at Mission SCDG (ca. 17th century) on St. Catherines Island, Georgia. One canine from 52 individuals were analyzed for internal enamel micro-defects (ASR) as indicators of childhood stress. Of these teeth, 28 were incrementally sampled for barium (Ba/Ca) values to estimate weaning age, and six were incrementally sampled for $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ values to reconstruct early life diet. Enamel defects are prevalent in the canines (96%), and individuals with the highest frequencies of ASR experienced increased risks for early death. Variations in childhood stress and subsequent mortality risk were in part related to weaning age and marine versus maize-based food consumption. A Cox hazard analysis indicates that weaning age is a significant predictor of age-at-death and ASR frequency. Moderate correlations also exist between ASR frequency and average post-weaning $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ values. These data suggest that individuals who weaned early and consumed less marine resources experienced heightened stress and mortality risks. Conversely, variations in these

experiences indicate that while Spain's political-economy was detrimental to indigenous health, some parents were faced with opportunities (e.g. weaning and dietary resources) to buffer their children from stress and long-term negative health outcomes.

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Growing during a catastrophe: ontogeny of body size and femoral bone strength in Late Medieval and Post-Medieval Europe

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Patterns of endochondral and appositional skeletal growth may vary between populations with shifts in subsistence economy, nutritional status, living conditions, and labor practices. Studies have demonstrated delayed growth in stature and body mass in populations experiencing significant environmental stressors. However, few studies have demonstrated similar growth delays in bone mass and strength.

This study compares ontogenetic trajectories of subadult body size and bone growth in two cemetery assemblages: Barton-upon-Humber (14th-19th centuries AD, Lincolnshire, UK, n=112) and Alytus (14th-18th centuries AD, Lithuania, n=153). Barton-upon-Humber experienced relative environmental and economic stability, with little evidence of disease. Whereas, Alytus had a high prevalence of malnutrition and infectious disease alongside periodic catastrophic events (war, famine, plagues), impacting health and survivorship. Growth in body size (stature, body mass), appositional growth (percent femoral cortical area [%CA]), and overall bone strength (polar section modulus [Zp]) and rigidity (polar second moment of area [J]) were compared. Alytus is expected to exhibit delayed growth in body size, elevated endosteal resorption (decreased %CA), and reduced bone strength.

Results indicate that stature and body mass are similar between assemblages during early childhood but diverge in older childhood and adolescence, with significantly smaller body size in Alytus. Additionally, appositional growth and bone strength are significantly lower in early childhood at Alytus relative to Barton-upon-Humber but similar in older childhood and adolescence. Comparing contemporaneous samples with distinct health profiles, results

support assertions for the influence of environmental perturbations on appositional growth in early developmental periods and body size in later stages of development.

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Faunal species identification from basic skeletal measurements: Differentiating 21 medium-to-large sized mammals

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Physical anthropologists commonly encounter faunal remains at field sites and in the laboratory, and the majority of remains presented to forensic anthropologists are actually non-human. Without an extensive zooarchaeological or comparative anatomical background, determining the non-human species from an isolated bone can be challenging. This study tests the ability of basic skeletal measurements to classify single bony elements into 21 North American faunal species. Fifty-eight length and breadth measurements were defined that could be collected reliably across 21 medium-to-large sized mammalian species (16 genera, 9 families). Data were collected from available humeri, radii, ulnae, femora, tibiae, fibulae, scapulae, ossa coxae, and fused metapodials from 652 individuals (~400 per element). Step-wise discriminant function analyses with a leave-one-out cross-validation were performed to evaluate accuracy in assigning each bone to its appropriate order, family, genus, and species. Species classification accuracies for long bones that were characterized by at least four measurements ranged from 75.8 to 92.0%, performing better than elements represented by fewer measurements. The humerus and femur were among the most reliable and higher performing elements, and when the two elements were combined species classification was 90.0%. As would be expected, taxa exhibiting greater size and morphological variation (e.g., Bovidae), and those with morphological similarities (e.g., dog vs wolf and coyote) displayed higher classification errors. The high classification rates, despite discriminating 21 species, suggest that a few basic measurements are highly useful for faunal species identification and may be used by physical anthropologists with limited faunal expertise to narrow down potential species.

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