of fossil brains problematic. Our ongoing work improves our understanding of current endocranial variability, which will allow more useful comparisons between extant humans and non-human *Homo* species.

Neurodevelopmental disorders as models for developmental interactions between brain and skull in human evolution

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The brain and skull develop and function as a tightly integrated system. This integration allows us the use of endocasts as proxies for the brain in extant and fossil specimens, affording the only direct evidence of brain evolution. As evolution occurs via changes in development, differences in endocast morphology among taxa result from divergent developmental patterns. However, it is unclear whether this affects the interdependence of brain and skull, and therefore the associated endocasts. One strategy for addressing this question is through study of distinct craniofacial morphologies within a species. For example, a number of developmental disorders have characteristic brain and skull features, such as Down Syndrome, Fetal Alcohol Syndrome, and Autism Spectrum Disorders.

In this study, premature cranial suture fusion, craniosynostosis, serves as an example for studying brain/skull interaction in differing craniofacial shapes. Size and shape of the brains and endocasts as measured from magnetic resonance images (MRIs) are statistically compared among four groups of infants with morphologically distinct head shapes following approved IRB protocols: infants with unilateral coronal, metopic, or sagittal craniosynostosis, and typically-developing infants. Results demonstrate no significant differences in brain or endocasts volumes among groups. However, volume of subarachnoid space (between brain and endocranium) differs significantly, with the location of increased/decreased space differing among groups. Surprisingly, the range of variation in all measures was greater within groups than among them. These results demonstrate additional study of both intra- and inter-specific variation in brain/skull interaction is needed to accurately interpret the fossil record.

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Migration Waves and Genetic Drift in the Peopling of Fuego-Patagonia

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The human colonization of Fuego-Patagonia is plagued with questions regarding the origin, timing and routes followed by its first colonizers (inland hunter gatherers), as well as the origin of later, highly specialized, marine populations. This study presents results obtained based on the analysis of mtDNA extracted from 20 prehistoric teeth, dated between 7,200 and ~700 cal yrs BP, and 38 modern individuals (Kawesqar, Mapuche-Huilliche and Yagan). The analysis shows that prehistoric settlers carry three distinct Native American founding haplogroups (C1, D1 and D4h3a), whereas modern groups correspond to the C1b, C1b13, D1, D4h3a, and B2i2 haplogroups among others. The prevalence of D1 and C1 haplogroups among modern Mapuche-Huilliches in the region (38.5% and 53.8% respectively) likely respond to a later migration, during historic or protohistoric times, that reflects the influence of populations from central Chile and Argentina that introduced lineages C1b13 and B2i2, while they mixed with local, long-time, resident groups. Haplogroups D1 and C1 account for most of the variation among the Yagan (40% each) which likely reflects processes of genetic drift characteristic of groups of small size, and the population decimation that resulted from the introduction of new diseases associated with European and Criollo colonization. Among modern Kawesqar 60% of those sampled present the D4h3a haplogroup, which is also found in prehistoric marine settlements in the archipelagos of Patagonia? This later haplogroup may reflect a second migration wave composed by individuals adapted to marine life that were moving along the Pacific coast, as early as 6,500BP.

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Beauty, brains, and brawn: phylogenetic and ecological interpretations of new virtual endocasts of large-bodied subfossil lemurs

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Extant primate suborders Strepsirrhini and Haplorhini display distinct endocranial shape differences that are correlated with suborder differences in encephalization and brain proportions. However, endocranial shape possesses a strong allometric component that may confound suborder differences, as modern anthropoids occupy a greater body size range than do extant strepsirrhines. Large-bodied subfossil lemurs expand the range of strepsirrhine body size and ecological diversity to greater overlap with haplorhines, allowing us to more fully evaluate the relationship between phylogenetic, allometric, and ecological correlates of endocranial diversity within and between primate suborders.

Virtual endocasts were reconstructed from micro-CT scans of subfossil lemur crania from the Duke Lemur Center (*Mesopropithecus*, *Archaeolemur*, *Babakotia,* and *Hapalemur*). A 3D morphometric analysis was conducted including a comparative sample of 54 extant primate species. Principal Component (PC) scores from Procrustes-aligned landmark sets were tested for correlation to endocast volume (ECV), body size (reconstructed from craniodental dimensions), and diet category (estimated from upper molar shear quotients).

Despite their large bodies and—in the case of *Archaeolemur*—relatively large brains for lemuroids, the subfossils are distinctly strepsirrhine-like in endocast shape. PC1 separates strepsirrhines and haplorhines, and is correlated with residual ECV (RSquare=0.33, $p<0.001$). PC2 weakly correlates with body mass (RSquare=0.12, $p=0.04$), indicating that strepsirrhine and haplorhine endocasts "get big" in somewhat the same fashion, while retaining key characteristics that are diagnostic of their suborder and related to brain proportions rather than overall size. Finally, residual ECV estimates for subfossil lemurs are not consistent with a strict relationship between diet and encephalization among strepsirrhines.

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On the edge of the empire: A craniometric analysis of group affinities from an Ottoman garrison in western Romania

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Recently, 160 human skeletal remains were excavated from the city center of Timişoara, Romania. This cemetery dates to the 15th and 16th centuries, a brief but dynamic time period when the Ottoman Empire expanded into Central Europe and utilized Timişoara as an important defense center. The inhumations are a representative sample of the population relocated into the fortified center during the ~150 years of Ottoman occupation. Here, we present a comparative study of craniometric variability that aims to better understand the population history of this group.

An inter-observer analysis of eight skulls from Howell's craniometric database was conducted to ensure comparability of data. Thereafter, 38 measurements were obtained from 28 crania in the Timişoaran sample. Two geographically-proximate populations from the Howell's database – Berg and Zalavar – were

employed as comparative data. Principal Component Analyses of size-adjusted data show broadly overlapping similarities among the three populations. However, MANOVA found all three groups to differ significantly, suggestive of different among-group shape patterns. Moreover, statistical analyses comparing males and females from the three groups indicate a substantial difference in average shape between the Timişoara males and females not found in the other two groups. These results might indicate inflated sexual dimorphism compared to the other European populations, or a different migration history for the Ottoman males and females buried in Timişoara. This study illustrates how biological data and historical information can be combined to better understand the effects of migration and military expansion in the past.

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Patterns of mutations in exome sequencing seen as an effect of sampled genes

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Human mutations are generally studied as individual or genome-wide approaches, and rarely the patterns of variations are studied for samples of genes for a group of individuals. This study shows the patterns of human variation for a group of genes, in order to assess the effects of gene sampling on the quantity of variations.

We performed whole-exome sequencing in 36 individuals and sampled 1000 lists of 143 random genes, from 16000 genes and performed a counting of variants found in each list. Each variant was separated by their impact on the protein in ten categories, frameshift, splicing, stopgain/stoploss, nonframeshift indels, missense (separated by in silico prediction of pathogenecity from zero to five), and synonymous. After the separation each individual had their variants counted as benign (population frequency above 0.05), polimorfism (frequency between 0.05 and 0.01), rare (frequency below 0.01), and private (exclusive of the individual). The quantity of variantions were normalized by the total of mutations in each category of mutations in each list.

We found that for mutations predicted to be loss-of-function there is not a clear separation of ratios between the frequencies groups, but for synonymous and missense mutations predicted as benign there is a clear separation and the quantitiy of benign mutations is not smaller than 0.1 for missense and 0.05 for synonymous. The ratio of private frameshift mutations is not superior to 0.25, and nonframeshift indel mutations have more benign variants than missense variants with pathogenicity three.

Mosaic and homoplastic evolution of the hominoid skeleton precludes 'overall' ancestral reconstructions based on single-taxon models

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For more than a century, models of human evolution have been guided by competing hypotheses of phylogenetic relationships. The 'molecular revolution' resolved the *Gorilla-Pan-Homo* trichotomy and, in combination with later paleontological discoveries and molecular clock advances, they confirm that *Pan* and *Homo* are sister taxa sharing an African last common ancestor (LCA) approximately 7-6 Ma. This finding is the primary basis of the 'chimp-like LCA paradigm,' which posits that *Pan* is a 'living fossil' reflecting the behavior, anatomy, and overall biology of the LCA.

The current fossil record is rich with partial skeletons of extinct apes and hominins that form part of the project presented here that analyzes the evolution of selected postcranial regions from a morphometric and phylogenetically informed viewpoint. Our results reveal stepwise mosaic evolution of the skeleton (i.e., fossil hominoids have no extant analogues) and pervasive homoplastic evolution of traits related to specialized antipronograde behaviors. Extinct and extant primate taxa can provide good LCA models for *specific* regions, but not for the whole organism –implying that Cuvier's principle of correlation of parts does not apply to hominoid evolution. Our results highlight that phylogenetic proximity does not necessarily predict phenotypic evolution. This inference agrees with modern genomics: humans and *Pan* share ~98% of their genes, but they exhibit remarkable phenotypic differences (resulting from changes in gene regulation rather than in the genes *per se*). Collectively, these results preclude using chimpanzees and bonobos as 'time machines' and indicate that fossils are critical in reconstructing the LCA's mosaic anatomy.

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Men's reproductive ecology and diminished hormonal regulation of skeletal muscle phenotype: An analysis of between- and within-individual variation among rural Polish men

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Human life history is characterized by several distinctive features—sexual division of labor, prolonged care of altricial young, multiple dependents of different ages, and male provisioning. Testosterone has been suggested to mediate a trade-off between men's reproduction and survival, through the regulation of sexually dimorphic musculature. This hypothesis predicts a relationship between testosterone and musculature in which mating effort, elevated testosterone, and dimorphic musculature covary positively. Testosterone is also posited to mediate a trade-off between mating and parenting effort, and accordingly, investing fathers show decreased testosterone production. Because men use their musculature not only in mating competition but also to support work demands, an important component of parenting effort, a relatively fixed relationship between testosterone and muscularity would seem maladaptive. We hypothesize that men's parenting effort, specifically provisioning and subsistence activities, becomes a primary determinant of muscularity. Life history, anthropometric, and hormonal data were collected from 122 rural Polish men (at the Mogielica Human Ecology Study Site) during the summer harvest and for 103 of these participants in the winter. We found that fatherhood jointly predicted heavier workload and decreased testosterone, but positively predicted muscle mass and strength measures. Furthermore, within-individuals, men experienced intensified workload and suppressed testosterone during summer, along with a concomitant increase in muscularity and strength. These findings provide preliminary support for our model, termed the 'Paternal Provisioning Hypothesis'. Between and within individuals, men's provisioning and subsistence activities were robust predictors of muscular development and performance, whereas their testosterone levels had no appreciable effect on skeletal muscle phenotype.

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