Sex-biased evolutionary constraints: how cross-sex genetic correlations and evolvability affect the evolution of canine size dimorphism

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Sexual dimorphism evolves due to differing selective pressures acting upon males and females. One target of sexual selection in primates is the maxillary canine, for which among-species differences in absolute and relative canine size and magnitudes of dimorphism are well documented. Less well understood is the impact of sexual selection on the genetic architecture (e.g., intralocus sexual conflict) that constrains the independent evolution of males and females. Using a pedigreed sample of *Papio hamadryas* (females, n = 321; males, n = 138), seventeen measurements were collected from casts of the permanent maxillary dentition (mesiodistal length and bucco/labio-lingual breadth for all teeth, as well as canine height). Using these measurements, two parameters, evolvability and cross-sex genetic correlation, were quantified. Evolvability measures microevolutionary potential, with sexually dimorphic traits predicted to have high evolvability. Cross-sex genetic correlation is a measure of the potential for male and female traits to evolve independently. Highly dimorphic traits are expected to have low cross-sex genetic correlations compared to sexually monomorphic traits. In line with these predictions, we find that for both sexes canine size has relatively high evolvability, with male canine measurements having the highest evolvability of all measurements. The cross-sex genetic correlations for canine measurements were the lowest. This suggest that intralocus sexual conflict resulted in the evolution of sex specific alleles or allele regulation of canine size in *Papio*. If other primates follow this pattern, this conflict, in conjunction with different selective pressures on each sex, is essential in the evolution of canine size dimorphism.

Age filtration in paleoepidemeological research: a cautionary tale and ways forward

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Issues of equifinality and hidden heterogeneity plague paleodemographic and paleoepidemeological research. In their 1992 paper ("The Osteological Paradox: Problems of Inferring Prehistoric Health from Skeletal Samples") Wood and colleagues highlight three core challenges that afflict paleoepidemeological inference: demographic non-stationarity, selective mortality, and hidden heterogeneity. We believe at least one additional phenomenon must be added to the list: age filtration bias. By age filtration bias, we mean that the scientific sample available for study has been selectively and systematically filtered so that certain ages are overrepresented while others are underrepresented. Failure to account for this effect will lead to incorrect reconstructions of mortality hazard, a vital measure in paleoepidemiology. Worse, it can lead to incorrect estimates of parameters that are assumed not to depend on age. We simulated skeletal data that showed evidence of a nominal disease (n=100) both with and without age filtration using a three-state illness-death model, where the transition hazard from the 'well' (nonlesioned) to 'ill' (lesioned) state was constant and the level of age filtration was large but not implausible. Across 100 simulations, the reconstructed value for the transition hazard was systematically biased by -16% for the filtered case but was not biased for the unfiltered case. This suggests that caution be used in interpreting datasets for which age filtration may exist and will inhibit our ability to accurately interpret past epidemics. We close by offering ways forward, notably the use of Bayesian priors to model age filtration when it may exist but cannot be directly measured.

Differential use of arboreal substrates during leaping in free-ranging primates and squirrels

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Primates and squirrels are both highly adept at navigating complex arboreal environments despite their disparate locomotor and visual adaptations. Experimental data suggest that primates' wide binocular field enables them to engage in leaps landed accurately on relatively narrow substrates. Here, we evaluate whether wild primates navigating a natural environment leap to relatively narrower substrates than wild squirrels, which have a significantly narrower field of binocular vision. Videos of leaping in free-ranging *Sciurus carolinensis* (n=98) and *Cebus capucinus* (n=46) were filmed at Hiram College and La Suerte Biological Field Station, respectively. For leaps with trajectories roughly perpendicular to camera orientation, the diameter of landing and launch substrates as well as leap length were measured in DLTdv8 and scaled to animal trunk width.

Wild primates both launched from and landed on branches that were relatively narrower than those used by squirrels ($p < 0.005$). In 21% of leaps to branches narrower than the animal's trunk, squirrels landed on clusters of branches. Primates used exclusively single-branch landings even at very small relative substrate sizes. Additionally, we found no significant relationship between leap length and launch substrate diameter in the wild squirrels, mirroring experimental findings that launch substrate diameter does not impact force production during leaping in squirrels. The significant difference in landing branch size and single- vs multi-branch landing at small substrate size between wild squirrels and primates supports the suggestion that primates' visual adaptations may facilitate precise arboreal leaping.

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Identifying candidate SNPs shaping dental morphological trait expression

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Dental morphological data are utilized as proxies for genetic variation to address various hypotheses within biological anthropology. However, the exact biological and genetic mechanisms responsible for the regulation of these traits remain mostly unknown. Recent work has sought to determine if genetic variants responsible for guiding the regulation of various ectodermal traits may also direct dental morphological trait expression due to a shared developmental origin. Through this approach, researchers successfully identified single nucleotide polymorphisms (SNPs) of the EDAR and WNT10A pathways that influence the morphological expression of both teeth and hair (Kimura et al. 2009, 2015). Here, we expand on these efforts by comparing the prevalence of SNPs influencing hair morphological variation with population-specific cusp 7 frequencies.

Data on cusp 7 trait frequency and genetic variants associated with hair morphology were collected from the literature focusing on ten populations (China, Japan, Vietnam, Colombia, Mexico, England, Finland, Nigeria, Kenya, and Gambia). Pearson's correlation with Holm's correction was performed to explore associations between the population frequencies of hair morphology SNPs and cusp 7 expression. Out of the 45 SNPs examined, 12 demonstrated a significant correlation ($p \leq 0.05$) to cusp 7 frequency, four were positive (rs6658216, rs310644, rs6841926, rs6912993) and eight were negative (rs7349332, rs12896399, rs499697, rs12116609, rs345542, rs12030667, rs10173381, rs10903929). These results highlight