

modern Amerindians. Under this hypothetical scenario, detection of relict groups deriving from the former Palaeoamerican population is expectable somewhere in the New World. Cranial samples consisting of digitized images in lateral view were analyzed for twelve groups of modern Amerindians, Asiatics, and Australians, and Late Pleistocene and Early Holocene remains from Africa, Asia, Australia and the Americas. Statistical analysis was focused on the observation of within and between-group variability of specific functional components of the skull by means of geometric-morphometric techniques. Results showed that some modern Amerindian groups, like those from Baja California peninsula in Mexico, shows clear affinities with Palaeoamericans and Late Pleistocene Asian and African skulls, rather than with modern Amerindians. Climatic changes during the middle Holocene probably generated the isolation conditions which restricted the gene flow between Baja California inhabitants and Northern populations, which resulted in the temporal continuity of the Palaeoamerican traits to the present.

Comparison of Y-chromosome and mitochondrial genetic diversity in Panamanian Amerinds.

A. González-Oliver, M.S. Ascunce, C.J. Mulligan. Department of Anthropology, University of Florida.

Differential modes of inheritance between the Y chromosome and the mitochondrial genome enable one to test for sex-based differences in evolutionary history. Different marriage practices may leave a distinct genetic signature that is independent of other cultural traditions, shared ancestry or linguistic affiliation. Specifically, matrilineal marriage practices (husband moves to wife's house) may result in increased Y variation and decreased mitochondrial variation while patrilineal practices may result in the opposite pattern of variation. In this study, we compare Y-chromosome and mitochondrial variation in four groups of Panamanian Amerinds: Chibcha-speaking Ngöbé (n=32) and Kuna (n=26) and Chocopeaking Emberá (n=22) and Wounan (n=19). The Ngöbé, Emberá and Wounan practice patrilineal marriage customs, while the Kuna group is matrilineal. Seven Y-chromosome STRs (DYS19, DYS388, DYS389-I and II, DYS390, DYS391, DYS392, DYS393) were amplified in two multiplex reactions. Mitochondrial D-loop sequence data were collected on larger sample sizes in a previous study.

Y-chromosome haplotype diversity was lowest in the Kuna (0.8615) and slightly higher in the patrilineal groups, Ngöbé (0.9012), Emberá (0.9177) and Wounan (0.9649), although the differences were not significant. Mitochondrial diversity was lowest in the Kuna (0.59), intermediate in the Ngöbé (0.76) and highest in the Emberá (0.94) and Wounan (0.91). The distribution of mitochondrial variation is consistent with differences in marriage practices among these groups. The lack of significant difference in Y variation, despite high levels of diversity in the assayed STRs, suggests that other processes may be influencing Y-chromosome variation in these groups.

Social network structure and human/HIV coevolution.

S.M. Goodreau. Center for Statistics and the Social Sciences, Center for AIDS Research, University of Washington.

The microevolution of sexually transmitted pathogens results from both the evolutionary mechanisms of the pathogen and the social behavior of the host. Nevertheless, attempts to understand patterns of HIV-1 genetic variation among human hosts have generally assumed that the host population mixes randomly. Here I simulate eight types of dynamic sexual networks whose general features are derived from insights of sexual network studies: one panmictic population, four assortative mixing populations, two core-periphery populations and one bridge (commercial sex worker / client / client's wife) population. Network simulation is accomplished using exponential random graph modeling (ERGM), a general framework adopted from social network analysis that allows for statistical inference and simulation of arbitrarily complex dependence patterns among social relationships. HIV transmission and evolution are then simulated within these networks using a model for HIV evolution that incorporates elements of the virus's complex intrahost dynamics. Resulting phylogenetic trees are analyzed using 'skyline plot' methods (Pybus 2000), which allows for a coalescent-based maximum likelihood estimate of effective population size at all points in the past. Existing parametric models for population growth are found to fare well when applied to viral sequences from a randomly mixing human population, but rather poorly from populations with more realistic patterns of sexual partnering, often overestimating current host populations by one or more orders of magnitude. Implications for HIV epidemiology are discussed, along with a

discussion of ERGM as a potential tool for better integrating human social dynamics and pathogen phylogenetics in the study of human pathogen co-evolution.

Selective forces and size change in the evolution of sexual size dimorphism in primates.

A.D. Gordon. Dept. of Anthropology, University of Texas at Austin.

Presented here is a new synthetic quantitative genetics model based on 1) Lande's (1980, 1981) model for the response of continuous characters to selection and 2) Bulmer's (1971) model for the reduction of additive variability due to directional or stabilizing selection. This iterative selection model describes the effects of selection on dimorphism and sex-specific relative variation of size over multiple generations. It also detects whether populations have recently undergone selection for size increase or decrease. The model was used to investigate the evolution and maintenance sexual size dimorphism (SSD) in 103 populations of 67 species representing the major radiations within the Order Primates. Cross-specific analyses of indices of 1) sexual size dimorphism and 2) sex differences in relative variability of body mass used phylogenetically independent contrasts to evaluate relationships within primate radiations.

Some radiations demonstrate violations of Cope's Rule (increase in size through an evolutionary lineage) and Rensch's Rule (positive allometry of size dimorphism). For example, the *fascicularis* group of macaques is shown to have undergone dwarfing since its divergence from other macaques, and dimorphism is negatively correlated with size in these populations. Consideration of patterns of size decrease across primates suggests that natural selection may play a larger role in generating differences in sex-specific selection pressures than previously thought. These findings suggest that reconstructed behavior of fossil primates inferred from dimorphism data alone may be missing an important component affecting size dimorphism: the relative contributions of sexual and natural selection pressures. Supported by NSF Dissertation Improvement Grant BCS-0137344.

Genome-wide linkage analyses of human stature in pedigree samples from different ethnicities.

H.H.H. Göring¹, R. Duggirala¹, J.W. MacCluer¹, A. Kissebah², M.P. Stern³, B. Towne⁴, S. Williams-Blangero¹, J. Blan-