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Genetic Evidence for the Phylogenetic Relationship between Na-Dene and Yeniseian Speakers

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Abstract Ruhlen's hypothesis, based on linguistic evidence, for a common phylogenetic origin of Na-Dene and Yeniseian speakers is tested using genetic data. Gene frequency data for the Kets, the only surviving Yeniseian speakers, were collected during a field study in 1993. Data for several Na-Dene groups, as well as other New World and Siberian populations, were compiled from the literature. These data were analyzed using R-matrix, principal components analysis, and Mantel tests. In a comparison of 10 New World and Siberian populations using eight alleles, 55.8% of the variation was accounted for by the first principal component, and 22.1% of the variation was subsumed by the second principal component. Contrary to Ruhlen's interpretation of the linguistic data, analysis of the genetic data shows that the Na-Dene cluster with other Native American populations, while the Kets genetically resemble the surrounding Siberian groups. This conclusion is further supported by correlations that are higher when the Kets are considered unrelated to Na-Dene speakers, and an insignificant partial correlation between genes and language when geography is held constant, indicating that spatial patterning accounts for most of the variation present in these populations.

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KEY WORDS: NA-DENE, YENISEIAN, KETS, POPULATION GENETICS

High Levels of Y-Chromosome Differentiation among Native Siberian Populations and the Genetic Signature of a Boreal Hunter-Gatherer Way of Life

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Abstract We examined genetic variation on the nonrecombining portion of the Y chromosome (NRY) to investigate the paternal population structure of indigenous Siberian groups and to reconstruct the historical events leading to the peopling of Siberia. A set of 62 biallelic markers on the NRY were genotyped in 1432 males representing 18 Siberian populations, as well as nine populations from Central and East Asia and one from European Russia. A subset of these markers defines the 18 major NRY haplogroups (A-R) recently described by the Y Chromosome Consortium (YCC 2002). While only four of these 18 major NRY haplogroups accounted for ~95% of Siberian Y-chromosome variation, native Siberian populations differed greatly in their haplogroup composition and exhibited the highest Φ_{ST} value for any region of the world. When we divided our Siberian sample into four geographic regions versus five major linguistic groupings, analyses of molecular variance (AMOVA) indicated higher Φ_{ST} and Φ_{CT} values for linguistic groups than for geographic groups. Mantel tests also supported the existence of NRY genetic patterns that were correlated with language, indicating that language affiliation might be a better predictor of the genetic affinity among Siberians than their present geographic position. The combined results, including those from a nested cladistic analysis, underscored the important role of directed dispersals, range expansions, and long-distance colonizations bound by common ethnic and linguistic affiliation in shaping the genetic landscape of Siberia. The Siberian pattern of reduced haplogroup diversity within populations combined with high levels of differentiation among populations may be a general feature characteristic of indigenous groups that have small effective population sizes and that have been isolated for long periods of time.

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Low Levels of STRP Variability Are Not Universal in American Indians

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Abstract Data related to 15 short tandem repeat polymorphisms (STRPs) are reported for five Brazilian Indian populations, and a set of them compared with results previously reported for Asian, neo-Brazilian, North American, Iberian, and African populations. The low variability observed for these markers among the Suruí Indians is confirmed, but the other populations show variability levels that are similar to those found elsewhere. Previous suggestions of population bottlenecks in the prehistorical colonization of the New World were not confirmed. On the other hand, STRPs again showed to be good markers for the establishment of population relationships.

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Craniometric Variation in the Americas

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Abstract Craniofacial variation is investigated in Latin America and the Caribbean. The samples included in this study are two historic and one prehistoric sample from Ecuador; prehistoric and modern Cuban samples; a prehistoric Peruvian sample; two prehistoric Mexican samples and one contemporary admixed Mexican sample; a 16th/17th-century Spanish sample; and Terry blacks. Biological distance is investigated using traditional craniometrics by computing size and shape variables according to Mosimann and colleagues. This study shows that there is much biological variation within the Americas.

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KEY WORDS: NEW WORLD, CRANIOMETRICS, MULTIVARIATE STATISTICS, HUMAN VARIATION

Genomic Diversities and Affinities among Four Endogamous Groups of Punjab (India) Based on Autosomal and Mitochondrial DNA Polymorphisms

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Abstract Nineteen insertion/deletion and restriction site polymorphisms on autosomal and mitochondrial genomes and mitochondrial DNA hypervariable segment 1 sequences were used to study genetic diversities and affinities among four endogamous groups of Punjab, India. High values of heterozygosity were noted in all four groups, both in the autosomal and mitochondrial genomes. The coefficient of gene differentiation among the groups, however, was found to be low. Genetic distance and phylogenetic analyses based on these data indicated that inferences on affinities among the populations were different when the two sets of loci (autosomal and mitochondrial) were considered separately. We have interpreted these results on the basis of some known historical data on migrations into this region. The results of this study when compared with the findings of some previous studies indicate that there are regional differences in the patterns of correlation between genomic and sociocultural affinities within India.

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Origin and History of the IVS-I-110 and Codon 39 β -Thalassemia Mutations in the Lebanese Population

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Abstract Using restriction fragment length polymorphisms (RFLPs) and sequence haplotype analysis, we studied the chromosomal background of the β -globin gene in 31 unrelated Lebanese IVS-I-110 or codon 39 (Cd39) subjects, and five normal β^A/β^A individuals. Our results are compared with those from similar studies in other parts of the Mediterranean in an attempt to provide insights into historical patterns of selection and disease. The great majority of the Lebanese chromosomes with the IVS-I-110 mutation are associated with the RFLP haplotype *I* and sequence haplotype *HT1*, which is probably the ancestral structure on which the mutation first emerged. The remainder of the IVS-I-110 alleles are linked to the 5'-subhaplotype 12 RFLP haplotype and/or *HTR* sequence haplotype. In contrast, in Turkey, IVS-I-110 is associated with six distinct sequence haplotypes and four distinct RFLP haplotypes, suggesting that the mutation probably emerged there. The diversity of sequence haplotypes described in Turkey was probably generated through recombination or gene conversion events with the most frequent β^A autochthonous structures. Our data on Lebanese β^A chromosomes and Algerian β^A chromosomes, along with previously described Turkish β^A chromosomes, strengthen this hypothesis. Following its emergence in Turkey, the IVS-I-110 mutation was probably introduced to Lebanon later, by migration or settlements. Cd39 demonstrates a remarkable level of sequence and RFLP haplotype heterogeneity in Algeria, in contrast to its relative homogeneity in Turkish samples. However, its rarity in the Near East, and more specifically in Lebanon, does not allow us to draw any conclusions concerning its origin and gene flow.

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Mode of Inheritance of Hand Osteoarthritis in Ethnically Homogeneous Pedigrees

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Abstract The aim of the present study was to investigate the extent and mode of inheritance of hand osteoarthritis (OA) using a large sample of ethnically homogeneous pedigrees. Two types of segregation analysis (SA) models were examined. Type I models used the data adjusted for potential significant covariates, particularly age and sex, prior to genetic analysis. Type II models incorporated effects of the potential covariates into major gene penetrance functions, permitting an account of the genotype covariate-specific effect on study variables. The results of this study strongly supported the hypothesis of a major gene effect and additional multifactorial component. The best-fitting model was the Mendelian one with an additive type of inheritance. The estimates obtained using the standard three-factor variance decomposition analysis suggest that age (72.8%) and major gene (14.5%) are the main sources of interindividual differences in the development of hand OA. The contribution of the putative major gene on age- and sex-adjusted OA phenotype variation was 55% in the present study.

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KEY WORDS: OSTEOARTHRITIS, SEGREGATION ANALYSIS, GENETICS

Evidence against a Relationship between Dermatoglyphic Asymmetry and Male Sexual Orientation

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Abstract Hall and Kimura (1994) studied the relation between dermatoglyphic asymmetry and male sexual orientation in a sample of 66 homosexual and 182 heterosexual men. They found that more homosexual men possessed a leftward dermatoglyphic asymmetry than did heterosexual men. In this paper, we report a comparative study about the relationship between sexual orientation and dermatoglyphic characteristics, including 60 homosexual men, 76 heterosexual men, and 60 heterosexual women, recruited from the general population, and also from a gay-rights nongovernmental organization, in Salvador, Brazil. Ulnar loops were the most frequent dermatoglyphic pattern in all groups, followed by whorls, arches, and radial loops. A chi-square analysis comparing the frequencies of the patterns in the three groups only showed an excess of ulnar loops in women ($p < 0.05$) and arches in men ($p < 0.01$), but did not reveal significant differences between homosexuals and the other groups studied. There was no significant difference between gay and straight men on total ridge count. We found a preponderance of rightward asymmetry in homosexual and heterosexual men, as well as in heterosexual women. Our results do not agree with Hall and Kimura's data indicating that more gay men possessed the minority leftward asymmetry than did straight men. There was no significant difference in leftward asymmetry in the sample studied. The results reported in this paper do not support any relation between dermatoglyphic asymmetry and male sexual orientation, and, thus, any hypothesis concerning a biological intrauterine contribution to adult sexual orientation somehow associated with dermatoglyphic development.

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Interpopulation Relationship by Isonymy: Application to Ethnosocial Groups and Illegitimacy

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Abstract The application of the isonymic method to establish interpopulation relationships is made difficult by such factors as: (1) a small population size; (2) the subdivision of the population into ethnosocial groups; and (3) the existence of individuals born extramaritally. The present study analyzes the validity of the isonymy method in populations where such difficulties exist. Lasker's R_{ij} relationship coefficients were calculated in base to marital records from six Pocho parishes (Argentina) for the period 1766 to 1840. Three endogamous ethnosocial groups were considered—Spanish, American Indians, “Mestizos”—and a fourth group combining mates of the three previous groups. For each ethnosocial category, and taking into account paternal surnames, maternal surnames (both for legitimate and illegitimate mates), and whole surnames merged, R_i interparish relationship matrices were obtained. All these matrices were correlated by means of the Mantel test. Maternal surnames of illegitimate mates show a similar pattern to the maternal surnames of legitimate mates and to all surnames of each category. Groups with larger sample size in every parish intercorrelate regardless of ethnosocial category. Results suggest the convenience of maximizing the sample size and using maternal surnames in populations with high illegitimacy.

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Sex Differential Patterns in Perinatal Deaths in Italy

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Abstract In industrialized countries, male excess is generally found in early deaths, despite the overall decrease in mortality. We studied the association between sex and some factors generally considered crucial for babies' survival, such as mother's age and education, birth order, and gestational age, in order to gain insight into the causes underlying the persisting higher vulnerability of male sex in early life. The analysis was performed on babies dying during the perinatal period. These were subdivided into those who were stillborn and those who died during the first week of extrauterine life. A higher male excess among babies dying during the neonatal period than among those who were stillborn was always found in all classes of all factors. The finding of such generalized male overmortality in the early extrauterine period of life, together with the patterns shown by the temporal sex ratio in stillbirths and in early deaths, supports the hypothesis of a postponement of male risk from late fetal into neonatal life.

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Sex Ratios at Birth in African Populations: A Review of Survey Data

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Abstract This study analyzes the distribution of sex ratio at birth in African populations using data collected in birth histories in sample demographic surveys (Demographic and Health Surveys and World Fertility Surveys). The average sex ratio from 56 surveys, totaling 1.130 million births, was 1.033 (95% CI, 1.029-1.037), significantly different from the world average of 1.055. The distribution of sex ratios across surveys was found to be heterogeneous, and different from what could have been expected from random fluctuations due to sample size. Three subsets were identified: a subset with lower sex ratios, primarily in countries of eastern and southern Africa of Bantu populations (1.010), a subset with average sex ratios (1.035), and a subset of countries with higher sex ratios, in particular Nigeria and Ethiopia (1.070). Further analysis revealed that African populations are as diverse as other populations, with sex ratios ranging from low values (below 1.00) to high values (above 1.08). Results are discussed in light of independent data sources and in comparison with other human populations.

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