H107 Shifting Morphological Structure: Comparing Craniometric Morphology in Founding and Descendant Populations

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The goal of this presentation is to explore the applicability of using cross-population data for individual biological profiling.

This presentation will impact the forensic community by highlighting the importance of understanding biological variation in the determination of ancestry in unidentified remains.

The Americas experienced an influx of morphologic diversity with the arrival of African slaves in the 17th Century. Derived primarily from countries along Africa's west coast, millions of Africans were transported in slave ships across the Atlantic Ocean, to either the Caribbean islands or North and South America. At present, more than 38 million U.S. residents are of African descent (U.S. Census Bureau 2007). Moreover, autosomal DNA markers suggest this segment of the American population exhibits 22.3 +/- 15.9% European admixture (Wassel Fry et. al 2007). Despite several generations of intermarriage and interbreeding between African-American and European-American populations, however, African-Americans are often treated as morphologically analogous to their founding population (i.e., Africans) in forensic analyses, particularly those which are nonmetric in nature. The conflation of these two populations may very well obscure patterns of morphological variation unique to African-Americans and thus could have major medicolegal implications for the identification of unknown remains.

The present study addresses this issue by applying geometric morphometric methods to the question of craniometric affinity in founding and descendant populations. The populations under investigation include native African slaves who died in Cuba (n=15) from the Morton Collection; modern Cubans (n=21) from a cemetery collection housed at the Museo de Montane, Havana; and, modern African-Americans from the Terry collection (n=47). Nineteen three- dimensional type 1 and type 2 anatomical landmarks were collected. The landmark data were transformed by generalized Procrustes analysis (GPA) which optimally translates, scales, and rotates the points into a common coordinate system. Multivariate statistical analysis was then conducted on the newly derived shape variables. In order to reduce dimensionality, a principal component analysis (PCA) was performed on the covariance matrix of the aligned coordinates. A multivariate analysis of variance (MANOVA) test, performed on the first 14 principal component scores accounting for approximately 83% of the total variation, detected significant shape differences among the groups (F=14.38; df=28, 134; Pr >F= <0.0001). A discriminant function analysis was conducted using the principal components to allocate crania into groups using crossvalidation or n-1 method. The modern African- Americans were correctly classified 97.87% of the time, while the African slaves and modern Cubans were correctly classified 100% and 52.38% of the time, respectively. Almost half (47.62%) of the modern Cubans were misclassified as modern African-Americans. The higher misclassification rate of the modern Cuban sample most likely reflects the greater admixture (Spanish) proportion of the sample. In addition, the misclassification of the modern Cubans into the African-American instead of the African slave sample may reflect the greater proportion of admixture in the Terry sample and the more homogenous nature of the slave sample.

Based on these results, the descendant populations under investigation (i.e., modern African-Americans and Cubans) are distinct from their founding population. Moreover, generations of admixture have produced two populations which bear more similarity to one another, in terms of potential misclassification, than native Africans, despite both geographic and cultural distance. These findings highlight the fluidity of cranial morphology within descendant populations. Incorporating such information into standard forensic practice may allow for a more informative assessment of unidentified human remains than is possible under current classification schemas of race in the United States.

Ancestry Determination, Populational Admixture, Geometric Morphometrics