A20 Craniometric Variation and FORDISC® Misclassification in Latin American and Asian Individuals

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Learning Overview: After attending this presentation attendees will better understand the impact of craniometric variation on the estimation of ancestry using a unique combination of Latin American and Asian samples.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by demonstrating the limitations of estimating ancestry for Latin American individuals using craniometrics in regions with population histories derived from both Latin American and Asian populations. This presentation will also demonstrate the need to include additional samples from these populations in FORDISC®.

This study explores cranial morphology and the usage of traditional morphometric ancestry estimation software to assist in the identification of deceased individuals in a Latin American sample. Recently, the complexity of morphological variation in Latin Americans has become increasingly discussed due to the changing demographics of the United States and the challenges admixture poses on identification cases.[1] Although the term Hispanic is traditionally used to classify individuals of Latin American descent, this classification fails to accurately describe populations in cultural and biological contexts, and this misrepresentation extends to modern methods of ancestry estimation.[2] In some areas of the United States, such as California, there are long histories of residency by both Latin Americans and Asians, which necessitates an ability to distinguish ancestry between the populations for cases in which context and visual examination do not point to a particular population. FORDISC 3.1® (FD3), a discriminant function analysis-based software, has been shown to misclassify Latin Americans as other ancestries, such as Japanese.[1]

In this study, FD3 was run on a sample (N=360) of Latin Americans (from the Hanihara dataset and Latin American Craniometric Database) comprised of individuals from Mexico, Colombia, Peru, Chile, Venezuela, Bolivia, and Argentina, along with individuals of Asian origins (N=470, including Japan, China, Philippines, and Java from the Hanihara dataset) to ascertain its accuracy in distinguishing between these populations. Analyses were separated by sex and include Mahalanobis D^2 (a biodistance measure), Principal Coordinates Analysis (PCoA), Canonical Variates Analysis (CVA), the Neighbor-Joining (NJ) method for construction of phylogenetic trees, and F_{st}. The hypothesis tested is that FD3 will be limited in classifying Latin Americans in the presence of selected Asian reference samples.

The results of these analyses show FD3 misclassifications exceeded 50% for Latin Americans as a group, and by individual sample, which is less than chance. The PCoA, which reflects the biodistance matrix, shows similarities between Asian and Latin American populations, and large differences among Latin American populations, such as Mexico and Peru. Further, CVA shows Asian populations spread across CV 1 and CV 2 in males, while Latin American samples were primarily constricted to positive values of CV 1 and the center of CV 2. Females yield similar CVA results where Asian and Latin American populations overlap one another with little clustering by sample. NJ analyses yield results consistent with CVA. F_{st} values (males=0.1152, females=0.1287) were high in comparison to populations around the globe.

FD3 as a tool is not currently helpful in scenarios in which context and visual assessment cannot narrow potential ancestries because the selection of reference groups may include both Latin American and Asian samples. For practitioners in areas such as California with a long and rich history of American Indian, Latin American, and Asian residents, among many others, these classification percentages leave much to be desired. These results join other studies that call for the need of representative samples, which can be applied to diverse populations and facilitate the work of forensic practitioners so that victims of homicide, genocide, exposure, and suicide can be identified and returned to their families. This is particularly critical for border crossers in the United States southwestern border.

Reference(s):

1. Dudzik B., Jantz R.L. 2016. Misclassifications of Hispanics using Fordisc 3.1: Comparing cranial morphology in Asian and Hispanic populations. *J For Sci* 61: 1311–18.
2. Ross A.H., Slice D.E., Ubelaker D.H., Falsetti A.B. 2004. Population affinities of 19th century Cuban crania: Implications for identification criteria in south Florida Cuban Americans. *J For Sci* 49: 1–6.

Cranial Variation, Admixture, Misclassification