A103 Assessing the Within-Group Structure of the "Hispanic" Sample in FORDISC® 3.1

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Learning Overview: After attending this presentation, attendees will better understand the limitations of ancestry estimation of "Hispanic" individuals in forensic contexts and gain insight on the misconception of utilizing the Hispanic population as a discretely defined population in typical applications of ancestry estimation methods.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by providing further research to suggest that ancestry estimation of continuously varying populations should not be employed in forensic contexts, as this may lead to greater errors in estimating biological profile parameters.

Recent decades have witnessed a significant push to improve and refine ancestry estimation methods in forensic anthropology. At the time of this writing, FORDISC® 3.1, the software for sex and ancestry estimation most commonly employed in forensic anthropology, includes a total of eight ancestries. Geographic groups characterized as Hispanic have been added in recent years, considering that a wider spectrum of representation for this generic ancestry should increase classification accuracies of unknown individuals. Thus, ancestry estimation methods have been expanding and diversifying Hispanic samples to encompass a greater range of variation. To test the effects of doing so, the within-group structure of the Hispanic sample in FORDISC® 3.1 was analyzed. Most individuals in the Hispanic reference group in FORDISC® 3.1 are of Central American origin, and the program divides them by specific country of origin (Guatemalan, Mexican, etc.). The goal of this study is to determine the validity of this reference group by using craniometric data of Hispanics from the Forensic Databank (FDB), a sample from the Dominican Republic (a Caribbean-Hispanic population), and positively identified Hispanic individuals from the New York City Office of the Chief Medical Examiner (OCME).

To assess group structure, K-means clustering analysis was performed on the pooled Hispanic sample and again on only FDB Hispanics. Analysis of the composition of clusters revealed no separation based on geographic origin in both cases. This strongly suggests that the Hispanic sample in FORDISC® 3.1 is largely an artificial group, comprised of a subjective, incomplete, and heterogeneous pool of individuals from different continental origins, rather than a real ancestry group in the traditional, geographic-origin sense. To emphasize the effects of this group composition, a modern Dominican sample was run in FORDISC® 3.1 using methods outlined in Jantz and Ousley.[1] Dominicans classified more frequently as American White and American Black, respectively, with only 10% of the sample classifying as Hispanic.

It is recommended that the Hispanic sample in FORDISC® 3.1 be discarded or divided and renamed as the specific geographic populations represented. Because the Hispanic population is difficult to define due to the ambiguity of characterizing the proportion of parent ancestries present on an individual basis (Native American, European, and African), it is suggested that the term "Hispanic" not be used to define an ancestral class, but an ethnicity. This would also imply that the use of craniometrics is not an appropriate approach for this type of analysis.

Reference(s):

1. Jantz R.L., Ousley S.D. *FORDISC® 3.0: Personal Computer Forensic Discriminant Functions.* University of Tennessee, Knoxville; 2005.

Hispanic, Ancestry Estimation, K-Means Cluster Analysis