A177 A Call for a Paradigm Shift in the Study of Ancestry

Ann H. Ross, PhD, North Carolina State University, Raleigh, NC 27695-7614; Jonathan D. Bethard, PhD*, University of South Florida, Tampa, FL 33620-8100; Elizabeth A. DiGangi, PhD, Binghamton University, Binghamton, NY 13902*

Learning Overview: After attending this presentation, attendees will understand the underlying factors responsible for human variation with implications for ancestry estimation.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by demonstrating a new paradigm for a better understanding of ancestry.

The estimation of ancestry is a crucial component in human identification but one of the most difficult parameters of the biological profile. Recently, antiquated and over-simplistic views of ancestry based on the trifecta of continental populations from Asia, Europe, and Africa have regained popularity. However, this facile presumption ignores underlying microevolutionary forces such as gene flow, drift, and migrations that are responsible for human diversification. Global population studies demonstrate that human craniofacial morphology fits a neutral evolutionary model because contiguous populations more frequently exchange genes and/or share common ancestry.

There is a need for broad synthesis to better understand the underlying patterns of modern human variation that will inform the estimation of ancestry. The purpose of this study is to explore craniofacial variation in Latin America and test the validity of using the tri-continental approach to ancestry. The sample totals 397 individuals, and samples were separated by biological sex when both were available for analysis (Chile: females *n*=34, males *n*=37; Colombia: females *n*=11, males *n*=53; Cuba: males *n*=19; Enslaved Africans from Cuba: males *n*=25; Guatemala: males *n*=71; Puerto Rico: males *n*=5; Panama: males *n*=10; Peru males: *n*=7; Spanish: females *n*=58, males *n*=67). Sixteen standard Type 1 and Type 2 craniofacial homologous coordinate landmarks were used in the analysis. Coordinate data must first undergo a Generalized Procrustes Analysis (GPA) transformation before subsequent statistical analyses can be performed. The shareware program MorphoJ was used to translate, rotate, and scale all coordinates into a common coordinate system using GPA. Shape is defined as all of the geometric information that remains after the effects of location, scale, and rotational effects are removed. Centroid size is a measure of geometric scale that is mathematically independent of shape. A Principal Component Analysis (PCA) of the covariance matrix was conducted on the GPA-transformed coordinates to reduce dimensionality of the data for subsequent multivariate statistical analyses. Shape and size variation among the groups was examined using a Procrustes Analysis of Variance (ANOVA). Among-group variation was examined using Canonical Variates Analysis (CVA). Mahalanobis distance or generalized distance, which considers the correlations among variables when computing the distance between means, was used to examine group relatedness. An average linkage hierarchical (or agglomerative) cluster analysis was performed using the generalized distance matrix to examine group similarity. Hierarchical clustering begins with every sample in a single cluster, then in each successive iteration, it merges the closest pair of clusters (distances between all pairs and averages all these distances) until all the data are in one cluster. The cluster analysis was performed in JMP® Pro 14.

The Procrustes ANOVA results show significant group variation for shape ($F_{(242, 15,785)}=6.82$, $p=<.0001$) and centroid size ($F_{(11,385)}=22.35$, $p=<.0001$). Ninety-one percent of the total variation is accounted for on the first five canonical variates. The generalized distance results show that all groups are significantly different from one another based on 1,000 permutations (p-values range from 0.01-<0.0001), except for Puerto Rico and Peru (D=4.14, p-value=0.347). The dendrogram produced from the hierarchical cluster analysis shows two distinct clusters: Chile/Spain. Panama, Cuba, Guatemala, and Colombia branch off the Chile/Spain cluster. The enslaved African sample clusters with Peru, and Puerto Rico is the most dissimilar. These results demonstrate that craniofacial morphology is much more complex than mere proportions of Asian, African, and European continental groups. Notably, these results are consistent with isolation-by-distance of early populations in the region and historical migrations, which underscores the need for a paradigm shift from a three-way continental approach to a population history approach to ancestry.

Ancestry, Paradigm Shift, Geometric Morphometrics

*Presenting Author