A173   What Are We Really Estimating? An Evaluation of What We Commonly Refer to as Ancestry Estimation

Kate Spradley, PhD*, Texas State University, San Marcos, TX 78666; Richard Jantz, PhD, University of Tennessee, Knoxville, TN 37996-0720

Learning Overview: After attending this presentation, attendees will better understand that the population history of the United States allows for providing estimates beyond what is usually considered ancestry estimation.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by suggesting that anthropologists can go beyond ancestry estimation when generating biological profiles.

While it has been stated that it is not possible to sort humans into more categories than continental origins, forensic anthropologists do this all the time, often working within a continent.[1] Forensic anthropologists commonly refer to this practice as ancestry estimation. But is ancestry what we are really estimating? Ousley et al. demonstrated that populations can be sorted by social race categories within the United States, by time period, by ethnic affiliation, and by geographic boundaries.[2] Why then is ancestry estimation the most commonly used terminology? The term "ancestry" was used to replace the word "race" to distance forensic anthropological estimations from a typological and racist past. However, the term ancestry refers to ancestral origins, which could include continental origins or ethnic affiliation. Ancestral categories such as European, African, or Asian are very broad and not especially informative for forensic case work. The purpose of this presentation is to address whether forensic anthropologists are estimating ancestry or something more specific, whether or not such estimations are informative, and how forensic anthropologists should refer to these estimations.

To address questions surrounding what is commonly referred to as ancestry estimation, particularly in the United States, craniometric data, following measurement definitions from Howells, from West Africa (Gold Coast and Cameroon: male=82, female=39), Europe (Germany and the Czech Republic: male=152, female=64), and the United States (American Black: male=213, female=175; and American White: male=282, female=193) were utilized in discriminant function analyses, using the custom import function in FORDISC® 3.0, with stepwise variable selection.[3,4] The West African and European groups represent the 19th century and American Black and American White groups are separated into 19th- and 20th-century groups. Analyses were run separately for males and females.

The results for the six female groups indicate the overall classification rate is 67.5%. The West African and European groups have the highest classification rates (97% and 73%) while the 19th- and 20th-Century American Black and White females range from 46%–68%. For the males, the West African and European groups have the highest classification rates (96% and 88%) while the 19th- and 20th-century American Black and White males range from 57%–65%. For both the males and the females, the plot of the Mahalanobis distances indicates that the 19th- and 20th-century American Black groups are intermediate between the European and American White groups and the West African group. The West African group is more dissimilar to the American Black groups, while the European group shows significantly more overlap with the American White groups, for both males and females. When 19th- and 20th-century American Blacks and American Whites are run separately, classification rates increased (up to 96%), suggesting that morphological differences exist in both groups that provide good classification rates.

The overall discriminant functions suggest that West Africans and Europeans can be differentiated from American Whites and Blacks with high classification rates. While American Blacks and Whites have ancestral origins in West Africa and Europe, they are also uniquely American and both can be assigned group membership to American subpopulations. The population history of the United States includes (but is not limited to) the migration of Europeans and the forced migration of enslaved Africans to the New World, resulting in admixture that shaped population structure. Correspondingly, miscegenation laws, institutional racism, and assortative mating practices have also shaped population structure in the United States to the degree that it is possible to estimate ancestral origins in addition to group membership suggestive of both present-day geography and population substructure. Therefore, an estimation is dependent upon the question asked, and the terminology used is largely context driven. What forensic anthropologists are, or should be, doing is estimating population affinity, a more specific and useful estimation than the more general estimation of ancestry.

Reference(s):
1.   Williams, F.L., R.L. Belcher, and G.J. Armelagos. Forensic misclassification of ancient Nubian crania: Implications for assumptions about human variation. *Current Anthropol*, 2005;46(2):340-346.
2.   Ousley, S., R. Jantz, and D. Freid. Understanding race and human variation: Why forensic anthropologists are good at identifying race. *Am J Phys Anthropol*, 2009;139(1):68-76.
3.   Howells, W.W. *Cranial Variation in Man: A Study by Multivariate Analysis of Patterns of Difference Among Recent Human Populations.* Papers of the Peabody Museum of Archaeology and Ethnolgy. Vol. 6. 1973: Harvard University Press.
4.   Jantz, R.L. and S.D. Ousley, *FORDISC 3.0: Personal Computer Forensic Discriminant Functions.* 2005, The University of Tennessee: Knoxville.

Ancestry, Biological Affinity, Estimation