A4 A Craniometric Recapitulation of Genetic Estimates of Ancestry for Individuals of Hispanic Identity: Temporal, Geographic, and Identification Trends

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After attending this presentation, attendees will better understand the importance that population dynamics plays in forensic anthropological casework, especially when considering individuals of Hispanic identity and Latin American geographic origin.

This presentation will impact the forensic science community by illustrating how craniometrically derived estimates of admixture recapitulate the results previously reported using forensic genetic markers, offering new evidence in support of a case identification bias.

Using genotypic data for United States-Mexico border-crossing fatalities, Hughes et al. reported greater indigenous ancestry in individuals who are currently unidentified and have been recovered in more recent years — what they called an "identification bias" in the forensic case analysis of individuals of Hispanic identity and Mexican origin.[1,2] These findings are consistent with recent demographic trends among living migrants and forensic casework statistics on undocumented border-crosser deaths. As such, they have significant implications for both casework logistics on the United States-Mexico border and the larger study of Hispanic population dynamics. It is necessary, therefore, to validate these genotypic trends using other sources of biological information relevant to the forensic context. Given the importance of craniofacial morphology to the estimation of ancestry and the historical use of quantitative cranial traits as reasonable proxies for neutral genetic markers, craniometrics were used to recapitulate these prior results.

The hypothesis that the dynamic temporal, geographic, and identification trends in United States-Mexico border casework revealed with genetic ancestry information can be equally accessed using craniometrically derived admixture estimates was tested. Hispanic cases were selected from the Forensic Anthropology Data Bank (FDB) such that craniometrics, birth year, geographic, and Identification (ID) status information were available. Proportions of admixture were sourced from the population structure analyses of Algee-Hewitt.[3]

To test for temporal trends, correlation coefficients, ρ, are calculated between birth year and the estimated admixture proportions. A significant correlation ($p < 0.05$) is found between birth year and the Native American (ρ=0.32) and European estimates (ρ=-0.31, p=0.0053). These analyses were repeated, after partitioning the sample into two groups: cases with documented place of birth and cases with recovery location only, serving as proxies for identified and unidentified cases, respectively. Significant correlations are obtained between birth year and the Native American estimates for the location born subset (ρ=0.31). For the recovery location subset, significant, and stronger, correlations are produced between birth year and both the Native American (ρ=0.50) and European (ρ=-0.49) estimates. When case year replaced birth year, the associations remain consistent and these two measures are positively related (ρ=0.60).

To assess identification bias, the location born and location recovered cases are compared for their level of indigeneity and identification status. Native American ancestry appears higher for the recovery location sample

(mean 50%, median 58%) than for the sample with known birthplace (46%, 39%). When grouped by ID status codes, the location born cohort contains many more cases with confirmed identifications (89%) than the recovery location cohort (63%). A cross-classification using identification status and location categories is significant (R^2=0.12, *df*=2, X^2=19.04, *Prob* > X^2= <0.0001). Inverse correlations between identification status and both case year (ρ=-0.33) and Native American proportions (ρ=-0.12) are produced for the location found subset. Identification status and case year (ρ=0.12) are positively related and Native American proportions (ρ=-0.12) are negatively related for the location born subset. Over time, confidence in identification decreases for the location found and increases for the location born data. Most importantly, for both analyses, case identification success decreases as indigenous ancestry increases. These findings are supported by regression analysis of the Native American proportions for the location found subset. The full model (R^2=0.28, *df*=3, *F* = 3.56, *Prob* > *F* = <0.0274) and effects tests for birth year (*F* = 8.13, *Prob* > *F*= <0.0082) and ID status-by-birth year (*F* = 5.95, *Prob* > *F*= <0.0216) are all significant, and lack of fit is not significant (*F* = 0.52, *Prob* > *F*= <0.8622) at α=0.05.

These results attest to an inverse relationship between the amount of European and Indigenous ancestry and suggest an increased case representation of peoples with more Indigenous ancestry in more recent years. These findings support an identification bias among the Hispanic-labeled cases in the FDB. Individuals with higher proportions of Native American membership have less frequent birth location information on record and are more often assigned low identity status scores. They most often represent individuals not yet positively identified by other means, such as DNA profile, fingerprint, or antemortem record matching.

Reference(s):

1. Hughes C.E., Algee-Hewitt B.F.B., Clausing E., Anderson B.E. Temporal Patterns of Mexican Migrant Ancestry: Implications for Identification. *Proceedings of the American Academy of Forensic Sciences*, 67th Annual Scientific Meeting, Orlando, FL. 2014.
2. Hughes C.E., Algee-Hewitt B.F.B., Clausing E., Anderson B.E. Temporal Patterns of Mexican Migrant Genetic Ancestry: Implications for Identification. *Amer Anth.* 2016: in review.
3. Algee-Hewitt B.F.B. Population inference from contemporary American craniometrics. *Am J Phys Anthropol.* 2016:160(4):604-24.

Hispanic Ancestry, Identification Bias, Geo-Temporal Trends