



Physical Anthropology Section - 2014

H124 A Structured Approach to Assessing Morphogenetic Variation in Mexico: Tests of Method Informedness for Improved Skeletal Identifications

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After attending this presentation, attendees will have a clearer understanding of population structure at a smaller geographic scale within Mexico. Additionally, attendees will learn how various statistical approaches applied to estimate population structure influence the conclusions drawn about biological patterning.

This presentation will impact the forensic science community by ameliorating the immediate need to improve skeletal identification methods for U.S.-Mexico border-crossing fatalities through a fine-scale approach to inferring skeletal and DNA variation across Mexico. By determining how heterogeneity within Mexico is expressed through differences in skeletal morphology and genetic profiles, forensic anthropologists are able to make informed decisions about method development and best practices for human identification contexts.

Population structure within Latin America has been well documented in previous studies. A clearer understanding of structure at a smaller geographic scale is a critical next step. Revealing latent structure that exists within morphogenetic data, and establishing its correspondence to geography, can improve forensic anthropological methods for estimating the biological profile. By demonstrating that Hispanic populations are biologically heterogeneous and determining how this variation is expressed through differences in skeletal morphology and genetic profiles, informed decisions can be made about method development in forensic anthropology and best practices for human identification contexts. The immediate need to improve skeletal identification methods for U.S.-Mexico border fatalities demands that such a fine-scale approach is applied to morphogenetic variation within Mexico.

Preliminary studies of both genetic and craniometric data demonstrate that population structure is detectable within Mexico and conforms to known geographic boundaries of population settlements and gene flow.^{1,2} Building on these recent observations, it is argued that patterning within Mexico itself may confound estimations of the biological profile; thus, further investigation into the effects of geography on morphogenetic variation can improve forensic methods by ensuring appropriate targeting and application. To this end, the present study examines how using various statistical approaches to estimate population structure influences the conclusions drawn about biological patterning. This study tests multiple strategies for inferring structure for genetic Short Tandem Repeat (STR) and cranial Icongruence Length Difference (ILD) data, each strategy with differing levels of *a priori* model informedness, using cases from the Pima County Office of the Medical Examiner. Approximately one-third of the 300+ sampled cases were identified individuals from Mexico. Using their state of origin, the study tested how different statistical approaches convey structure within Mexico and evaluated how well these inferred groupings correspond to geography.

Three tiers of model informedness were tested: low- (LLI); mid- (MLI); and full- (FLI) level informedness. LLI models were assayed using unsupervised model-based clustering, implemented with MCLUST and Structure 2.3.1 software, for ILD and STR datasets, respectively. Components and model parameterization were determined for the LLI analyses in the absence of any known identifiers. For each case, STR or ILD data was input, while region of origin was excluded; the biological data alone drove the clustering. For the MLI-level analyses, structure was assessed for ILD and STR data using k-means clustering. While region of origin data was excluded, the cluster-seed approach was designed to maximize the biological data variation among clusters. Finally, the FLI tests included a mixture model-based discriminant function analysis for ILD data, and a Structure 2.3.1 analysis, following the recommendations of Hubisz *et al.*, for STR data.^{3,4} For both FLI models, region of origin data was combined with the biological data for cluster partitioning, thus making these models fully “informed.”

The resulting clustering for the LLI, MLI, and FLI approaches revealed a clear trend: increased informedness yields increased correspondence with geography and between cluster memberships from ILD and STR data. LLI models showed no significant indications of population structure for either ILD or STR data (when $K \geq 2$). In contrast, both MLI and FLI approaches yielded geographically structured clusters, with the FLI outperforming the MLI. The results of this study demonstrate that sub-population structure can be detected using ILD and STR data from Mexico and that the level of method informedness greatly affects its ability to convey this structure. In the case of Mexico, where variation is regional and differences, while present, are nuanced, it is critical researchers consider adequate samples and select the most appropriately informed models.



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References:

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