A76 Improvement to the Estimation of Hispanic Ancestry Through the Combination of Cranial and Dental Traits

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After attending this presentation, attendees will understand how the simultaneous analysis of multiple datasets, in this case cranial morphoscopic and dental morphological traits, improves the accuracy of estimating ancestry in the forensic context.

This presentation will impact the forensic science community by highlighting the utility of combining data from different sources when estimating ancestry. Additionally, this presentation demonstrates the power of non-metric ancestry estimation methods in a statistical framework.

With respect to ancestry, "Hispanic" is an umbrella term that fails to account for population histories in different regions of the United States; however, in common usage, "Hispanic" refers to populations with a history of European and Native American admixture, with an added component of African ancestry in southeast and Caribbean populations.[1] The Hispanic population in the United States is growing, and forensic anthropologists increasingly encounter the remains of these individuals in their casework. Several methods have been developed that address the estimation of Hispanic ancestry, but each focuses on a single source of variation.[2-4] This presentation explores whether estimates are improved by combining data.

The present research is based on data from modern Hispanic individuals from a combination of medicolegal and research collections (n=154). It is important to note that many of these individuals are presumed migrants and have yet to be positively identified; however, an ancestry estimate of "Hispanic" has been established using other methods.[5] For each individual, cranial (n=11) and dental (n=23) variables were recorded based on published standards.[6-8] Ancestry estimates were produced using both random forests based on conditional inference trees and naïve Bayes classification on cranial data, dental data, or combined data, resulting in a total of six models for ancestry estimation. The models were tested on each of 30 randomly generated training and test sets to account for variability in correct classification rate. Differences between models were assessed using a paired sample t-test, since classification rates were generated from the same sample across models for each run.

Results reveal that models based on the combined data have higher Positive Predictive Values (PPV) for individuals of Hispanic ancestry ($p < 0.01$). The PPV is a measure of how often the models are correct when giving an estimate of "Hispanic;" because that is the only group considered here, it can be interpreted as a measure of model accuracy. Models based on both types of data have a mean PPV of 0.93 for random forests, and 0.81 for naïve Bayes. In contrast, dental variable-only models performed about 10% worse (0.82, Random Forest Modeling (RFM); 0.72, Bayes) and cranial-only models about 15% worse (0.78, RFM; 0.64, Bayes).

Previous research concluded that the improvement observed when simultaneously analyzing cranial and dental data was of practical, if not statistical, significance, especially in the estimation of Hispanic ancestry. The results presented here demonstrate a statistically significant improvement to ancestry estimation for Hispanic individuals. Future research that combines multiple types of data within a statistical framework will lead to improved estimates of ancestry.

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