A92 Morphoscopic Trait Expression Within and Among Hispanic Populations

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After attending this presentation, attendees will understand the frequency distribution of morphoscopic traits within two Hispanic populations, the utility of those traits for assessing ancestry at the regional population level, and the necessity of population-level ancestry assessments.

This presentation will impact the forensic science community by providing quantitative data on the distribution of morphoscopic traits for multiple Hispanic populations and a novel method for ancestry assessment using a forensic dataset.

Establishing the ancestry of human remains located along the United States-Mexico border is not a straightforward affair. The Latin American Diaspora is increasing the number of deaths along the United States southern border with Mexico, and consequently, along the major borders between Mexico and its southern neighbors. In the United States, the ancestry of these individuals is generally identified as Hispanic, a term that seemingly covers an intentionally large number of Spanish-speaking (cultural) groups, although doing so without justification in many instances. Previous authors identified craniometric differences among various populations recovered along these borders; however, limited research has focused on the differences in morphoscopic trait expression between Mexican, Guatemalan, and other Latin American groups and the utility of those traits for the assessment of ancestry.

This study evaluated population variation of eight cranial morphoscopic traits using samples of known Southwest Hispanics (n=72), Guatemalans (n=106), American Blacks (n=146), and American Whites (n=218). This study applied the Support Vector Machine (SVM) method to build a prediction model based on a sub-sample (20%) of the data; the remainder of the data was used as a test sample. SVMs are supervised learning models for data analysis and pattern recognition, useful for classification purposes. The model searches for a linear boundary (the support vector) between groups using the observations situated between groups, rather than using a centroid value (as in discriminant function analyses). When a linear boundary is not possible — which is often the case with biological data — a kernel trick is used to create non-linear classifiers to best fit the model. SVMs perform well for datasets that are non-linear, sparse, or have high-dimensionality, which are all issues that can occur when working with categorical variables in classification models.

The SVM approach effectively differentiated between the four groups with correct classification rates between 72% (Guatemalan group) and 94% (American Black group). However, when the Guatemalan and Southwest Hispanic samples were pooled, the same model correctly classified all groups with a higher degree of accuracy (American Black=96%; American White=77%; and the pooled Hispanic sample=91%). This study also identified significant differences between the two Hispanic groups in six of the eight traits using univariate statistical tests. These results speak to the unique population histories of these samples and the current use of the term "Hispanic" within forensic anthropology. Finally, it is argued that the SVM can be used as a classification model for ancestry estimation in a forensic context and, as a diagnostic tool, may broaden the application of morphoscopic trait data for the assessment of ancestry.

Morphoscopic trait analysis can be used to assess ancestry, both at the population level and using larger, geographic-based (grouped) ancestries. Although Guatemalan and Hispanic individuals differ significantly in the distribution of character states, combining these two groups under the umbrella-term "Hispanic" is useful in the United States, where ancestry assessments using broad terms are generally sufficient for the identification process.

Ancestry, Morphoscopic Traits, Support Vector Machines