

Using rASUDAS to estimate population affinity for unidentified remains in Tucson, Arizona

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SUMMARY

This study used rASUDAS to estimate population affinity in a sample of 24 unidentified individuals presumed to be undocumented migrants in Tucson, Arizona. The results call for the inclusion of more complex populations in reference samples to improve model's accuracy.

Keywords: ASUDAS, tooth morphology, statistics

Introduction

The prerogative of a forensic anthropologist is to establish a biological profile for a set of skeletal remains, which includes population affinity. As migration continues to increase, accurate population affinity estimates are more essential. Nonmetric dental traits exhibit dramatic patterns of variation at the global scale. Scott and colleagues (2018) pioneered a new method (rASUDAS) to estimate population affinity using crown and root morphology and a naïve Baye classification algorithm to calculate the probability of an individual's assignment to a particular geographic group. rASUDAS is used in the current study to estimate population affinity of migrants at the United States/Mexico border.

Objectives

To estimate population affinity of unidentified skeletal remains from Tucson, Arizona using rASUDAS to gain a better idea of geographic origin and facilitate identification.

Methods

A sample of 24 unidentified individuals provided by the Pima County Office of the Medical Examiner was scored using the protocols described in ASUDAS (Turner et al., 1991). The posterior probabilities for each group assignment were compared to previously tested populations to determine the

model's effectiveness in assigning unknown individuals with complex population histories.

Results and Discussion

Most individuals (~71%) were classified in an Asian or Asian-derived group, followed by the Western Eurasian group (~21%). Based on previously tested populations using this application, these results reflect individuals with complex population histories, including Hispanic individuals. However, more data are required to make a definitive assessment because of the small comparative groups (n=14).

Conclusion

Currently, this new application successfully predicts group assignments and performs better when assignment group numbers are limited. It is a complement to existing techniques in estimating population affinity. However, additional data from complex populations are critical. Implementing more data to train this model will allow this application to act as a stand-alone method for assessing a vital part of the biological profile of a set of remains.

Bibliographic references (ABNT standard)

SCOTT, G. Richard *et al.* rASUDAS: A New Web-Based Application for Estimating Ancestry from Tooth Morphology. **Forensic Anthropology**, vol. 1, no. 1, p. 18-31, 2018.

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