A12 Assessing the Accuracy of Current Ancestry and Sex Estimation Methods on a Japanese Sample

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Learning Overview: After attending this presentation, attendees will have gained a better understanding of the accuracy of current ancestry and sex estimation methods on a Japanese skeletal sample.

Impact on the Forensic Science Community: This study will impact the forensic science community by investigating the suitability of currently available reference samples. As these reference samples serve as the basis to estimate ancestry and sex within a medicolegal context, it is critical to understand their accuracy in estimating these parameters on known skeletal samples. This work also highlights the diversity present in skeletal populations and the need for large diverse reference samples.

According to the Migration Policy Institute, from 1960 to 2014 there was a 2,597% increase in Asian migrants to the United States, thus representing 30% of the United States' foreign-born population.[1] Further, the 2010 Census reported that the Asian population is the fastest growing of any population in the United States. Specifically, the Japanese population experienced an increase of up to 59%.[2] However, most current biological profile estimation methods in the United States are based on individuals of European and African ancestry, which are then used to estimate the biological profile of unknown decedents in forensic cases. Despite studies stating the need for population-specific biological profile estimation methods, there is a scarcity of research that has focused on ancestry and sex estimation methods for Asian populations. As Asian migration into the United States continues to rise, so will the necessity for Asian-specific methods and reference data.

Heritable traits under investigation in biological anthropology include four major data types: craniometrics, cranial non-metrics and macromorphoscopics, odontometrics, and dental morphology. Each data type reflects different biological, environmental, and evolutionary influences. While similar research projects typically utilize only one or two data types, this study includes all four data types in a single project to present a holistic approach to analyzing ancestry and sex estimation methods on an Asian sample. The aims of this study are: (1) to test the accuracy of current ancestry and sex estimation methods on a Japanese sample, and (2) to explore the applicability of available reference populations when estimating the biological profile of unknown Asian decedents.

Data were collected from a modern Japanese sample curated at the Jikei University School of Medicine in Tokyo, Japan (n=33). Data for each individual were input into various statistical estimates typically used by forensic anthropologists. Craniometric data were assessed using FORDISC® 3.1 to estimate sex and ancestry.[3] Cranial non-metric and macromorphoscopic data were analyzed using tetrachoric Mahalanobis distance and visualized using multidimensional scaling to assess population affinity.[4] Odontometric data were compared to data presented in Pilloud et al. using FORDISC® 3.1 to estimate sex and ancestry.[5] Dental morphological data were input into the statistical program rASUDAS to estimate ancestry.[6]

Preliminary results using the craniometric, odontometric, and dental morphology datasets produced correct classification rates from 21.10%–36.40% for ancestry, and the craniometric and odontometric datasets produced correct classification rates from 24.20%–36.40% for sex. The craniometric dataset produced the most accurate estimates of ancestry, while the odontometric dataset provided the most accurate sex estimates.

These varied results likely stem from inappropriate or insufficient reference samples, unexplored variation in the study sample, and/or the statistical treatments used in the current ancestry and sex estimation methods. Within forensic anthropology, there is a need to establish more robust reference samples that represent a broad range of global variation. It may also be necessary to explore additional statistical treatments and the incorporation of more than one type of data to accurately quantify population variation and sexual dimorphism.

Reference(s):

1. Zong, Jie, and Jeanne Batalova. Asian Immigrants in the United States. *Migration Information Source* (2016).
2. Hoeffel, Elizabeth M., Sonya Rastogi, Myoung Ouk Kim, and Shahid Hasan. *The Asian Population: 2010.* US Department of Commerce, Economics and Statistics Administration, 2012.
3. FORDISC® 3.1 Personal Computer Forensic Discriminant Functions. University of Tennessee, Knoxville, Tennessee.
4. Konigsberg, Lyle W. Analysis of Prehistoric Biological Variation under a Model of Isolation by Geographic and Temporal Distance. *Human Biology* 62, no. 1 (1990): 49-70.
5. Pilloud, Marin A., Joseph T. Hefner, Tsunehiko Hanihara, and Atsuko Hayashi. The Use of Tooth Crown Measurements in the Assessment of Ancestry. *Journal of Forensic Sciences* 59, no. 6 (2014): 1493-501.
6. Scott, G. Richard, Marin A. Pilloud, David Navega, João d'Oliveira Coelho, Eugénia Cunha, and Joel Irish. Rasudas: A New Web-Based Application for Estimating Ancestry from Tooth Morphology. *Forensic Anthropology* 1, no. 1 (2018): 18-31.

Ancestry Estimation, Sex Estimation, Asian Population