A174 The Biogeographic Profile in Forensic Anthropology: An Alternative to Ancestry for Casework Along the United States-Mexico Border

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Learning Overview: After attending this presentation, attendees will be aware of how the place of origin can be inferred from unknown case variables and how place of origin in Mexico, trihybrid ancestry, case reporting date, and place of recovery on the border are interrelated. This study is relevant to the identification of Hispanics of Mexican origins, especially for Undocumented Border Crossers (UBC) casework from Arizona.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by introducing biogeography as an alternative parameter to single-group ancestry. This presentation shows how novel geospatial and machine learning methods can be used to develop a biogeographic profile for unknown remains recovered along the United States-Mexico border.

Increasing fatalities and shifting demographics of Latin American migrants demand multi-focused research that works to improve rates of positive identification for UBCs.[1-5] Morphogenetic analyses of trihybrid ancestry have distinguished among many bio-cultural groups in Mexico, represented in UBC casework.[6-11] Demographic studies on migration networks have found distinctive transit pathways to "El Norte," whereby migrants of different origins are associated with particular destinations along the United States-Mexico border at different times.[12] Predictions of individual sending region/origin are argued here to be more valuable for forensic case evaluation than single-group ancestry classifications.

While "ancestry" is an essential component of the biological profile, when defined as a single group category, such as Black, White, or Hispanic, its utility is limited in the border Identification (ID) context, as many UBCs will be classified as the same ancestry. Prior work has advocated for replacing single ancestry with probabilistic estimates of continental ancestry, which, under a trihybrid model, correspond to the relative quantities of European, Indigenous American, and African ancestry. It has shown that these ancestry proportions better account for admixture and the history of colonialism, slavery, and migration in the Americas.[6-9] Expanding this discussion to UBC casework, the present study rejects single ancestry classification in favor of reporting "biogeography": an identity parameter that reflects the patterned association between ancestry proportions and geographic place of origin. It demonstrates how this "biogeographic profile" can be produced and mobilized in statistical models that predict location of origin from place of recovery. This information on sending region can direct the forensic case investigation by providing probable locations for finding next of kin and by reducing the pool of potential matches from missing persons lists.

Sampling ≈150 cases from the Pima County Office of the Medical Examiner (PCOME) in Arizona, finite-mixture, geospatial, machine learning, and traditional statistical methods are used to: (1) produce biogeographic profiles; (2) investigate the relationships among ancestry composition, geographic location of remains, and case-reporting date; and (3) build models that predict the individual's documented origin as a microregional category or Geographic Information Systems (GIS) coordinates. Initial geospatial analysis shows global clustering relative to a random distribution (average nearest neighbor ratio=0.53), persisting at a range of scales (5–100km). Visual examination of mapped cases suggests clustering by both sending regions and ancestry, implying preset transit-corridors or routes. Autocorrelation analysis indicates clustering for trihybrid ancestries and latitudes/longitudes. Significant differences exist in ancestry quantities for paired microregions: Southeast cases carry more Indigenous and less European ancestry than North (+32, -27%) and Traditional (+25, -23%) cases. Correlations suggest that quantities of ancestry are structured by space/time. Individuals with more Indigenous ancestry originate in the southeast, more European ancestry in the northwest, and more African ancestry in the northeast. Individuals with higher African ancestry are more commonly recovered in earlier years. European and Indigenous ancestry are inversely related. Indigenous ancestry is a proxy for latitude, as it increases along a north-south axis and changes with the latitude-longitude of the recovery site. Tests of spatial relationships find that the north-south origin location is related to the north-south and east-west recovery location. Bootstrap forest methods confirm the significance of trihybrid ancestry and geo-temporal variables for predicting microregions and coordinates. While logistic regression explains only 38% of the variation and misclassifies 43% of cases, remarkable improvement is gained with more complex machine learning methods. The optimal neural network, fitted using k-fold validation, predicts place of origin with an overall model R^2=0.99. Latitudes and longitudes are estimated, respectively, with R^2=0.99 and 0.93. Reducing the training sample, using 33% holdout-validation, produces a slightly lower overall model R^2=0.75.

This study provides a novel framework for producing a biogeographic profile and predicting individual place of origin using both biological and case-context information. It also identifies potential migration pathways that track from place of origin to place of recovery along the border and are related to trihybrid, especially Indigenous, ancestry. This study posits that patterns of spatio-temporal clustering (in case numbers, ancestry composition, reporting year, sex, origin) may reflect evolving motivations, collective knowledge, and barriers to migration. This information provides additional lines of evidence to direct case investigations or support partial identifications. Any new tool that holds the promise of increasing the number of UBC identifications is welcomed and will be put into practice at the PCOME.

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