TOWARD ESTIMATING GEOGRAPHIC ORIGIN OF MIGRANT REMAINS ALONG THE UNITED STATES–MEXICO BORDER

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Due to the diverse demographics within the United States, ancestry estimation in the biological profile created by forensic anthropologists is helpful in facilitating a positive identification, narrowing down the parameters when searching through missing persons databases. The U.S.–Mexico border has seen an increase in migrant fatalities during the year 2012. In particular, Brooks County, Texas, has seen a dramatic increase in migrant remains. Until recently, the remains in Brooks County have been buried as unidentified individuals with no forensic pathological or anthropological analyses. Collaborative efforts by Baylor University, University of Indianapolis, and Texas State University are underway to exhume and analyze these individuals and work toward positive identification. Using the term Hispanic to describe these remains is of little use as individuals in Latin America do not refer to themselves as Hispanic and it is not informative to the geographic origins of these individuals. Because different countries that comprise Latin America have different population histories that have led to different population structures, it may be possible to use craniometric data to more precisely estimate the geographic origin of migrant fatalities found along the U.S.– Mexico border. Preliminary results suggest that, with larger data sets, it is possible to take a finer-grained approach to estimating geographic origin to facilitate a more rapid positive identification and repatriation. [unidentified migrant remains, identification, ancestry]

Cranial morphology is polygenic, highly heritable (Carson 2006; Devor 1987), and can be used to estimate the geographic origin of an individual or group of individuals (Jantz and Ousley 2005; Ousley et al. 2009). These estimations are based on statistical methods, strength of the reference data, and understanding of the population structure of the reference data. The most popular method of ancestry estimation in the United States is FORDISC 3.1 (Jantz and Ousley 2005). FORDISC 3.1 (Jantz and Ousley 2005) uses discriminant function analysis (DFA) to compare measurements from an unknown cranium to multiple reference groups, for the purpose of classification (Jantz and Ousley 2005). Currently, the reference groups in FORDISC include American white, American black, Hispanic, Guatemalan, Japanese, Chinese, Vietnamese, and American Indian (Jantz and Ousley 2005).

If an unidentified skeleton is estimated to be Hispanic based on interpretation of FORDISC 3.1 output, that means that the unidentified individual is most
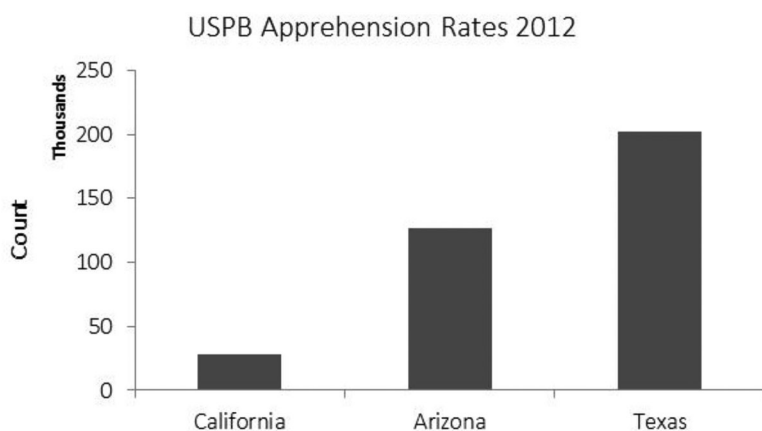
FIGURE 1. USBP apprehension rates in 2012 by State (U.S. Customs and Border Patrol 2012).

morphologically similar to the reference group Hispanic. The Hispanic reference group in FORDISC consists mainly of U.S.–Mexico border-crossing fatalities that died between 2000 and 2012 and positively identified individuals submitted by practicing forensic anthropologists from the late 20th century to present (Jantz and Ousley 2005). Approximately 30 percent of the positively identified Hispanics in the FORDISC 3.1 reference group have a known country of origin, the majority from Mexico. In most areas of the United States, the ancestry designation Hispanic can be useful in narrowing down a list of potential matches from missing persons databases. However, human remains found along the U.S.–Mexico border, in known migrant corridors, present a different perspective on anthropological criteria and local vernacular commonly used in ancestry estimation.

In Brooks County, Texas, in particular, death rates rose between dramatically between 2011 (52 deaths) and 2012 (126 deaths; Collette 2013). Data from the Pima County Office of the Medical Examiner (PCOME) in Tucson, Arizona, suggest that the majority of migrants that die crossing the border in Arizona are from Mexico (Anderson 2008). Apprehension rates from Texas suggest that, in addition to Mexico, migrants are also from Honduras, Guatemala, and El Salvador (Isacson and Meyer 2013). Regardless of country of origin, if ancestry is estimated as Hispanic, it will not help narrow down a list of potential matches from missing person databases that exist in foreign governments or human rights organizations.

In 2012 and 2013, migration increased approximately 15 percent along the U.S.–Mexico (WOLA). Texas and Arizona have the highest apprehension rates along the shared border with Mexico (Isacson et al. 2013). During the fiscal year 2012, U.S. Border Patrol (USBP) apprehended 28,461 individuals in California, 126,500 in Arizona, and 201,912 in Texas (Figure 1; U.S. Customs and Border Patrol 2012). The USBP categorizes apprehensions as "Mexican" or "other than Mexican" (U.S. Customs and Border Patrol 2012), meaning that an apprehended individual is a Mexican national or from some other country. As

previously mentioned, it is presumed that most of the individuals categorized as "other than Mexican" are from Honduras, Guatemala, and El Salvador (Isacson and Meyer 2013). Of the USBP apprehensions, Texas has the highest rate of "other than Mexican" migrants (37 percent) as compared to Arizona (14 percent), and California (4 percent; U.S. Customs and Border Patrol 2012). The geographic origin of the individuals apprehended is informative to the geographic origins of the deceased migrants and in turn is helpful for assessing reference samples needed.

The ten largest Hispanic origin groups in the US (as defined by the U.S. Census Bureau) include Mexico, Puerto Rico, El Salvador, Dominican Republic, Guatemala, Columbia, Honduras, Ecuador, and Peru (Motel and Patten 2012). Genome-wide analysis of population structure among Mexican, Ecuadorian, Columbian, Puerto Rican, and Dominican Republic groups indicates different patterns and magnitudes of European, Native American, and African admixture (Bryc et al. 2010). In turn, these differing levels of admixture should be reflected in cranial morphology due to its high heritability. Unfortunately, skeletal data derived from groups in Latin America and the Caribbean have not accumulated at the rate of those for American blacks and whites, as most recent skeletal collections contain the latter two groups (Spradley 2008). However, large-scale data collection efforts on migrant remains found in Arizona and Texas provide data that can begin to facilitate a finer-grained approach to ancestry estimation along the U.S.–Mexico border (Spradley 2013).

The purpose of this research is to begin to explore the biological variation within a sample of migrants recovered from Brooks County, Texas. Understanding the biological variation through craniometric analysis and comparison to migrants from Arizona can shed light biological similarities and differences that could help with finer-grained ancestry estimation. More precisely pinpointing the geographic origin an individual is from, provided samples become large enough, can help expedite the identification process. If the country of origin can be pinpointed, the search for potential missing persons matches will be narrower and could take less time.

MATERIALS AND METHODS

Four groups are used in the present analyses. Two groups represent unidentified migrants who died crossing the border in Texas (Unidentified Texas Migrants, male $n = 8$ and female $n = 5$) and in Arizona (Unidentified Arizona Migrants, male $n = 127$ and female $n = 18$). Two additional groups represent positively identified or contextually identified individuals from Mexico (Mexican, male $n = 82$ and female $n = 24$) and Guatemala (Guatemalan, male $n = 72$ and female $n = 3$). The majority of data were collected by the author or graduate students or technicians trained by the author. A portion of the PCOME data was collected by several graduate students at the University of Tennessee or forensic anthropologists working at the PCOME. If data existed on other contemporary Central American groups, they would have been included for comparison. The Unidentified Texas Migrants are from exhumations in Brooks County, Texas. The exhumations were carried out by Dr. Lori Baker of Baylor University in conjunction with

TABLE 1. Groups Used in Present Analysis

Group	Male (*n*)	Female (*n*)	Total
Unidentified Arizona Migrants[*]	127	18	145
Unidentified Texas Migrants[**]	8	5	13
Mexican	82	24	106
Guatemalan	72	3	75
Total			339

*Sex estimated from skeletal morphology or DNA.
**Sex estimated from skeletal morphology.

Dr. Krista Latham at the University of Indianapolis. These exhumations were necessary because Brooks County became overwhelmed with the increase in migrant deaths and began to bury the migrants as "unknown" because the county lacked the resources to obtain proper forensic analyses, including DNA sampling. These exhumations and analyses that followed provided the only opportunity for identification of these deaths.

Following the exhumations, many of these remains ($n = 65$) were taken to Texas State University for intake, processing, analysis, and long-term curation until identification. While there is currently only one positive identification thus far, the cultural profile (Birkby et al. 2008), circumstances surrounding death, and anthropological examinations suggest that all individuals exhumed are most likely migrants. Although this sample used in the following analyses is small (female = 5 and male = 8), it does allow for preliminary exploration of morphological variation as compared to unidentified migrants that cross the border in Arizona and groups that are known to migrate to the United States (Mexican and Guatemalan).

The Mexican skeletal data comes from two sources, the PCOME, located in Tucson, Arizona, and the Xóclan contemporary cemetery collection from Mérida, Yucatan in Mexico. All individuals from the Xóclan collection (female = 21 and male = 44) have 20th century birth years and are from an overflow cemetery for the main burial ground in the city (Chi-Keb et al. 2013). In 2006, the Facultad de Ciencias Antropológicas (School of Anthropological Sciences) of the Universidad Autónoma de Yucatán (UADY) started to curate skeletal remains from the cemetery that are positively identified (Chi-Keb et al. 2013).

The PCOME receives a high number of U.S.–Mexico migrant fatalities each year due to their location near what the USBP labels the "Tucson Sector" of the border, spanning 281 miles along the border (Anderson 2008). During the course of a long-term (2009–13) data collection project at the PCOME funded by the National Institute of Justice, 533 skeletons of recently deceased migrants were measured at the PCOME (Spradley 2013). Of those, 105 (at the time of this writing; female = 14 and male = 91) are positively identified although a smaller number of identified and unidentified are used in the present analysis because not all crania were complete (Table 1).

**TABLE 2.** Landmarks Used in Geometric Morphometric Analyses

1	Alare L	17	Inferior nasal border L
2	Alare R	18	Inferior nasal border R
3	Asterion L	19	Opisthion
4	Asterior R	20	Parietal subtense point
5	Basion	21	Porion L
6	Bregma	22	Porion R
7	Dacryon L	23	Prosthion
8	Dacryon R	24	Minimum frontal breadth point L
9	Ectoconchion L	25	Minimum frontal breadth point R
10	Ectoconchion R	26	Cheek height inferior point L
11	Frontomalar anterior L	27	Cheek height superior point R
12	Frontomalar anterior R	28	Minimum nasal breadth L
13	Glabella	29	Minimum nasal breadth R
14	Lambda	30	Zygion L
15	Metopion	31	Zygion R
16	Nasion		

The Guatemalan group (female = 3 and male = 72) is composed of Mayans, victims of human rights violations during Guatemalan's Civil War (1960–96; Spradley et al. 2008). The individuals in this group are likely to have little European admixture. Data were collected at the Forensic Anthropology Foundation in Guatemala (FAFG) and curated in the Forensic Anthropology Data Bank at the University of Tennessee. Some are positively identified, while others contextually identified based on the circumstances surrounding the burial exhumations.

Geometric morphometric analyses were chosen over analyses using traditional inter-landmark distances for purposes of exploring shape variation and morphological visualization. Landmarks were selected to represent overall craniofacial morphology and to maximize the sample sizes for each group. Table 2 provides a list of the 31 landmarks used for geometric morphometric analyses. A Generalized Procrustes analysis (GPA) was used to center, scale, and rotate all individuals into a common coordinate system and eliminate nonshape-related variation (i.e., size; Mitteroecker and Gunz 2009; Slice 2007). Because size is separated from shape during the GPA, males and females were pooled to increase sample sizes. Because the goal of this research is to explore shape variation for the purposes of statistical discrimination for identification purposes, a canonical variates analysis (CVA) was performed in MorphoJ (Klingenberg 2011) to maximize shape variation among groups and determine the shape features that distinguish the groups. Wireframe graphs were used to help assess the morphological shape differences among groups.

TABLE 3. Mahalanobis Distances among Arizona Migrants, Texas Migrants, Guatemalans, and Mexicans

Group	Arizona Migrants	Guatemalan	Mexican
Arizona Migrants	-		
Guatemalan	3.95	-	
Mexican	2.07	4.21	-
Texas Migrants	5.06	6.92	5.08
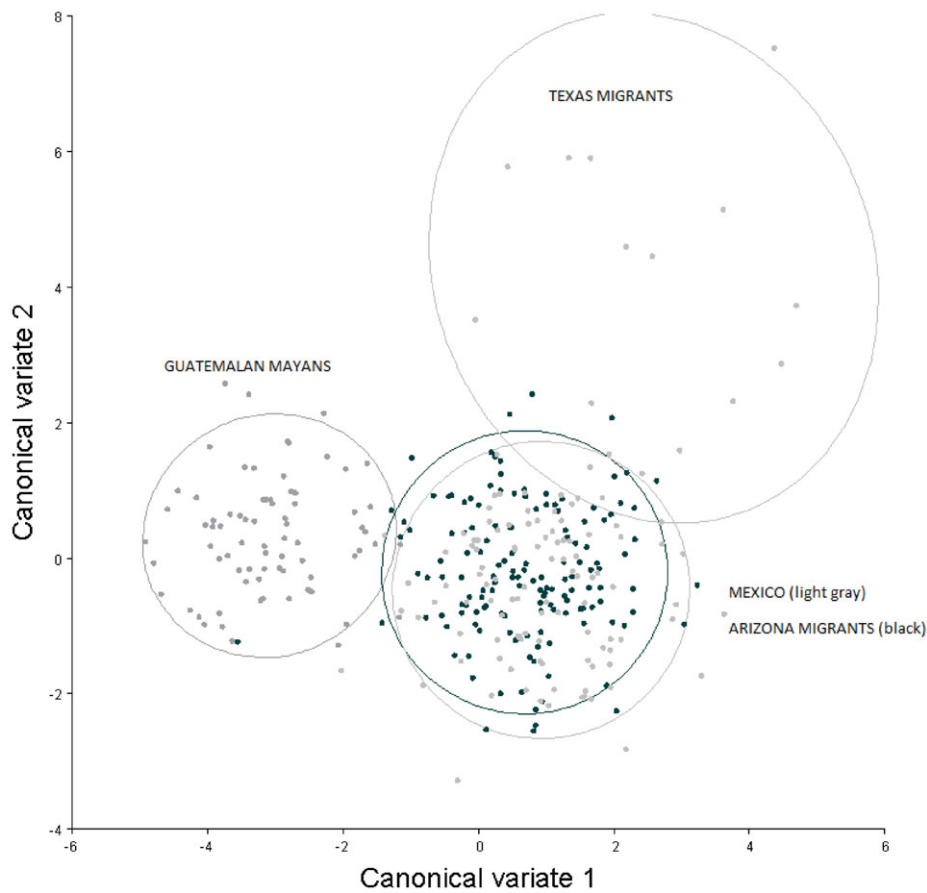
FIGURE 2. Canonical variates plot of Arizona Migrants, Texas Migrants, Mexicans, and Guatemalans.

RESULTS

The Mahalanobis distances generated from the CVA (Table 3) are all significant at the <.001 level. Interpretation of these distances suggests that the Texas Migrants are most differentiated from all other groups and the Arizona Migrants and Mexicans are most similar to one another. The canonical variates (CV) plot further (Figure 2) displays

the separation of the Texas Migrants from other groups. The first axis (CV1, 62 percent variation) separates Guatemalans from all other groups. The second axis (CV2, 18 percent variation) separates the Texas Migrants from all other groups. The Arizona Migrants and the Mexican group overlap suggesting morphological similarity.

The wireframe graphs associated with CV1 are in units of Mahalanobis distances (Figure 3). The light gray outline (Figure 2) is the average shape of all groups and the black line represents a change in ten Mahalanobis distance units from the geometric mean (Klingenberg 2011). Shape variation in the positive direction along CV1 suggests that Texas Migrants, Arizona Migrants, and Mexicans display a more anteriorly projecting nasion and glabella, a more superiorly projecting frontal subtense (metopion), basion, and opisthion in comparison to Guatemalans. Shape variation in the positive direction along CV2 (Figure 3) separates the Texas Migrants from other groups based on a more inferior nasion, influencing a smaller nasal and facial height, an inferiorly located inferior malar height point suggesting larger malar height. Further, CV2 suggests the superior vault including the landmarks metopion, bregma, parietal subtense are all superiorly projecting from the mean suggesting overall larger cranial vault heights for the Texas Migrants. The left and right asterion are also positioned more posteriorly suggesting not only higher cranial vaults but also wider cranial vaults.

DISCUSSION

The overall results of the CVA analysis suggest that it is possible to take a finer-grained approach to ancestry estimation, meaning it is possible to estimate geographic origin (i.e., country or region of origin) rather than using broad categories such as white, black, or Hispanic. In particular, the present analysis suggests good statistical separation of Guatemalan Mayans and Mexicans. The Unidentified Arizona Migrants and Mexicans show considerable overlap suggesting they are similar to one another. A portion of the Mexican sample comes from the PCOME so it is not surprising that the two groups (Unidentified Arizona Migrants and Mexicans) are similar. However, at the same time the results are congruent with previous reports (Anderson 2008) that migrants from the PCOME are predominantly from Mexico. The Texas Unidentified Migrants are differentiated from the Guatemalan Mayans and Mexicans, although overlap with Mexicans exists.

Although Guatemalans are differentiated from all other groups, this group consists of Mayans and does not represent the entire range of variation found within Guatemala. If Guatemalans with more European admixture were included in the present analyses, results may differ. However, at this time no other Guatemalan data are available. Furthermore, the Texas Migrant sample is small, however these results are meant to illustrate the beginning of long-term research goals and suggest the potential in studying the remains of the migrants to fulfill the ultimate goal of better identification criteria along the U.S.–Mexico border. Despite these limitations, the results suggest that Texas Migrants, who are more likely to include individuals from countries other than Mexico, can be craniometrically distinguished from Mexicans and Guatemalan Mayans.
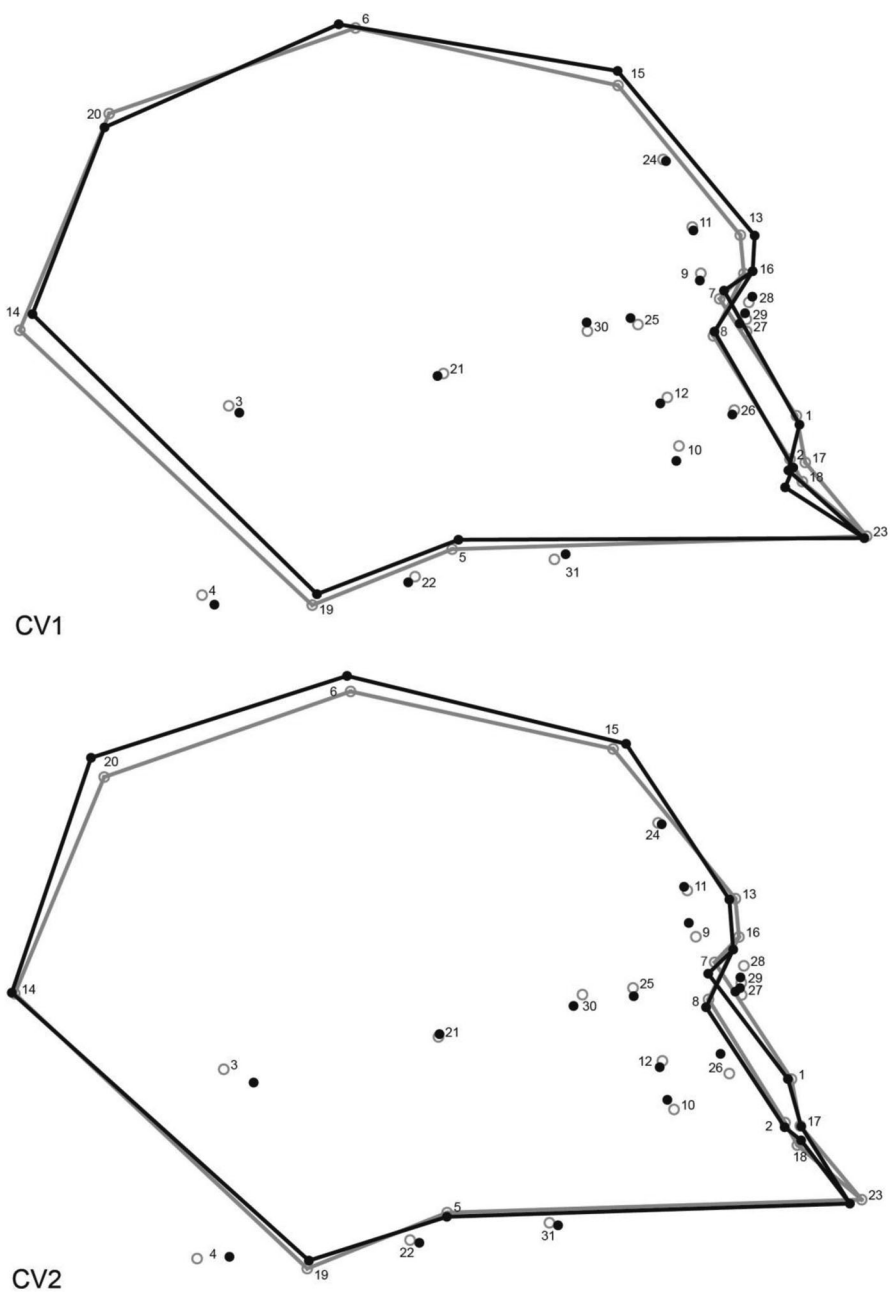
FIGURE 3. Wireframe graphs representing morphological shape differences along CV1 and CV2.

Long-term goals of this research will depend upon the positive identifications of migrant deaths along the U.S.–Mexico border. If craniometric data are systematically collected, then the data can be updated to include country of origin when an identification is made. Once enough data from positive identifications have accumulated from countries other than Mexico (e.g., Honduras, El Salvador) then further analyses will

include assessing which landmarks are best for discrimination among groups and testing nontraditional approaches to ancestry estimation such as machine learning algorithms in addition to traditional approaches such as DFA. The ultimate goal will be to provide an end-user application, within FORDISC or a stand-alone graphic user interface (GUI), for estimation of geographic origin from U.S.–Mexico migrant fatalities. Combing craniometric analyses with isotopic data could add an additional line of evidence for estimating geographic origin.

CONCLUSIONS

When estimating the ancestry of an unidentified migrant along the U.S.–Mexico border, the term Hispanic is of little use. With more population-specific reference data, it is likely that anthropologists may be able to estimate the geographic origin of the migrant in order to narrow down the initial search for potential missing persons. However, more data are needed from Latin American countries before new criteria can be developed and validated. Further, it is always important to remember that estimation is not definitive and should be expressed as a degree of statistical probability. If the associated probability of estimation is low, then a wider search parameter should be used. If the associated probability is high, then the initial search can be narrow and expanded if no results are returned. Using craniometric data to estimate geographic origin of migrant fatalities along the border, provided reference data accumulates, is quick and could facilitate a more rapid search and identification.

The process of identification of migrant remains in Texas, as in every other border state requires collaboration with multiple agencies. Currently, the author is working with the Colibrí Center for Human Rights and the Argentine Forensic Anthropology Team to facilitate migrant identifications along the U.S.–Mexico border. Collaboration with human rights organizations, human rights activists, and foreign consulates in addition to working with local and state law enforcement and medico-legal agencies is a necessity. Resources for decedent identification within the United States, such as the National Missing and Unidentified Persons System (NamUs) and the Combined DNA Index System (CODIS) often lack missing persons information for individuals or appropriate DNA family reference samples for comparison to migrant remains. Because of the lack of centralization of these missing persons data, narrowing down the search criteria by focusing on country of origin using craniometric data will help to expedite the identification process.

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