

Biological Distance, Migrants, and Reference Group Selection in Forensic Anthropology

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Biological distance, or biodistance, has been a useful way to aid in the reconstruction of population structure within prehistoric populations and to gain further knowledge about processes that affect the biological relationships of historic or recent population groups. In prehistoric populations, biodistance can provide information otherwise unavailable (Jantz, 1977; Jantz and Owsley, 2001; Powell and Neves, 1999; Stojanowski and Schillaci, 2006). Biodistance in historical investigations can help corroborate historical documentation (Edgar, 2009; Owsley et al., 2005). Biodistance studies involving recent groups can inform forensic anthropological practice by gaining a better understanding of reference samples used in classification statistics and to understand the relationship of an unknown individual to known reference groups (Jantz and Moore-Jansen, 1988; Owsley et al., 2009; Ross et al., 2004; Spradley, 2014).

Classification statistics, including discriminant function analysis (DFA) or machine learning techniques such as random forest modeling can provide an estimate of geographic origin for an unknown individual. However, the major assumption that goes along with any classification statistic is that the

unknown individual belongs to one of the reference groups. Therefore, having appropriate reference groups and understanding where those reference groups are from, how they biologically relate to one another, and how the unknown relates to the reference groups is the key to a good classification. No matter the method, an important consideration is the appropriateness of reference groups. This is a pressing issue as a classification (estimate) of geographic origin (where in the world the person is from) is produced for use within the medico-legal community and will be compared against missing persons records, making accuracies in such classifications important. As such, the reference groups need to represent the population groups they are applied to, necessitating a need to fully understand the reference groups themselves and their biological similarities to one another. If groups are similar, pooling may be the appropriate option given the nature of the desired outcome. For example, is a broad classification (African, European, Native American) enough to assist with identification, or is something more specific needed that denotes the actual geographic origin and self-described group membership (American Black, American White, Central American)? If a broad classification is desired, pooling groups may be appropriate if they are from the same or similar geographic areas and temporal period. If a more specific classification is desired, pooling may not be the best solution.

Along the US/Mexico border there is a continual flow of migration and, unfortunately, an increasing number of deaths. In recent years, the majority of migrants who die crossing the US/Mexico border are found in Arizona and Texas. Previous research supports the supposition that the majority of migrants that cross the Arizona/Mexico border are from Mexico ([Anderson, 2008](#); [Pima County Office of the Medical Examiner, 2013](#)), predominantly central and south Mexico. Within Texas, the majority of migrants are termed by the US Border Patrol (USBP) as “other than Mexican,” or OTMs. Apprehension statistics indicate the majority of migrants who cross the Texas/Mexico border are from Honduras, El Salvador, and Guatemala followed by Mexico ([U.S. Customs and Border Patrol, 2012](#)). The majority of anthropological analyses on the undocumented migrants have been focused within a forensic context, generating case reports and attempting to facilitate identifications and repatriations. Systematic data collection during forensic anthropological analysis has provided valuable information for better understanding of the biological variation within and among these migrant populations ([Birkby et al., 2008](#); [Hughes et al., 2013](#); [Hurst, 2012](#); [Spradley, 2013, 2014, 2015](#); [Spradley et al., 2015](#); [Tise et al., 2013](#)).

In order to discuss migrant populations, an understanding of migration is important. Until recently, few definitions of migration were provided in the biological anthropology literature ([Cabana and Clark, 2011](#)). Clark defines migration as “a long-term residential relocation by one or more social groups across community boundaries in response to spatially uneven changes in social and economic conditions” (2011, p. 84). Within bioarchaeology, the investigator is typically trying to reconstruct the act and rate of migration, using model-bound methods. Model-bound methods have more assumptions, incorporate measures of similarity, and are meant to provide estimates of specific parameters such as admixture and kinship, while model-free methods evaluate the degree and pattern among groups ([Relethford and Lees, 1982](#), p. 176). However, both are used to quantitatively assess populations that have already experienced the act and long-term effects of migration. The present study differs from most studies of migration in that it uses model-free methods to assess the structure and scale of migration ([Cabana and Clark, 2011](#)). Structure and scale are defined by Cabana and Clark as addressing questions relating to who is migrating, what border is traversed, and how the migrant groups are organized.

The purpose of this chapter is to use biodistance techniques to better understand the biological variation of these migrants and to further explore biological relationships of migrants who die in Arizona

versus those who die in Texas. As forensic anthropologists are called to estimate geographic origin of unidentified individuals, biological distance is also used to understand the biological relationships of these migrants to other reference groups commonly used in forensic anthropological practice.

BACKGROUND

Migration (as defined by [Clark, 2011](#)) is a natural process in the course of human history and is a continual process along the US/Mexico border. The United States has a long history with migration at the US/Mexico border, both authorized and unauthorized. During the late 1930s, the Bracero program was initiated within the US to recruit workers from Mexico and provide them with temporary visas, mostly for work in agriculture within border states ([Brick et al., 2011](#)). Central Americans also took advantage of the program. The Bracero program ended in 1964 and subsequent changes in US policy fueled a demand for immigrant labor beginning in the 1970s. The demise of the Bracero program meant that the majority of Mexicans and Central Americans supplying the continued labor demand were unauthorized. Mexico currently makes up the largest group of naturalized and unauthorized immigrants in the United States followed by Central American countries, particularly El Salvador, Guatemala, and Honduras ([Brick et al., 2011](#); [Ramirez and de la Cruz, 2002](#)).

Currently, the demand for immigrant labor has not diminished and it is estimated that without immigrant labor the US would be short 7.3 million workers in the workforce over the next decade ([Myers et al., 2013](#), p. 5). There are a number of reasons why Mexicans and Central Americans continue to migrate to the United States, including escaping economic circumstances and violence. In response to unauthorized migration, in 1994 the USBP adopted the policy “Prevention through Deterrence” as their operational strategy of choice for securing the US/Mexico border. This strategy deterred migrant crossings in populated areas that were relatively safe and instead forced migrants to cross in more remote and dangerous areas such as the Sonoran Desert ([Haddal, 2010](#)). As a result, a funnel effect was created that led to an increase in migrant apprehensions and deaths ([Martinez et al., 2013](#)). Although USBP strategies have historically aimed to stop migrants before entering the United States, migration continues and the problem remains: deaths continue, creating a humanitarian crisis at the US/Mexico border. Until recently the majority of migrant deaths occurred in Arizona despite the fact that the Texas/Mexico border covers 1254 miles of the 1900 miles of the entire border. However, in 2012 Texas surpassed Arizona in deaths. The majority of these deaths occur in the Rio Grande Valley and more specifically in Brooks County, Texas ([U.S. Customs and Border Patrol, 2012](#)).

The Pima County Office of the Medical Examiner (PCOME) located in Tucson, Arizona receives the majority of migrant remains, due to their proximity to the border. The PCOME also keeps official statistics on border deaths. In 2000, as a result of “Prevention through Deterrence,” migrant death rates began to rise. Between 1990 and 1999, 129 deaths occurred along the Arizona/Mexico border in contrast to 802 deaths that occurred over the next 5 years ([Martinez et al., 2013](#)). The identification rate of the migrants at the PCOME is approximately 60%. Based on information collected by the PCOME, the majority of migrants analyzed in the W.H. Birkby Forensic Anthropology Laboratory since 2001 were from Mexico (1285/85%), followed by Guatemala (120/8%), and El Salvador (40/3%) ([Pima County Office of the Medical Examiner, 2013](#)).

In Texas, unlike Arizona, not all migrant deaths are sent to a medical examiner’s office. Brooks County, Texas (942 mi²) receives the highest reported number of undocumented migrant deaths each

year (80 in 2011, 129 in 2012, and 87 in 2013). These deaths fall under the jurisdiction of a justice of the peace (JP), since there is no medical examiner within the county. Due to the lack of a centralized location for medico-legal investigation of migrant remains, there exists a lack of centralized record keeping on information pertaining to the identification rate of migrants and their countries of origin. Therefore, the USBP apprehension rates are used as a proxy for country of origin. As stated previously, the majority of apprehensions are from Central America, specifically Honduras, El Salvador, and Guatemala.

Because the geographic origins of apprehensions should correlate with the geographic origins of decedents, these two migrant samples offer a unique insight into biodistance studies. Both source populations are from Latin America, a broad geographic location; however, Arizona receives high numbers of Mexicans while Texas receives high numbers of Central Americans. Cranial morphology has been shown to be a proxy for genetic data, in that quantitative continuous traits can provide information about genetic similarities (Carson, 2006; Devor, 1987; Herrera et al., 2014; Relethford, 2004; Relethford and Blangero, 1990; Strauss and Hubbe, 2010). Because Arizona and Texas migrants represent Mexico and Central American groups, respectively, craniofacial morphology from these migrant groups can be used to explore among and within group biological variation and their morphometric similarities to other forensic reference groups.

The objective of this research is to ascertain, through biological distance measures, how the migrant groups are organized in terms of population structure. Can the migrants who cross into Arizona be distinguished from the migrants who cross into Texas? As these groups represent active forensic anthropology cases it is important to establish if these two groups can be distinguished from other relevant reference groups for purposes of improving ancestry estimation.

MATERIALS AND METHODS

Population Groups

Migrant Groups

Two migrant groups representing deaths along the Arizona and Texas borders are from (1) the PCOME located in Tucson, Arizona and (2) from exhumations carried out in Brooks County, Texas housed at the Forensic Anthropology Center at Texas State (FACTS). Due to the high volume of migrant deaths along the border and because these deaths are taken to the PCOME for anthropological or pathological examination, systematic craniometric data collection was possible (see Spradley, 2013). In the late 2000s, Texas saw an increase in migrant deaths, most notable in the USBP Rio Grande Valley Sector. Due to this dramatic increase in deaths and lack of resources, the local JP and Brooks County Sheriff's Office were overwhelmed with deaths and began to bury the deceased individuals, most without proper analyses or collection of DNA samples, leaving little chance for identification and repatriation.

During the summers of 2012 and 2013, Drs. Lori Baker (Baylor University) and Krista Latham (University of Indianapolis) and their students performed voluntary exhumations of burials within Brooks County for the purposes of skeletal analysis and DNA sampling in hopes of facilitating positive identifications. From these exhumations and the cases sent from a South Texas Medical Examiner, a total of 80 migrant individuals were sent to Texas State University for processing and analyses. The majority of these individuals had significant amounts of flesh that required extensive processing prior to analysis. To date, 40 individuals have been processed and analyzed.

Group	N
Migrants	
Arizona female	39
Arizona male	182
Texas female	19
Texas male	20
Forensic reference groups	
Guatemalan male	87
American Black female	86
American Black male	151
American White female	306
American White male	543
^a These sample sizes reflect the starting sample sizes; each analysis will have a different sample size based on missing data due to trauma, taphonomic factors, or age-related changes.	

The undocumented migrants from the PCOME (Arizona) and from FACTS (Texas) are used in all subsequent analyses (Table 12.1). The PCOME data come from two sources, the Forensic Anthropology Data Bank (FDB), and a long-term data collection project between Texas State University and the PCOME (Spradley, 2013). Because various aspects of biological variation between males and females are of interest, only individuals with known sex from DNA or from pelvic morphology were used in the present analyses. Many individuals from the PCOME are crania only and sexing reliability from cranial morphology alone has been shown to be difficult for this particular population group. Both samples contain identified and unidentified individuals.

Forensic Reference Groups

Additional forensic reference groups include American Black and White males and females and Guatemalan males (see Table 12.1). The American Black and White groups are from the FDB (Jantz and Moore-Jansen, 1988); the Guatemalan sample was collected by the author at the Forensic Anthropology Foundation of Guatemala on behalf of the FDB. The FDB is a repository of data collected by forensic anthropologists, curated by Dr. Richard Jantz at the University of Tennessee. While the cases in the FDB are predominantly from the United States, it does contain a southeastern bias as the majority of the data were collected through the efforts of Dr. Jantz. The Guatemalan sample contains only males and represents Mayans who were victims of Guatemala's Civil War. These particular forensic reference groups were chosen based on the fact that they contain birth-years post-1930 and minimally contain the standard craniometric data found in Moore-Jansen et al. (1994).

Craniometric Data

The craniometric data selected for use in the subsequent analyses were collected according to standards found in Moore Jansen et al. (1994) or Howells (1973). The migrant and Guatemalan data were all collected with the Microscribe digitizer and the program 3Skull (SD Ousley, 2004). For the FDB,

Glabella-occipital length (GOL)	Bimaxillary subtense (SSS)
Basion-nasion length (BNL)	Dacryon subtense (DKS)
Basion-bregma height (BBH)	Inferior malar length (IML)
Biasterronic breadth (ASB)	Minimum malar height (WMH)
Minimum frontal breadth (WFB)	Frontal chord (FRC)
Basion-prosthion length (BPL)	Frontal subtense (FRS)
Nasion-prosthion height (NPH)	Parietal chord (PAC)
Nasal height (NLH)	Parietal subtense (PAS)
Nasal breadth (NLB)	Occipital chord (OCC)
Maximum alveolar breadth (MAB)	Occipital subtense (OCS)
Orbital breadth (OBB)	Bregma radius (BRR)
Interorbital breadth (DKB)	Basion radius (BAR)

some data were collected with calipers while in other instances data were collected using the Microscribe. The craniometric data selected for the following analyses are presented in [Table 12.2](#) and were selected for representing the overall craniofacial morphology and to maximize sample sizes.

Analyses

Arizona and Texas Migrants

In order to assess similarity among the Arizona and Texas males and females, Mahalanobis squared Euclidean distance (D^2) was obtained as a measure of biological similarity between the two groups. A canonical discriminant analysis (CANDISC) was used to reduce the dimensionality of the data and assess the overall morphological similarities and dissimilarities between the two migrant groups. The variables chosen for the CANDISC include 24 interlandmark distances representing the overall craniofacial complex and maximize sample sizes (see [Table 12.2](#)). A discriminant function analysis (DFA) with cross-validated classification rates was used to determine how well the two groups classify. Prior to running the DFA, a stepwise variable selection procedure was employed, by sex, to reduce the number of variables as to not overfit the data.

Arizona and Texas Migrants and Forensic Reference Groups

The same procedures described for Arizona and Texas migrants were employed for the comparison of the migrant groups to other forensically relevant reference groups, American Black and White males and females and Guatemalan males. Because the Arizona and Texas migrants and Guatemalans are all from Latin America, it is expected, based on an isolation by distance model, that they will be more similar to one another than to the American Black and White groups. Therefore, the Mahalanobis D^2 was evaluated for all groups. If the distances between the groups are small and insignificant, then the analyses are repeated by combining the groups with small D^2 values.

Results

Arizona and Texas Migrants

The D^2 values ([Table 12.3](#)) derived from the DFA suggest that the Arizona and Texas females are the most similar to each other followed by the Arizona males. The Arizona males and females are more similar to

Group	Arizona Female	Texas Female	Arizona Male
Arizona female	—		
Texas female	4.94	—	
Arizona male	11.45	13.74	—
Texas male	10.28	8.00	5.20

^aVariables: GOL, BNL, BBH, ASB, WFB, BPL, NPH, NLH, NLB, MAB, OBB, DKB, SSS, DKS, IML, WMH, FRC, FRS, PAC, PAS, OCC, OCS, BRR, and BAR.

each other than the Texas males and females; this could be due to differences in sample size. However, the Texas group has a more equal distribution of males to females than the Arizona group. The canonical plot (Fig. 12.1) represents 93% of the total variation. The males and females are separated on the first axis while the two population groups on the second axis. Based on the first axis, the males exhibit larger values for all variables in the between canonical structure with the exception of the frontal subtense (FRS). The second axis is separating the Texas males and females from the Arizona males and females based on larger values for parietal subtense (PAS), FRS, interorbital breadth (DKB), and minimum frontal breadth (WFB).

The DFA (Table 12.4) results produce good classification, higher than random chance, with 78% of the Arizona migrant females correctly classified and 76% of the Texas migrant females. The variables used

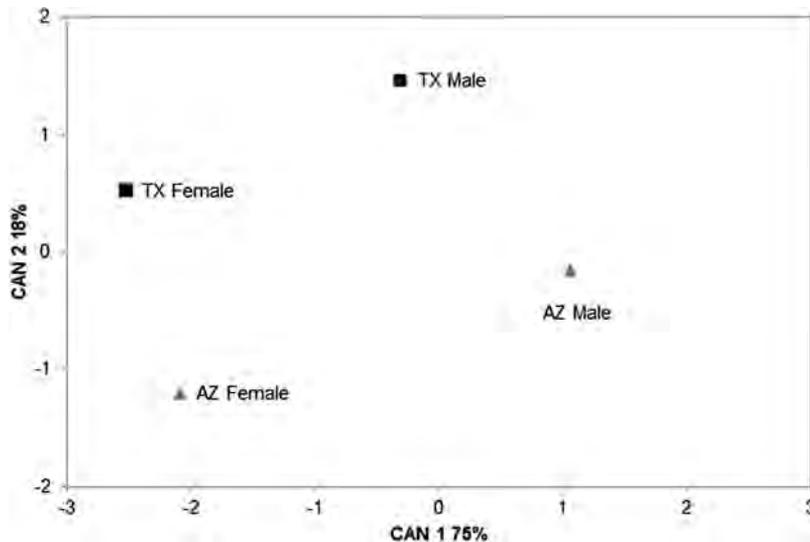


FIGURE 12.1 Plot of canonical means for Arizona and Texas males and females.

Variables: GOL, BNL, BBH, ASB, WFB, BPL, NPH, NLH, NLB, MAB, OBB, DKB, SSS, DKS, IML, WMH, FRC, FRS, PAC, PAS, OCC, OCS, BRR, and BAR.

Group	N	Cross-Validated Classification Rate (%)
Arizona female	18	76.47
Texas female	17	77.78
Arizona male	77	80.52
Texas male	15	73.33

^aStepwise selected variables for females: BAR, DKS, MAB, IML, OCS, OCC, and PAS.
^bStepwise selected variables for males: IML, BAR, NLB, DKS, WFB, MAB, OBB, and DKB.

for discrimination include basion radius (BAR), dacryon subtense (DKS), maximum alveolar breadth (MAB), inferior malar length (IML), occipital subtense (OCS), occipital chord (OCC), and PAS. The Arizona migrant males have an 81% classification rate and the Texas migrant males a 73% classification rate. The variables used to discriminate male migrants include IML, BAR, nasal breadth (NLB), DKS, WFB, MAB, orbital breadth (OBB), and DKB.

Arizona and Texas Migrants and Forensic Reference Groups

The D^2 values indicate that the smallest distances are found among the Texas, Arizona, and Guatemalan groups (Table 12.5). In the canonical plot (Fig. 12.2), the first axis separates American White females and males from all other groups, with American Black males intermediate. The American White group is the most differentiated based on larger values for DKS, frontal chord (FRC), FRS, biasterionic breadth (ASB), basion-bregma height (BBH), WFB, glabella-occipital length (GOL), bregma radius (BRR), parietal chord (PAC), basion-nasion length (BNL), OCC, BAR, bimaxillary subtense (SSS), and OCS. The second axis separates American Black and White, Arizona, and Guatemalan males from all other groups. The second axis separates males and females with the exception of the Texas males.

The American Black males are most differentiated from all other groups on the second axis based on larger values for basion-prosthion length (BPL), IML, DKB, nasion-prosthion height (NPH), MAB, NLB, and nasal height (NLH). Fig. 12.2 The American Black and White males and American White females are differentiated from all other groups on the plot with the American Black females clustering with the Arizona and Texas migrants and Guatemalan males.

The DFA results classify 50% of the Arizona migrant females correctly, as well as 53% of the Texas migrant females, 80% of the American Black females, and 89% of the American White females. (Table 12.6) of the males, 52% of the Arizona migrant males classified correctly, as well as 74% of the Guatemalan males, 80% of the American Black males, 40% of the Texas migrant males, and 79% of the American White males.

Combining Groups for Discriminant Function Analysis

Due to the small D^2 values among the Arizona, Texas, and Guatemalan migrants, these groups were combined into a general Hispanic group. The term Hispanic is a generic category that erases cultural identity and nationality. These groups are combined and labeled Hispanic due to the small D^2 values

Table 12.5 Mahalanobis D² for Arizona, Texas, and Other Forensic Reference Groups^a

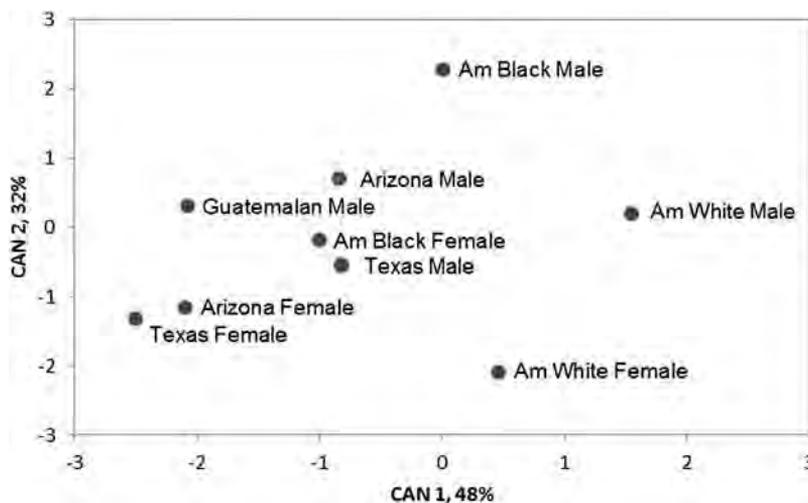
Group	Arizona Female	American Black Female	Texas Female	American White Female	Arizona Male	American Black Male	Guatemalan Male	Texas Male
Arizona female	—							
American Black female	6.37	—						
Texas female	4.01	8.00	—					
American White female	9.98	8.52	11.09	—				
Arizona male	7.69	6.78	9.62	11.01	—			
American Black male	19.34	8.47	21.04	20.25	7.35	—		
Guatemalan male	7.01	8.78	7.06	13.70	3.46	12.62	—	
Texas male	7.67	7.91	6.23	6.18	3.75	12.86	4.46	—
American White male	17.49	11.52	20.69	6.98	6.52	9.32	13.76	7.70

^aVariables: GOL, BNL, BBH, ASB, WFB, BPL, NPH, NLH, NLB, MAB, OBB, DKB, SSS, DKS, IML, WMH, FRC, FRS, PAC, PAS, OCC, OCS, BRR, and BAR.

Table 12.6 DFA Cross-Validation Classification Rates for Arizona, Texas, and Other Forensic Reference Groups

Group	Female N	Female Classification Rate (%) ^a	Male N	Male Classification Rate (%) ^b
Arizona	18	50	75	52
Texas	17	53	15	40
Guatemalan	—	—	66	74
American Black	20	80	44	80
American White	71	89	177	79

^aFemale stepwise selected variables: NLB, GOL, IML, BPL, BNL, BPL, BRR, FRS, MAB, BBH, ASB, and PAS.
^bMale stepwise selected variables: GOL, DKS, MAB, IML, BNL, BPL, FRS, DKB, WFB, NLB, OCS, PAC, PAS, OBB, BAR.

**FIGURE 12.2** Plot of canonical means for Arizona and Texas and other forensic reference groups.

Variables: GOL, BNL, BBH, ASB, WFB, BPL, NPH, NLH, NLB, MAB, OBB, DKB, SSS, DKS, IML, WMH, FRC, FRS, PAC, PAS, OCC, OCS, BRR, and BAR.

indicating similarity to one another. The plot of the canonical means (Fig. 12.2), showing 80% of the total variation, indicates that the Hispanic groups cluster together on the first axis along with the American Black females.

The first axis also separates American White females and males from all other groups, with American Black males intermediate. The American White group is the most differentiated based on larger values for DKS, FRC, FRS, ASB, BBH, WFB, GOL, BRR, PAC, BNL, OCC, BAR, SSS, and OCS. The second axis

Table 12.7 DFA and Cross-Validated Classification Rates for Combined Hispanic Groups and Other Forensic Reference Groups^{a, b, c}

Group	Female N	Female Classification Rate (%) ^b	Male N	Male Classification Rate (%) ^c
Hispanic	36	79	194	84
American Black	19	19	48	85
American White	71	71	189	83

^aIncluding Guatemalan males (n = 66) separately with TX and AZ combined results in AMB 81%, Guatemalan 68%, Hispanic 51%, and White 82%.

^bStepwise selected variables for females: GOL, BNL, BPL, BBH, NLB, MAB, DKB, IML, FRS, ASB and BRR.

^cStepwise selected variables for males: GOL, BNL, BPL, DKB, NLB, MAB, OBB, IML, WMH, WFB, ASB, FRC, FRS, PAS, and OCS.

separates American Black and White, Arizona, and Guatemalan males from all other groups. The second axis separates males and females with the exception of the Texas males. The American Black males are most differentiated from all other groups on the second axis based on larger values for BPL, IML, DKB, NPH, MAB, NLB, and NLH.

The classification results for females and males improved when combining the population specific groups into a broad Hispanic category. For the Hispanic females 79% classified correctly, as well as 78% for the American Black, and 92% for the American White. The Hispanic males achieved an 84% classification rate, American Black males achieved 85%, and American White males achieved 83% (Table 12.7).

DISCUSSION

Addressing issues of structure and scale as defined by Cabana and Clark (2011), partitioning the migrant groups by the location where they were found, Arizona and Texas, suggests both demographic and morphological differences are evident between the groups. Texas receives an equal male-to-female distribution while Arizona receives an unequal sex distribution, with more males than females. The D^2 values and DFA indicate that the Texas and Arizona migrants are morphologically dissimilar enough for classification accuracy, suggesting that it is possible to distinguish the two groups from one another, as previously suggested using craniometric data and genetic data.

Spradley (2014), using smaller sample sizes and geometric morphometric methods, found that Texas migrants were dissimilar from Arizona migrants based on several facial features and more projecting anterior vault landmarks including metopion (FRS point), bregma, and PAS in the Texas migrants. The present analyses found the crania of the Texas migrants larger than Arizona migrants based on overall values for anterior vault measurements, including FRS and PAS and DKB, allowing these two groups to achieve good classification rates. Further, Salazar-Flores et al. (2015) using short tandem repeats and Nei genetic distances found that although Central American and Mexican Mestizos are genetically more similar to each other than South Americans and Caribbeans, the two groups are still genetically differentiated from one another.

When the migrants are compared to the forensic reference samples, the migrants cluster together and classification rates drop for the migrants and Guatemalans. This clustering and drop in classification rates are primarily related to size with the American White males and females and American Black males exhibiting larger values for all variables. When the migrant groups are pooled with the Guatemalan group to form a broad Hispanic group, classification rates increase. These results suggest that the Latin American groups are more similar to one another than to the other groups. Further, these groups are considered complex population groups having Spanish, Native American, and some African admixture and often show an intermediate position between parental groups, making them more challenging to classify.

Though pooling the Latin American groups does not address the structure or scale of migration, it does inform forensic anthropological practice. Using nonmetric traits, [Hefner et al. \(2015\)](#) previously found that when a broad classification is needed, it is statistically sound to pool the groups considered Hispanic. While pooling specific groups from Latin America may be useful to achieve a broad classification of Hispanic in general anthropological practice within the United States, when working with individual cases with enough circumstantial evidence that fits the profile of a migrant, a more specific classification may be of greater use.

Thus, once the classification of Hispanic is identified, it may be useful to attempt a separate DFA using more population-specific groups. At present, positively identified Mexican and Guatemalan reference groups exist. However, for Central American groups (ie, Honduran, El Salvadoran) enough data do not exist. Rather, these data are contextually inferred in that the Texas migrants are from Central America and can be differentiated from Arizona migrants predominantly from Mexico.

The issue of the mass disaster along the US/Mexico border and the humanitarian crisis it has created suggests that anthropologists need to know that an individual fits the overall migrant profile; in this case the designation of Hispanic in addition to other contextual information (see [Birkby et al., 2008](#) for a discussion of the cultural profile of migrants) may be helpful. However, saying someone is Hispanic on the border is not necessarily helpful if the goal is to figure out where they are from within Latin America. Collecting data on these migrants can further research and development in forensic anthropological practice while also informing modern human variation and issues of population structure through morphological analysis.

Arizona and Texas are not the primary destinations for all migrants. While the states that traditionally receive Latin American immigration vary based on country of origin, California and Texas are the states with the largest immigrant communities from all four countries. However, as of 2010 Mexicans and Central Americans began to settle in Georgia, Nevada, North Carolina, New York, Colorado, New Jersey, Washington, and Florida ([Telford, 2014](#)). Therefore, these immigrants, authorized or unauthorized, are no longer heavily clustered within certain regions of the United States. While it was once forensic anthropologists in the Southwest who were faced with the majority of immigrants or naturalized citizens from Latin America, today practitioners from all over the country are likely to see an increase of Latin Americans in their casework. The data collected by forensic anthropologists used in the present research highlight the role forensic anthropologists play in the data collection that is used to further understanding of modern human variation, migration, and practice.

The results presented here suggest that within the United States, the use of a broad Hispanic reference sample will increase classification accuracy. However, if the goal is to estimate where in the world the individual is from, comparing the unknown forensic case to more specific geographically defined groups will be more informative.

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