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Project IDENTIFICATION:

DEVELOPING ACCURATE IDENTIFICATION CRITERIA FOR HISPANICS

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Abstract

The population considered Hispanic is the second-largest population group in the United States, and there are no skeletal collections with large numbers of Hispanics. If there are no criteria to accurately assess the sex and ancestry, two fundamental components of a biological profile, then Hispanic individuals will remain unidentified as they show up in forensic anthropological cases across the nation. The Hispanic population in the United States consists mainly of individuals of Mexican origin. There are no population-specific reference data or criteria available for Hispanics of Mexican origin. The goal of this project is threefold: 1) to obtain cranial and postcranial skeletal measurements from individuals from Mexico to establish a database of available reference data for further research and development; 2) to create sectioning points and classification functions for population-specific sex estimates applicable to the majority of Hispanics within the United States; and 3) to utilize traditional and geometric morphometric methods with the new reference data to explore morphological variation of among Mexicans, American Blacks, and Whites, to provide better classification accuracy in ancestry estimation. It is expected that new reference data from positively identified Mexicans will improve sex and ancestry estimation.

The Mexican skeletal data comes from three sources: the Pima County Office of the Medical Examiner (PCOME) located in Tucson, Arizona, and two documented cemetery collections from Mexico from Zimapan, Hidalgo, and Mérida, Yucatan. Data that was previously collected data from the PCOME for the Forensic Anthropology Data Bank (FDB) were included to increase sample sizes. Only positively identified Mexicans were included in all analyses. Secondary reference data was obtained from the FDB for comparison purposes. A reference group of recent Guatemalans was included in analyses, as once inside the borders of the U.S., they are considered Hispanic.

A discriminant function analysis (DFA) was employed to generate sex classification functions for each long bone, clavicle, scapula, and calcaneus. Sectioning points were also created for individual measurements from the bones with high Mahalanobis D^2 values. Geometric morphometric methods were utilized to explore differences in craniofacial morphology size and shape between two Hispanic groups (Mexicans and Guatemalans) as compared to American Blacks and Whites. DFA was employed using principal component scores derived from geometric morphometric analyses and using traditional craniometrics. The traditional craniometric DFA utilized both standard data (Buikstra and Ubelaker 1994; Moore-Jansen et al. 1994) and the Howells (1973) measurement set.

New population-specific classification functions are presented that provide cross-validated classification rates up to 96%. Results of the geometric morphometric analyses indicate that Mexicans and Guatemalans are smaller in size than American Whites and Blacks, and all groups differ in craniofacial morphology, particularly in the mid-facial region. An analysis of shape shows that Mexicans and Guatemalan have small cranial vaults in height and length, exhibit alveolar prognathism, and have a wide mid-facial area. However, using principal components with centroid size fails to achieve classification rates as high as traditional craniometric data in ancestry estimation. When running a DFA with all reference groups, the Mexican sample provides the lowest classification values. When Guatemalans are removed from the analysis, the classification rate for Mexicans increases.

The data collected for Project IDENTIFICATION provide new reference data to further research and development in forensic anthropology. Population-specific sex estimation criteria are now available that are appropriate for the majority of Hispanics (of Mexican origin) in the U.S. Ancestry estimation criteria are also improved with appropriate, population-specific data. Because ancestry classifications improve with the addition of Howells measurements, it is recommended that these measurements are incorporated into data collection protocol for forensic anthropologists.

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Executive Summary

1 RESEARCH PROBLEM AND GOALS

Forensic anthropologists tasked with the identification of severely decomposed or skeletal remains must generate a biological profile. This biological profile can then be used to compare with missing persons records to help narrow down the identity of the remains in question. The biological profile includes sex, ancestry, age, and stature. Of these profile components, sex and ancestry are critically important. If the sex is incorrect, the remains are likely to remain unidentified. If the ancestry is incorrect, the remains may remain unidentified or the investigation may be delayed. Assessments of sex and ancestry are dependent upon population-specific skeletal reference data. Currently in the United States, the second largest population group is referred to as Hispanic and there are no skeletal collections with large numbers that represent this group. If there are no criteria to accurately assess the sex and ancestry, two fundamental components of a biological profile, then individuals considered Hispanic will remain unidentified as they show up in forensic anthropological cases across the nation.

The majority of data available to forensic anthropologists for research and development in forensic anthropology comes from late 19th- and early 20th-century skeletal collections of American Blacks and Whites. Even more recent documented collections such as the William M. Bass donated skeletal collection at The University of Tennessee at Knoxville and the Documented Skeletal Collection at Texas State University-San Marcos contain mostly American White and Black skeletons (Shirley et al. 2011). The Forensic Anthropology Data Bank (FDB) is the largest repository with metric reference data for Hispanic skeletons (Jantz and Moore-Jansen 1988). However, the problems surrounding the FDB data is that the majority are assumed to be Hispanic based on the context (e.g., found in close proximity to the U.S.–Mexico Border) or have a designation of Hispanic with no further information regarding geographic origin[1].

As the second-largest population group in the country, the population considered Hispanic in the U.S. consists mainly of individuals of Mexican origin (Figure 1). The goal of this project is to: 1) obtain

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[1] Data from the FDB was made available by Dr. Richard Jantz.

cranial and postcranial skeletal measurements from individuals from Mexico to establish a database of available reference data for further research and development by forensic anthropologists; 2) to create sectioning points and classification functions for population-specific sex estimates applicable to the majority of Hispanics within the U.S.; and 3) to utilize traditional and geometric morphometric methods with the new reference data to explore morphological variation of among Mexicans, American Blacks, and Whites, to provide better classification accuracy in ancestry estimation. It is expected that new reference data from positively identified Mexicans will improve sex and ancestry estimation.

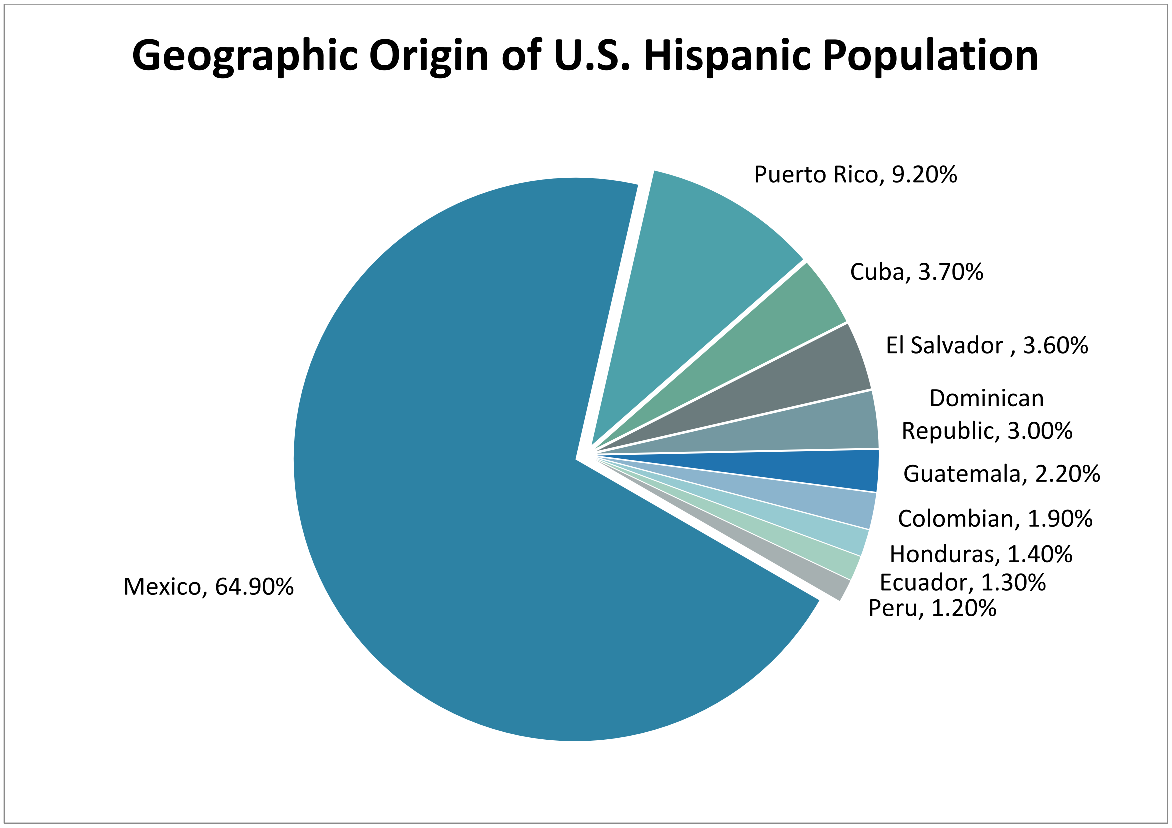

Figure 1. Geographic origin of U.S. Hispanic population (data from Motel and Patten [2012]).

2 RESEARCH DESIGN

A. REFERENCE SAMPLES

The Mexican skeletal data comes from three sources: border-crosser fatalities from the Pima County Office of the Medical Examiner (PCOME) located in Tucson, Arizona; a documented cemetery collection from Zimapan, Hidalgo, Mexico, held at Universidad Nacional Autónoma de México UNAM; and a documented collection from the Xoclán cemetery, held at Universidad Autónoma de Yucatán UADY in Mérida, Yucatan, Mexico. These cemetery collections represent modern Mexicans with birth years spanning the early 19th century to 1980. The UNAM collection represents slightly earlier birth years than the collection at UADY. Of the 2,000 miles of shared border between the U.S. and Mexico, 281 miles are located in what the U.S. Border Patrol (USBP) refers to as the Tucson Sector (Anderson 2008). It is from the Tucson Sector that the PCOME receives border-crossing fatalities. During the course of Project Identification, 533 skeletons were measured (Table 1). Of those, 215 are positively identified. The identification process is ongoing at the PCOME, and data collected during this project will continue to be updated with reference to positive identifications for inclusion into the FDB, and subsequently FORDISC 3.0 (Jantz and Ousley 2005). FORDISC is, a personal discriminant function program that uses reference data from the FDB.

Secondary reference data was obtained from the FDB for comparison purposes. A reference group of Guatemalans was included in analyses due to the fact that once inside the borders of the U.S., they are considered Hispanic. This group is composed of victims of human right's violations during Guatemalan's Civil War (Spradley et al. 2008). Data was collected at the Forensic Anthropology Foundation in Guatemala (FAFG) and curated in the FDB. American Blacks and Whites from the FDB are also included, along with Hispanic groups, because they represent the three largest population groups in the U.S. The American Blacks and Whites are from positively identified forensic cases and documented skeletal collections.

Table 1. Reference Groups for Analysis.*

Institution	Country of Origin	Female	Male	Unknown	Total
PCOME					
Identified	Mexico	9	68		77
	El Salvador	2	3		5
	Guatemala	1	5		6
	Honduras		1		1
	Peru	1			1
	USA	1	12		13
	Unknown		2		2
Unidentified**		23	170	125	318
UADY					
Xoclán Collection	Mexico	21	44		65
UNAM					
Zimapan Collection	Mexico	16	29		45
FDB					
American White	USA	306	521		827
American Black	USA	86	148		234
Mexican	Mexico	5	51		56
Total		471	1054	125	1650

* Project IDENTIFICATION funded data collection at the PCOME and UADY.
**Sex is based on DNA.

B. DATA COLLECTION

Craniometric data was collected using a Microscribe® G2X digitizer in conjunction with the program 3Skull (Ousley 2004). The Microscribe® G2X digitizer collects landmark or coordinate data. 3Skull archives the coordinate data in one table and calculates the inter-landmark distances, archiving these data in another table. The end result is a database containing inter-landmark distances (or traditional craniometric data) and the landmark data. The traditional craniometric data archived includes all the standard craniometric data and additional craniometric data defined by Howells (1973) (Table 2). Standard postcranial metric data were also collected (Buikstra and Ubelaker 1994; Moore-Jansen et al. 1994), as were additional postcranial metrics following the definitions outlined in Zobeck (1983) (Table 3). These additional postcranial measurements have shown to differentiate population groups better than the standard measurements (Zobeck 1983).

Table 2. Howells Cranial Measurements and Abbreviations.

Abbreviation	Measurement	Abbreviation	Measurement
GOL	glabella-occipital	PAS	parietal subtense
NOL	nasion-occipital	PAF	parietal fraction
BNL	basion-nasion	OCC	occipital chord
BBH	basion-bregma	OCS	occipital subtense
WFB	minimum frontal breadth	OCF	occipital fraction
XCB	max cran br	FOL	foramen magnum length
XFB	max frontal br	FOB	foramen magnum breadth
ZYB	byzygomatic breadth	NAR	nasion radius
AUB	biauricular breadth	SSR	subspinale radius
ASB	biasterionic breadth	PRR	prosthion radius
BPL	basion-prosthion length	DKR	dacryon radius
NPH	nasion-prosthion height	ZOR	zygoorbitale radius
NLH	nasal height	FMR	frontomalare radius
JUB	bijugal breadth	EKR	ectoconchion radius
NLB	nasal breadth	ZMR	zygomaxillare radius
MAB	external palate breadth	AVR	M1 alveolar radius
MAL	external palate length	BRR	bregma radius
MDH	mastoid height	VRR	vertex radius
OBH	orbital height	LAR	lambda radius
OBB	orbital breadth	OSR	opisthion radius
DKB	interorbital br	BAR	basion radius
NDS	nasion-dacryon subtense	NAA	nasion angle
WNB	simotic chord	PRA	prosthion angle
SIS	simotic subtense	BAA	basion angle, nasion-prosthion
ZMB	bimaxillary br	NBA	nasion angle
SSS	zygo-maxillary subtense	BBA	basion angle, nasion-bregma
FMB	bifrontal breadth	BRA	Bregma angle
NAS	nasio-frontal subtense	SSA	zygomaxillary angle
EKB	bi-orbital breadth	NFA	nasio-frontal angle
DKS	dacryon subtense	DKA	dacryal angle
IML	inferior malar length	NDA	o-dacryal angle
XML	maximum malar length	SIA	simiotic angle
MLS	malar subtense	FRA	frontal angle
WMH	minimum malar height	PAA	parietal angle
SOS	supraorbital projection	OCA	occipital angle
GLS	glabella projection	RFA	radio-frontal angle
STB	bistephanic breadth	RPA	radio-parietal angle
FRC	frontal chord	ROA	radio-occipital angle, lambda-opisthion
FRS	frontal subtense	BSA	basal angle, prosthion-opishtion
FRF	frontal fraction	SBA	sub-bregma angle
PAC	parietal chord	SLA	sub-lambda angle

Table 3. Postcranial Measurements Used in Sex Estimation.

Measurementnt	Source*	Measurement	Source*
1.Clavicle maximum length	1	32.Ulna med/lateral diam of shaft	2
2. Clav. ant/post diameter midshaft	2	33. Ulna least circumf of shaft	1
3. Clav. sup/inf diam midshaft	2	34. Innominate height	2
4. Scapula maximum height	1	35. Iliac breadth	2
5. Scapula maximum breath	1	36. Femur maximum length	1
6. Scapula spine length	1	37. Femur bicondylar length	3
7. Scapula supraspinous length	1	38. Femur trochanteric length	3
8. Scapula infraspinous length	1	39. Fem subtroch ant/post diam	1
9. Scap. glenoid cavity breadth	3	40. Fem subtroch med/lateral diam	1
10. Scap. glenoid cavity height	3	41. Fem ant/post diam midshaft	1
11.Scap. glenoid to inf. angel	3	42. Fem med/lateral diam midshaft	1
12.Humerus maximum length	1	43. Fem max vert diam of head	3
13. Humerus prox epiph breadth	3	44. Femur max horiz diam of head	3
14. Hum max diam midshaft	1	45. Fem ant/post diam of lat condyle	3
15. Hum min diam midshaf	1	46. Fem ant/post diam of med condyle	3
16. Hum max diam of head	1	47. Femur epicondylar breadth	3
17. Humerus epicondylar breadth	3	48. Femur bicondylar breadth	3
18. Hum least circumf of shaft	1	49. Femur min vert diam of neck	3
19. Radius maximum length	1	50. Femur circumference midshaft	2
20. Radius maximum diam of head	3	51. Tibia condylo-malleolar length	3
21. Radius ant/post diam of shaft	2	52. Tibia max breadth of prox epiph	3
22. Radius med/lateral diam of shaft	2	53. Tibia max breadth of distal epiph	3
23. Rad neck shaft circumference	3	54. Tibia ant/post diam nutr. foramen	1
24. Ulna maximum length	1	55. Tibia med/lateral diam nutr. foramen	1
25. Ulna physiological length	1	56. Tibia position of nutr. foramen	3
26. Ulna max breadth olecranon	3	57. Tibia circum at nutr. foramen	1
27. Ulna min breadth olecranon	3	58. Fibula maximum length	1
28. Ulna max width olecranon	3	59. Fibula maximum diam midshaft	2
29. Ulna olec-radial notch	3	60. Calcaneus maximum length	2
30. Ulna olec-coronoid length	3	61. Calcaneus middle breadth	2
31. Ulna ant/post diam of shaft	2		

**Measurements from 1 and 2 are considered standard (Buikstra and Ubelaker 1994)*

1 Bass 1987

2 Moore-Jansen and Jantz 1989

3 Zobeck 1983

C. METHODS

Sex Estimation

Discriminant Function Analysis

A discriminant function analysis (DFA) was employed to generate classification functions for each long bone, clavicle, scapula, and calcaneus. A stepwise discriminant analysis (STEPDISC) was performed in SAS 9.3 (2002-2010) using the Wilks' lambda criterion and an alpha of .05 in order to find the best subset of variables, per individual bone, for discrimination of sex. The stepwise selected variables were then run in a DFA for each bone in order to generate Mahalanobis D^2, cross-validated classification rates, and Fisher's linear discriminant scores. The STEPDISC process was run using the standard measurements and the Zobeck measurements in order to determine if the Zobeck measurements provide additional discrimination power.

Sectioning Points

Sectioning points were created for individual measurements from the bones with high Mahalanobis D^2 values and classification rates by taking the average of the male and female means, per measurement, and dividing by two. For each sectioning point, the male and female sample size, mean, and standard deviation of each measurement are provided along with the overall classification rate. All analyses were performed in SAS 9.3 (2002-2010) and used measurements from the left side. In cases where the left side was missing a measurement, the value for the right side was substituted when available.

ANCESTRY ESTIMATION

With new population-specific craniometric data from Mexico, it is necessary to recognize how the overall craniofacial morphology of this group compares to other reference groups commonly used in forensic anthropological practice. Three questions relating to ancestry estimation are addressed in this report:

1. How do the reference groups differ in overall craniofacial morphology?
2. Do standard measurements provide better classification rates for ancestry over Howells' measurements?
3. Do traditional linear measurements (e.g. standard or Howells) provide better classification rates than data derived from geometric morphometrics?

Geometric Morphometric Analyses

Landmarks were selected to represent overall craniofacial morphology and to maximize the sample sizes for each group. Table 4 provides a list and definitions of the 30 landmarks used for geometric morphometric analyses. A General Procrustes Analysis (GPA) was used to center, scale, and rotate all individuals into a common coordinate system and eliminate non–shape-related variation (i.e., size) (MItteroecker and Gunz 2009; Slice 2007). Because size variation is removed in the GPA, males and females were pooled to increase sample sizes.

Table 4. Cranial Landmarks Used in Geometric Morphometric Analyses.

No.	Landmark	No.	Landmark
1	Alare L	16	Nasion
2	Alare R	17	Inferior nasal border L
3	Asterion L	18	Inferior nasal border R
4	Asterior R	19	Occipital subtense point
5	Basion	20	Opisthion
6	Bregma	21	Parietal subtense point
7	Dacryon L	22	Prosthion H
8	Dacryon R	23	Minimum frontal breadth point L
9	Ectoconchion L	24	Minimum frontal breadth point R
10	Ectoconchion R	25	Cheek height inferior point L
11	Frontomalar anterior L	26	Cheek height superior point R
12	Frontomalar anterior R	27	Frontotemporale L
13	Glabella	28	Frontotemporale R
14	Lambda	29	Zygion L
15	Metopion	30	Zygion R

An analysis of variance (ANOVA) in SAS 9.3 (SAS 2002-2010) was used to determine if groups exhibit significant differences in centroid size; a Tukey multiple comparison test was used to determine which groups differ significantly. Separate ANOVAs were run on males and females due to sex differences in size. A canonical variates analysis (CVA) was performed in MorphoJ (Klingenberg 2011) to determine the shape features that distinguish the four reference groups. Interpretation of wireframe graphs were used to help assess the morphological shape differences among groups. Principal components and centroid size from the GPA were exported for DFA using SAS 9.3 (SAS 2002-2010) in order to ascertain whether traditional morphometric methods or geometric morphometric methods provide better classification accuracy for ancestry estimation.

Traditional Morphometric Analyses

To address whether standard measurements provide better classification rates for ancestry over Howells' measurements, two DFAs were run. All measurements were imported into FORDISC 3.0 (Jantz and Ousley 2005) using the custom import function. DFA analyses were performed by selecting the "no classify" option. This option allows FORDISC to be used as statistical software that will run a DFA with a variety of options. The first DFA included the standard measurements, while the second used the Howells' measurements. Both DFAs included a Forward Wilks stepwise discriminant analysis to determine the variables that best maximize group differences and to maintain appropriate variable numbers relative to sample size.

3 RESULTS AND CONCLUSIONS

A. SEX ESTIMATION

Discriminant Function Analysis

Standard postcranial measurements

The results of the DFA using the standard postcranial measurements indicate that the scapula provides highest overall classification rate of 95.55%. The femur, tibia, radius, and clavicle also provide classification rates greater than or equal to 90%. The fibula has the lowest classification rate at 80.36%. The stepwise selected measurements are provided in Table 5 along with classification functions. Table 6 provides a list of sample sizes, Mahalanobis D^2, female and male cross-validated classification rates, and the overall classification rates.

Table 5. Classification Functions with Stepwise Selected Variables[†,‡].

Bone	Classification Function†
Clavicle	(0.214*maximum length) + (0.586*anterior-posterior diameter) + (-36.980)
Scapula	(0.233*height) + (0.322*breadth) + (-64.974)
Humerus	(0.306*epiphyseal breadth) + (0.385*maximum head diameter) + (0.534*minimum diameter mid-shaft) +(-41.584)
Radius	(0.070* maximum length) + (1.466*anterior-posterior diameter mid-shaft) + (-31.026)
Ulna	(0.104* maximum length) + (0.310*dorso-volor diameter mid-shaft) + (-29.136)
Ulna*	(0.641*ORLL) + (0.417*BOPL) + (0.517*MBOL) + (-40.919)
Femur	(0.153*epiphyseal breadth) + (0.589*maximum head diameter) + (0.355*medio-lateral diameter at mid-shaft) + (-44.912)
Tibia	(0.612*maximum distal epiphyseal breadth) + (0.506*anterior-posterior diameter at nutrient foramen) + (-45.420)
Fibula	(0.067*maximum length) + (-22.302)
Calcaneus	(0.323*maximum length) + (0.349*middle breadth) + (-37.484)

[†] Section point is 0; females are negative and males positive.

[‡] All measurements recorded in mm.

[*] Classification function using Zobeck stepwise selected measurements.

Table 6. Cross-validated Classification Rates from DFA for Mexican Reference Data Using FDB Stepwise Selected Measurements.

Bone	Female n	Male n	D^2	Female %	Male %	Overall %
Clavicle	35	52	5.19	91.43	86.54	88.99
Scapula	31	41	8.30	93.55	97.56	95.55
Humerus	32	60	6.00	90.63	85.00	87.82
Radius	35	53	4.95	94.29	86.79	90.54
Ulna	32	46	3.64	90.63	71.74	81.19
Femur	27	64	6.20	100	85.94	92.97
Tibia	32	65	6.56	96.88	86.15	91.52
Fibula	32	56	2.27	87.5	73.21	80.36
Calcaneus	22	30	4.39	90.91	73.33	82.12

The length and breadth measurements for the scapula, clavicle, and calcaneus were selected for use in the DFA. For the long bones, the length measurements were only found significant to include in the DFA for the radius, fibula, and ulna, with the radius biting the most dimorphism and the fibula the least. The femur, tibia, and humerus exhibit the most dimorphism based on joint surfaces (e.g. epiphyseal breadth and head diameter) rather than length. Femoral distal epiphyseal breadth, head diameter, and medio-lateral midshaft diameter provide a cross-validated classification rate of 93%. Tibial distal epiphyseal breadth and maximum nutrient foramen provide a classification rate of 91.5%.

Zobeck measurements

The Zobeck measurements established as significant in the stepwise discriminant analyses are found in the scapula, radius, ulna, and femur (Table 7). For these bones, sex estimation improved for the radius and ulna; however, the Mahalanobis D^2 increased for all bones. The radius classification rate improved 1%; however, the ulna classification improved by over 4%, and the femur and scapula rates remained almost the same. Because classification rates increased only for the ulna, classification functions are not provided for the other bones.

Table 7. Cross-validated Classification Rates from DFA for Mexican Reference Data Using Zobeck Stepwise Selected Measurements.

Bone	Female n	Male n	D^2	Female %	Male %	Overall %
Scapula	28	30	9.85	96.55	93.75	95.15
Radius	34	50	5.56	97.06	86.00	91.32
Ulna	26	31	5.86	89.66	81.58	85.62
Femur	25	38	9.19	100.00	86.36	93.18

Sectioning Points

Male and female sample sizes, means, and standard deviations are provided in Table 8, along with the sectioning point and the percentage of the reference sample correctly classified. Clavicle length, scapula height, and radial length provide the highest classification rates; however, with the exception of the femur MTV measurement, all sectioning points provide high classification rates.

Table 8. Sectioning Points and Percent of Reference Sample Correctly Classified for Select Postcranial Measurements.

Measurement	Female			Male			Sectioning Points	
	N	Mean	Std Dev	N	Mean	Std Dev	Value	Percent Correctly Classified
Tibia max breadth of distal epiphyses	32	45.06	2.30	65	51.57	3.14	48	0.96
Tibia ant/post diam nut foramen	34	28.88	2.28	78	34.08	2.71	31	0.94
Femur epicondylar breadth	28	69.21	3.87	64	79.58	5.93	74	0.91
Fem max vert diam of head	34	38.71	1.70	78	44.64	2.89	42	0.91
Fem med/lateral diam midshaft	33	23.67	1.80	81	26.78	2.41	25	0.82
Radius maximum length	35	209.89	9.65	53	236.23	17.12	223	0.99
Humerus epicondylar breadth	33	52.21	2.78	64	59.70	4.02	56	0.91
Hum max diam of head	32	39.31	2.91	63	45.29	3.02	42	0.96
Scapula maximum height	32	133.56	7.37	41	153.15	8.12	143	1.00
Scapula maximum breadth	32	92.28	4.35	49	103.31	5.47	98	0.93
Maximum clavicle length	35	134.09	6.37	52	151.44	9.36	143	0.99

B. ANCESTRY ESTIMATION

Geometric Morphometric Analyses

Size

The ANOVA indicates significant differences in size for both males ($p < .0001$) and females ($p < .0001$). The American Black females have the largest values for centroid size, followed by American Whites, although they do not significantly differ from one another (Tables 9 and 10). The Mexican females have the smallest centroid size, and based on the Tukey multiple comparisons, differ significantly when compared to American Blacks and Whites. The males follow the same pattern as the females. The American Black and White males have the largest values for centroid size and do not significantly differ from one another. The Guatemalan males have the smallest centroid size and do not significantly differ from the Mexican males. Significant differences in centroid size are found between American Black and White males when compared to Guatemalan and Mexican males.

Table 9. Female Centroid Size Means and Standard Deviations.

Group	N	Mean	Std Dev
American Black	17	400.16	12.87
American White	134	395.72	10.32
Mexican	29	379.96	11.78

Table 10. Male Centroid Size Means and Standard Deviations.

Group	N	Mean	Std Dev
American Black	61	419.16	11.28
American White	247	418.19	11.24
Mexican	95	403.26	12.80
Guatemalan	71	398.96	8.75
Note: Mexican and Guatemalans are significantly different to both American Whites and Blacks in centroid size, but do not differ between each other.			

Shape

The Mahalanobis distance matrix (Table 11) and associated p-values indicate that all groups are significantly different. The Mexican and Guatemalan groups are more similar to one another than the American Black and White groups. The first canonical variate (CV) explains 69.72% of the total variation, followed by 17.15% and 13.12% for CVs 2 and 3, respectively (Figure 2). The first CV separates the American Whites and Blacks from the Mexican and Guatemalan groups. Shape changes are visualized in wireframe graphs associated with each CV (Figures 3 and 4). The light blue lines represent the average configuration of all individuals and the dark blue lines represent a change in 10 Mahalanobis distance units on the positive axis. The first CV reflects morphological differences between the American White (negative axis) and Guatemalans and Mexicans (positive axis) (see Figure 2A).

Table 11. Mahalanobis Distances from Canonical Variates Analysis.

Group	**American Black**	**Guatemalan**	**Mexican**
American Black (n=78)	-	< 0.0001	<0.0001
Guatemalan (n=75)	4.54	-	<0.0001
Mexican (n=124)	4.65	3.42	-
American White (n=381)	3.45	4.86	4.86
*Mahalanobis distances below diagonal, p-values for permutation test of distances above.			

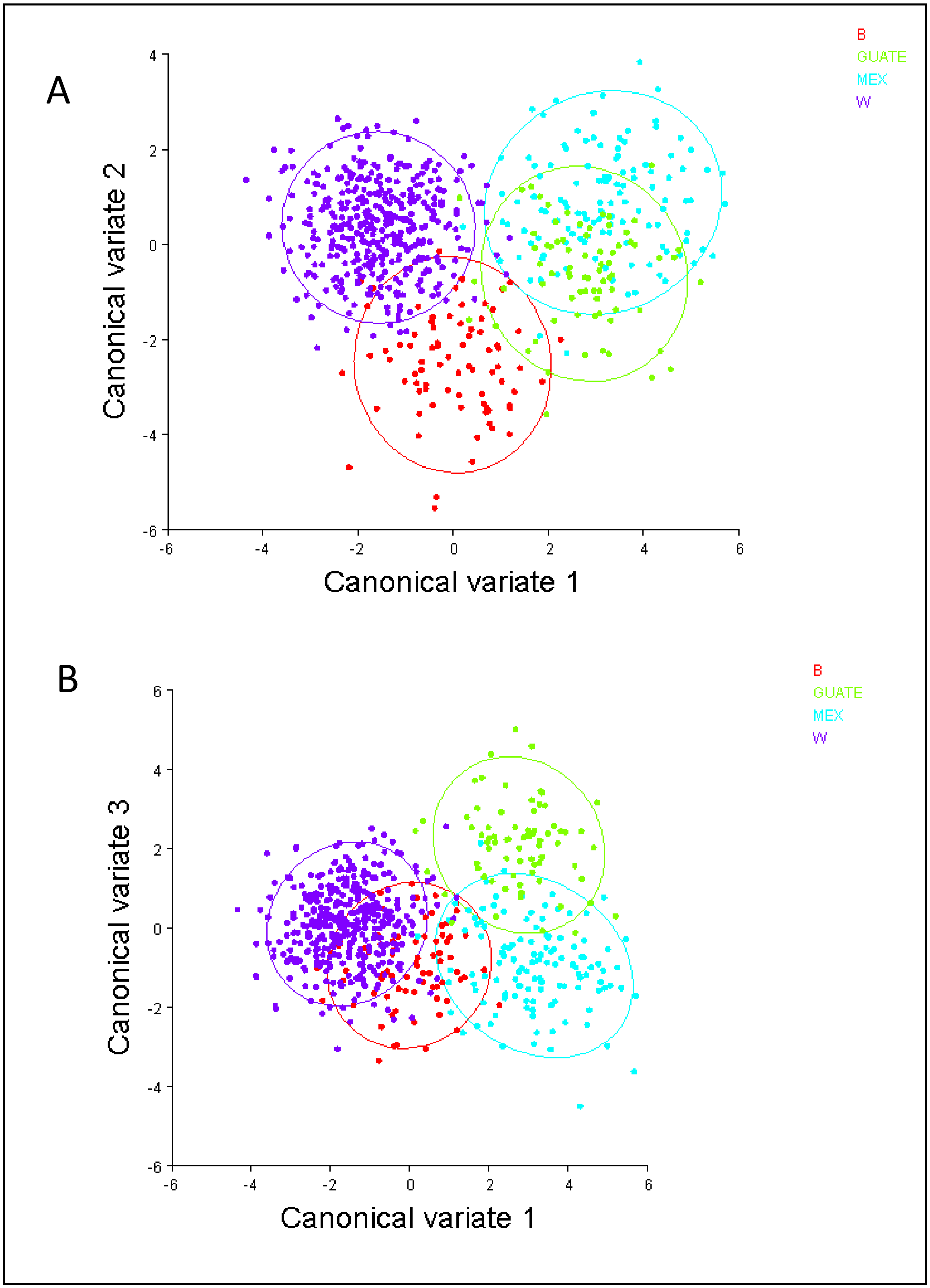

Figure 2. A) Canonical variates 1 (69.72%) and 2 (17.16%) and B) canonical variates 1 (69.72%) and 3 (13.12%).

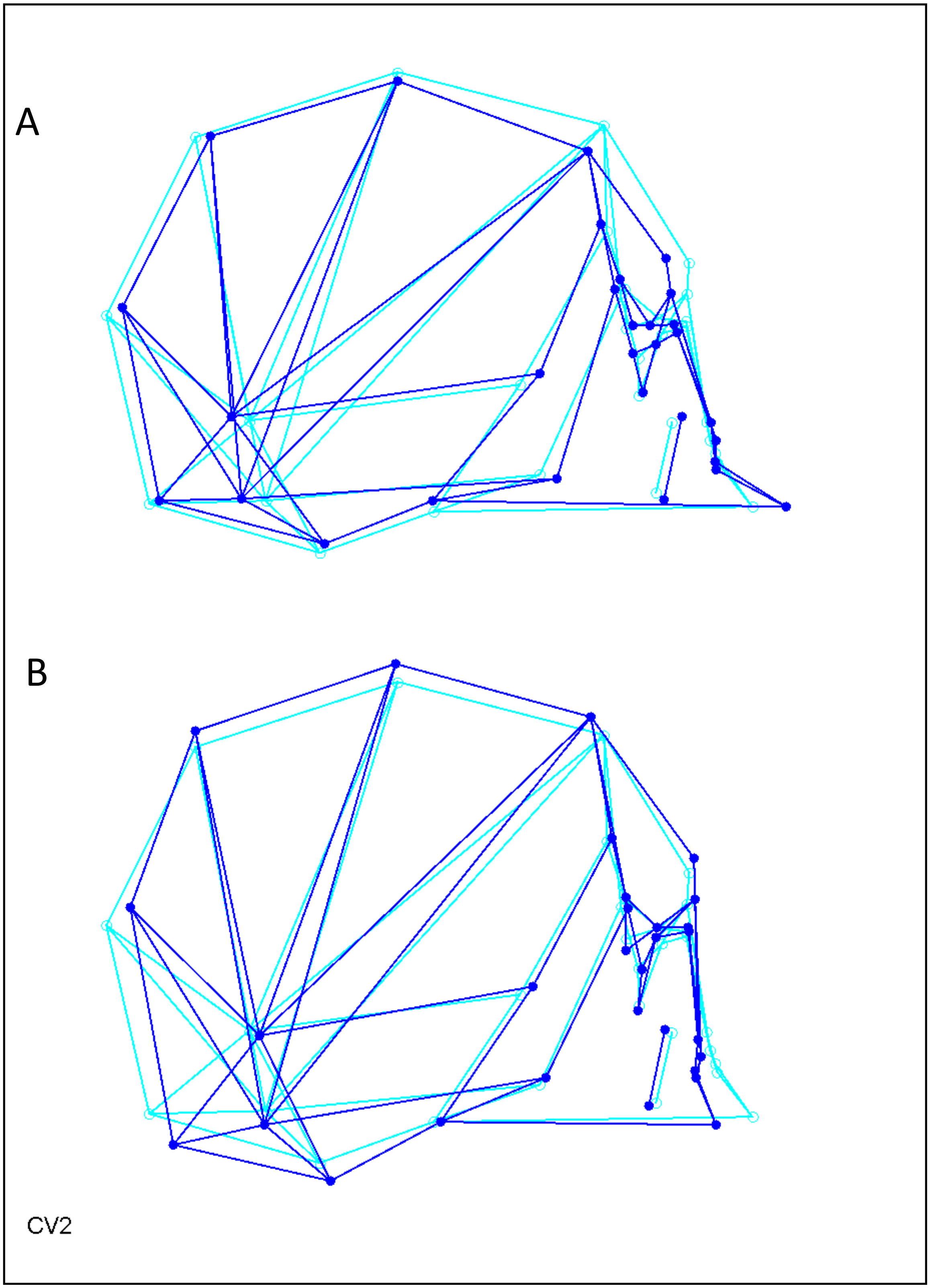

Figure 3. Lateral view of A) shape changes associated with CV 1 and B) shape changes associated with CV 2.

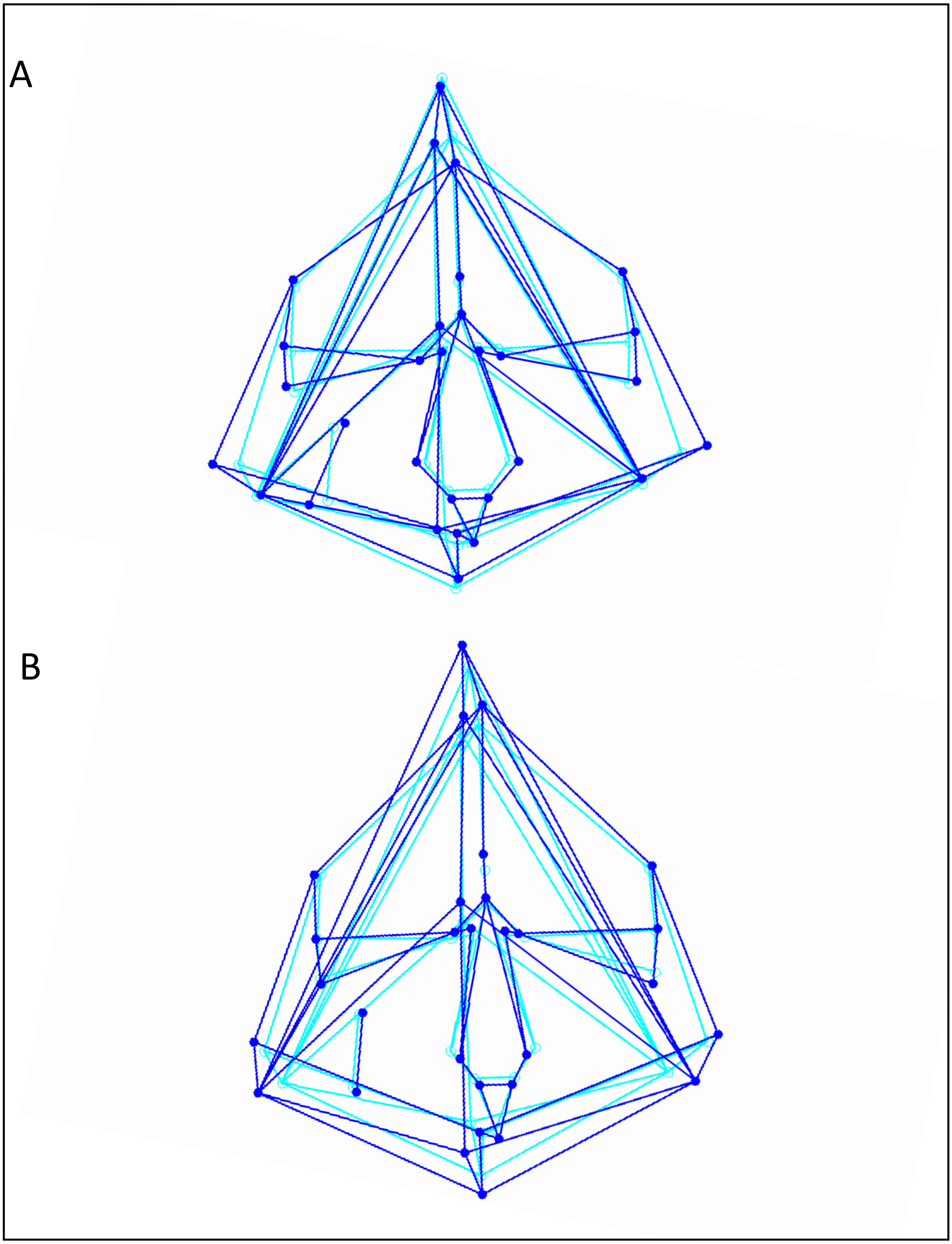

Figure 4. Anterior view of A) shape changes associated with CV 1 and B) shape changes associated with CV 2.

The Guatemalans and Mexicans on the first axis are separated primarily due to overall smaller cranial vaults, pronounced prognathism, wide zygomatics, and larger values for cheek height and nasal breadth. The second CV is separating the American Blacks from other groups based on a longer and lower cranial vault, more pronounced prognathism, a less pronounced glabellar region, superiorly projecting posterior cranial vault, narrower face and vault, and wide nasal aperture. The third CV separates the Guatemalans from the other groups based on short and high cranial vaults.

Ancestry Estimation

The first 10 principal components account for 60.3% of the total variation and were included with centroid size in DFAs. Because the test of homogeneity of the covariance matrices was found significant at the 0.1 level, the within-covariance matrices were used in quadratic DFAs. The cross-validated classification rates are provided in Table 12. American Whites have the highest classification rate (84%) and American Blacks the lowest (60%), with the Mexican (61%) and Guatemalan (57%) groups intermediate. The majority of misclassified Guatemalans classified into the Mexican group and vice versa. When Guatemalans are removed from the DFAs (Table 13), classification rates improve for all groups, especially Mexicans (78%).

Table 12. Cross-validated Classification Rates using Principal Components and Centroid Size, All Groups.

Group	n	Percent Classified Into			
		American Black	Guatemalan	Mexican	American White
American Black	78	**60.26**	7.69	6.41	25.64
Guatemalan	71	5.63	**57.75**	32.39	4.23
Mexican	126	9.68	20.97	**61.29**	8.06
American White	383	11.29	2.89	2.10	**83.73**

Table 13. Cross-validated Classification Rates using Principal Components and Centroid Size, Guatemalans Removed.

Group	n	Percent Classified Into		
		American Black	Mexican	American White
American Black	78	**64.10**	10.26	25.64
Mexican	126	12.90	**78.23**	8.87
American White	383	11.81	2.89	**85.30**

Traditional Morphometric Analyses

Males

DFA results for males using the 12 stepwise selected variables from the standard measurements set provides an overall cross-validated classification rate of 82.2% using the reference groups American Black and White, Guatemalan, and Mexican (Table 14). Using the standard measurement subset, 89% of American Whites, 80% of American Blacks, 74.6% of Guatemalans, and 61.0% of Mexicans correctly classified into their own group. The 17 stepwise selected variables from the Howells measurements provide an overall cross-validated classification rate of 85.8%. Using these measurements, 91% of American Blacks, 85% of Guatemalans, 87% of American Whites, and 76% of Mexicans correctly classified into their own group.

Table 14. DFA results for Mexican, Guatemalan, American Black, and American White Males Standard vs. Howells Measurements.

Group	DFA Results Using Mexican Reference Group			
	12 Stepwise Selected Standard Measurements[1]		17 Stepwise Selected Howells Measurements[2]	
	N	% Correct	N	% Correct
American Black	70	80	34	91
Guatemalan	71	74.6	59	85
Mexican	41	61	53	76
American White	227	89	149	87

[1] GOL MAB BBH OBH OBB NLB AUB DKB BNL BPL XCB UFHT

[2] GOL PRA DKA DKB OBH XFB MLS AUB EKB BAA JUB FRS BRA FRF MAB MDH PAC

Females

Because the Guatemalan female sample is too small (n=5), it was not included in the female DFAs. DFA results for females using the 12 stepwise selected variables from the standard measurements set provide an overall cross-validated classification rate of 89.1% using the reference groups American Black and White, Guatemalan, and Mexican (Table 15). Using the standard measurement subset, 92% of American Whites, 84% of American Blacks, and 82.0% of Mexicans correctly classified into their own group.

Table 15. DFA results for Mexican, American Black, and American White Females Standard vs. Howells Measurements.

Group	DFA Results Using Mexican Reference Group			
	12 Stepwise Selected Standard Measurements[1]		10 Stepwise Selected Howells Measurements[2]	
	N	% Correct	N	% Correct
American Black	37	84	15	93
Mexican	17	82	13	85
American White	102	92	53	98

[1] NLB BBH MAL AUB OBH GOL BPL BNL FOB WFB ZYB XCB

[2] NAA OBH GOL NLB ZYB NDA WFB ASB XFB ZOR

C. DISCUSSION

The first goal of Project IDENTIFICATION was to obtain population-specific cranial and postcranial skeletal measurements from individuals from Mexico to establish a database of available reference data for further research and development by forensic anthropologists. Osteometric data is now available for 215 positively identified individuals from Mexico. Metric data was collected for an additional 318 undocumented border crossers. These remains are not identified at this time, although efforts to are underway for their identification. All data is available through the FDB, curated at The University of Tennessee at Knoxville by Dr. Richard Jantz. As positive identifications are made, the data will be updated.

The second goal of this project was to create sectioning points and classification functions for population-specific sex estimates applicable to the majority of Hispanics within the U.S. Because the majority of Hispanics in the U.S. are of Mexican ancestry, the new sexing criteria provided should be the most appropriate for forensic anthropology practice. The classification functions provided for long bones should be considered more robust than the sectioning points, as multivariate methods are more robust than univariate. The classification rates from postcranial metrics, classification functions, and sectioning points are higher than those presented by Tise et al. (2013). Although Tise et al. (2013) were using data from this project, their sample sizes were smaller and not positively identified, and sex was estimated from the pelvis. The use of a test sample at this time was not feasible due to small sample sizes, particularly for the females. As more positive identifications are made at the PCOME, males and females will be used as a test sample for provided error rates.

The third goal of this project was to utilize traditional and geometric morphometric methods with the new reference data to explore morphological variation of among Mexicans, American Blacks, and Whites. Within this goal, three main questions were addressed: 1) how do the reference groups differ in overall craniofacial morphology; 2) do standard measurements provide better classification rates for ancestry than Howells measurements; and 3) do traditional linear measurements provide better classification rates than data derived from geometric morphometric data? Geometric morphometric analyses using the new Mexican data and data from Guatemalans, American Blacks, and American Whites was used to explore the biological variation of these groups. Differences in both size and shape are noted for all groups. Although the two groups considered Hispanic (Guatemalan and Mexican) are more similar to each other than American Whites and Blacks, they differ significantly in their overall craniofacial morphology.

Results from DFAs for males and females both suggest that use of additional Howells measurements improves overall classification accuracy in ancestry estimation. Classification rates were the lowest for Mexicans among both males and females. The female rates were higher; however, that is most likely because no Guatemalan females were included in the analyses. Based on the geometric morphometric results, the Guatemalans and Mexicans—although morphologically different from one another—are more similar to each other than American Blacks and Whites. Thus, the inclusion of the Guatemalan sample in the male DFA sample lowers the classification rate for the Mexicans, as both groups commonly misclassified as each other. The low sample sizes of the Mexican females could also skew the results. When the DFA results from the data (centroid size and principal components) derived from the geometric morphometric analysis and the traditional linear measurements were used, the latter performed better in ancestry estimation based on classification rates.

D. IMPLICATIONS FOR POLICY AND PRACTICE

Sex and ancestry estimation are crucial components of the biological profile. The demographic structure of the U.S. has rapidly changed over the past decade, with Hispanics now the second-largest population group. Further, the majority of Hispanics are of Mexican origin (Motel and Patten 2012). The present study has investigated the cranial morphological differences between two groups considered Hispanic by the U.S. Although the Guatemalans and Mexicans are more similar to each other than to American Whites and Blacks, they do exhibit significant differences in morphology. These results suggest that population groups considered Hispanic with different geographic origins should not be lumped together when creating new criteria and methods for forensic identification. Furthermore, because most Hispanics in the U.S. are of Mexican origin, the Mexican data derived from this project should be the most appropriate reference data for the U.S. However, it should be noted that the data collected from the PCOME represents individuals that died in their attempt to enter the U.S. These individuals most likely represent a portion of the Mexican population that is considered to be of low socioeconomic status (SES) (Anderson 2008).

Main Body of Technical Report

1 INTRODUCTION

A. STATEMENT OF PROBLEM

Forensic anthropologists tasked with the identification of severely decomposed or skeletal remains must generate a biological profile that includes sex, ancestry, age, and stature. This biological profile can then be used to compare with missing persons records to help narrow down the identity of the remains in question. Of the profile components, sex and ancestry are critically important. If the sex is incorrect, the remains are likely to remain unidentified. If the ancestry is incorrect, the remains may remain unidentified or the investigation may be delayed. Assessments of sex and ancestry are dependent upon population-specific skeletal reference data. Currently in the United States, the second largest population group is referred to as Hispanic and there are no skeletal collections with large numbers that represent this group. If there are no reference data or criteria to accurately assess the sex and ancestry, two fundamental components of a biological profile, then individuals considered Hispanic will remain unidentified as they show up in forensic anthropological cases across the nation.

Further complicating the issue surrounding the development of forensic anthropological identification criteria, the term Hispanic is a social construct with no precise biological meaning. The term Hispanic refers to various national origin groups from Latin America lumped into one category in order to better track the fastest growing U.S. population. From a human variation point of view, the term lumps national origin groups with diverse population histories and population structures into one ambiguous term that complicates studies of biological variation that can be applied to a forensic setting. For the purpose of this report, the term Hispanic cannot be avoided. When the term Hispanic is used in this report, it refers to the U.S. Census Bureau definition of a person of Spanish speaking origin regardless of country of origin (Ramirez and de la Cruz 2002). Therefore, a goal of this report is to provide new reference data that can help better understand the biological variation of national origin groups from Latin America for application in forensic anthropology.

B. REVIEW OF THE LITERATURE

Sex and Ancestry Estimation

The pelvis is the most reliable estimate of sex due to differences in pelvic morphology between men and women related to childbirth (Phenice 1979; Stewart 1979; Walker 2005). However, not all skeletal remains found in forensic contexts provide a complete pelvis. Following the pelvis, a metric analysis of the long bones provides the next most reliable indicator of sex (France 1998; Spradley and Jantz 2011). Because there are no reference samples of Hispanic skeletons, in the past White methods were most often used to estimate sex of Hispanic. In a previous publication, Spradley et al. (2008) demonstrated that when criteria from Whites are applied to Hispanic skeletons, female skeletons are classified as females 100% of the time, although males were correctly classified only 73.5% of the time. Tise et al. (2013), using data obtained from Project Identification, found that population-specific criteria applied to Hispanics improves the overall classification rates. However, the classification rates are not as high as those for American Blacks or Whites (Spradley and Jantz 2011). While the Tise et al. (2013) article provided relevant, needed criteria, the sample sizes utilized for development of sectioning points and classification functions are small, and the majority of individuals in the sample are unidentified, presumed to be Hispanic, and thus the results should be considered only preliminary.

Ancestry estimation is possible because craniometric data is moderately to highly heritable (Carson 2006; Devor 1987; Relethford 2009). Although craniometric data can be influenced by the environment , the underlying genetic structure is not erased, allowing craniometric data to be useful for ancestry estimation (Relethford 2004). The most commonly employed for method for ancestry estimation in forensic practice is the use of craniometric data applied to statistical methods such as discriminant function (Jantz and Ousley 2005). Previously, Spradley et al. (2008) found difficulty in estimating ancestry for Hispanic skeletal remains using discriminant function analysis and available reference data from American Black and White and Hispanic groups. The Hispanic reference sample used in Spradley et al. (2008) publication was composed largely of unidentified, undocumented border crossers found in the Arizona desert and individuals labeled Hispanic in the Forensic Anthropology Data Bank (FDB). The FDB individuals are from forensic cases around the country, and the majority of these individuals have no specific information as to the geographic origin or cultural identity of the individual.

More recently, Ross and Slice (2009) developed a 3D-ID program that uses three-dimensional landmark data and geometric morphometric methods . Geometric morphometrics focuses on the geometric properties of shape and form (size and shape) using two- or three-dimensional data. In the field of biology, geometric morphometric methods have been shown to better discriminate among closely related species (Adams et al. 2004). In 3D-ID, the landmark data is subjected to geometric morphometric analyses, followed by traditional multivariate classification statistics (Mitteroecker and Gunz 2009; Slice 2007). Although their reference data has groups considered Hispanic, the sample sizes are relatively small. Ross et al. (2011) use both traditional craniometrics and data derived from geometric morphometrics in discriminant analyses to explore regional variation within the Iberian Peninsula. However, there have been no formal tests regarding whether data derived from geometric morphometric analyses perform better than traditional metrics for ancestry estimation within the U.S for the purpose of ancestry estimation.

Non-metric data, as well use the use of a cultural profile, have also been published for use in ancestry assessment for Hispanic individuals. Birkby et al. (2008) provide a list of non-metric traits of the skull based on skeletal remains from the Pima County Office of the Medical Examiner (PCOME) in Tucson, Arizona, that receives a high number of undocumented U.S.–Mexico border crossing decedents. Hurst (2012), using the Birkby et al. (2008) trait list and additional non-metric traits from Hefner (2009), achieved good classification rates for Hispanics in a three-group model (Southwest Hispanic, American White, and Black) with discriminant function analysis. The cultural profile (Birkby et al. 2008) employed at the PCOME also works well for identifying undocumented border crossers from U.S. citizens. This profile includes examination of personal effects such as voter cards, foreign currency, and religious icons in conjunction with certain skeletal indicators of low socioeconomic status that do not fit the profile of US citizens found near the border. This profile works well in examination of decedents found at the PCOME, although it may not be as useful in forensic investigations further away from the border, or for cases involving American citizens.

FORDISC 3.0 (Jantz and Ousley 2005), a widely used personal discriminant function program that can classify an unknown into one of the available reference groups, uses metric data from positively identified American Blacks and Whites (ancestry is self-reported from forensic case submissions and recent documented collections) from the FDB. However, the Hispanic reference group in the FDB and FORDISC remains largely contextually identified. At the time Project IDENTIFICATION was written, there were only 65 positively identified individuals designated Hispanic in the FDB. Of those, only 21 were associated with known national origin.

In order to obtain and implement population-specific criteria for forensic practice, an understanding of the complexity of the social construct Hispanic and the biological variation of population groups from national origin groups considered Hispanic is needed.

What Does Hispanic Mean?

In order to keep track of the demographics of U.S. population, the Office of Management and Budget provides race and ethnic categories that are used by the U.S. Census Bureau (Office of Management and Budget 1994). For anyone who self-identifies as Hispanic, they must first choose a race (White or Black), followed by the ethnic category of Hispanic. Therefore, the second- largest population group in the U.S. is an ethnicity, rather than a race. An ethnicity can consist of individuals from various geographic, linguistic, and cultural origins (Itzigsohn and Dore-Cabral 2000; Melville 1988; Stephan and Stephan 2000). Contrary to the U.S. Census Bureau definition of Hispanic, Melville writes that for individuals of Spanish-speaking origins, “the most common practice is for each national origin group to use the name of their country” (Melville 1988). Genetic and morphological research provides evidence that the national origin of various groups considered Hispanic contains genetic structure that can be used for identification purposes (Bonilla et al. 2005; Cerda-Flores et al. 2002; Klimentidis et al. 2009; Lisker et al. 1996; Rangel-Villalobos et al. 2008; Rubi-Castellanos et al. 2009; Seldin et al. 2007).

The genetic structure of the various groups considered Hispanic differs in terms of the degree of admixture from parental groups. Typically complex groups with at least two parental groups, such as African Americans, display an intermediate position between parental groups in terms of genetics and morphology (Parra et al. 1998; Spradley 2006). In terms of Hispanics, with three parental groups (European, African, and Native American) the genetic structure can be more complex (Bonilla et al. 2005; Lisker et al. 1986; Rubi-Castellanos et al. 2009) and the morphological variation is not fully understood. When considering the various geographic locations in Latin America and Europe that are considered Hispanic, they all have unique population histories that provide different population structure (Martínez-Cruzado et al. 2005; Ross et al. 2004; Rubi-Castellanos et al. 2009; Seldin et al. 2007). For example, using ancestry informative markers (AIMs), Seldin et al. (2007) found that Argentinians exhibit a higher degree of European admixture than Mexican Americans, and that the degrees of European and Native American ancestry differed regionally. Martinez-Cruzado et al. (2005) examined biological ancestry frequencies among Puerto Rican municipalities and found Native American ancestry the highest, followed by sub-Saharan African.

Regional variation and varying levels of African admixture has also been documented in Mexico. Rubi-Castellanos et al. 2009 found that higher levels of European admixture are found in the North, with decreasing levels in the South with constant rates of African admixture. Further, within each region of Mexico, heterogeneity exists due to the complex population history of Mexico (Bonilla et al. 2005). Within the United States, Klimentidis et al. (2009) explored the relationship between self-identified Hispanics in Arizona and admixture proportions using 76 AIMs. This study is of particular interest because the study participants were allowed to answer the question, "What would you say your ethnicity is (if you could describe it in any way you wanted)?" (Klimentidis et al. 2007:378). While some identified as Hispanic, others described themselves as Mexican, Mexican American, Spanish, and half Hispanic/half White (Klimentidis et al. 2007:378). When the genetic admixture analysis was run using European, African, and Native American parental groups, the self-identified Mexican and Mexican Americans had higher degrees of Native American ancestry than other self-identified Hispanics.

Research involving morphological variation of national origin groups considered Hispanics has been limited due to lack of data. Using three-dimensional cranial morphology data, Ross et al. (2004) found Cubans to be more similar to American Blacks. Ross et al. (2004) suggest that Cubans make up Florida's largest Hispanic community, and that the unique population history of Cubans makes them more similar to American Blacks and less likely to have genetic Native American ancestry. Whereas individuals originating from Mexico, Central, and Latin America derive genes primarily from Spanish and Native American sources, in coastal geographic regions African ancestry is prevalent (Lisker et al. 1986; Lisker et al. 1996; Lisker et al. 1990; Long et al. 1991; Martinez-Abadias et al. 2006).

While Cubans would be most likely to consider themselves Cubans, and Mexicans likely to consider themselves Mexican rather than Hispanic, once inside the U.S., for political and policy purposes, both groups are considered Hispanic (Melville 1988; Ramirez and de la Cruz 2002). Because of the many geographic localities individuals considered Hispanic originate from and their distinct population histories, the term Hispanic does not adequately capture any cultural, biological, or genetic meaning. The national origins for the majority (92%) of Hispanics in the United States (Figure 5) are Mexico (67%), followed by Puerto Rico (9.2), Cuba (3.7%), El Salvador (3.6%), Dominican Republic (3.0), Guatemala (2.2%), Columbia (1.9%), Honduras (1.4%), Ecuador (1.3%), and Peru (1.2%) (Motel and Patten 2012a). Further data indicate that 37% of the Mexican origin group is foreign born (Motel and Patten 2012a). Because the majority of Hispanics in the U.S. are of Mexican origin, a Mexican reference sample is needed along with further clarification on the usage of the term Hispanic in forensic anthropological practice.

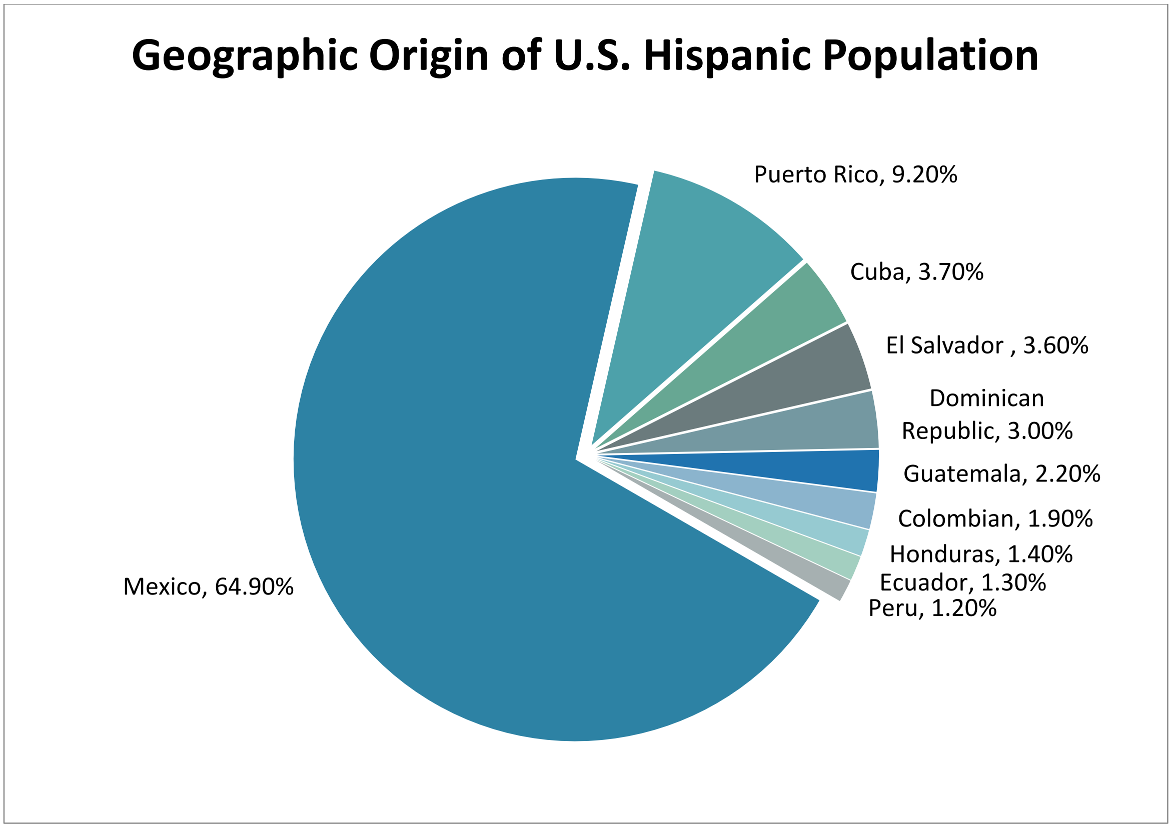

Figure 5. Geographic origin of U.S. Hispanic population (data from Motel and Patten [2012]).

C. RATIONALE FOR RESEARCH

The FDB is the largest repository with metric reference data for individuals considered Hispanic skeletons (Jantz and Moore-Jansen 1988). As discussed in the previous sections the majority are assumed to be Hispanic based on the context (e.g., found in close proximity to the U.S. Mexico Border) or have a designation of Hispanic with no further information regarding geographic origin[2]. Even more recent documented collections such as the William M. Bass donated skeletal collection at The University of Tennessee at Knoxville (Shirley et al. 2011) and the Documented Skeletal Collection at Texas State University-San Marcos contain mostly American White and Black skeletons.

The Scientific Working Group in Forensic Anthropology (SWGANTH, www.swganth.org) suggests that best practice in sex and ancestry assessment should include sound methodology that utilizes appropriate, population-specific data. There are no population-specific reference data or criteria available

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[2] Data from the FDB was made available by Dr. Richard Jantz.

specifically for Hispanics of Mexican origin, the largest national origin group considered Hispanic. The goals of this project are to:

1. obtain cranial and postcranial skeletal measurements from individuals from Mexico to establish a database of available reference data for further research and development by forensic anthropologists;
2. create sectioning points and classification functions for population-specific sex estimates applicable to the majority of Hispanics within the United States; and
3. utilize traditional and geometric morphometric methods with the new reference data to explore morphological variation of among Mexicans, American Blacks, and Whites, to provide better classification accuracy in ancestry estimation.

It is expected that new reference data from positively identified Mexicans will improve sex and ancestry estimation.

2 METHODS

A. REFERENCE SAMPLES

The Mexican skeletal data comes from three sources, the PCOME, located in Tucson, Arizona, and two cemetery collections from Mexico from Zimapan, Hidalgo, and Mérida, Yucatan. All individuals had birth years from the 20th century. Of the 2,000 miles of shared border between the U.S. and Mexico, 281 miles are located in what the U.S. Border Patrol (USBP) refers to as the Tucson Sector (Anderson 2008). It is from the Tucson Sector that the PCOME receives border-crossing fatalities. The USBP reported in 2004 that 43% of all undocumented border crossers were apprehended in the Tucson Sector, and the majority of border crossers are from Mexico (Anderson 2008). During the course of Project Identification, 533 skeletons were measured (Table 1). Of those, 203 are positively identified. The identification process is ongoing at the PCOME, and data collected during this project will continue to be updated with reference to positive identifications for inclusion into the FDB, and subsequently FORDISC 3.0. Previously collected data at the PCOME for the FDB were included to increase sample sizes.

Table 16. Reference Groups for Analysis.*

Institution	Country of Origin	Female	Male	Unknown	Total
PCOME					
Identified	Mexico	9	68		77
	El Salvador	2	3		5
	Guatemala	1	5		6
	Honduras		1		1
	Peru	1			1
	USA	1	12		13
	Unknown		2		2
Unidentified**		23	170	125	318
UADY					
Xoclán Collection	Mexico	21	44		65
UNAM					
Zimapan Collection	Mexico	16	29		45
FDB					
American White	USA	306	521		827
American Black	USA	86	148		234
Mexican	Mexico	5	51		56
Total		471	1054	125	1650

* Project IDENTIFICATION funded data collection at the PCOME and UADY.
**Sex is based on DNA.

The Zimapan, Hidalgo, cemetery collection is curated at the Universidad Nacional Autónoma de México (UNAM) in Mexico City and represents individuals born in the early to mid–20th century. This collection is from a cemetery relocation project in the municipality of Zimapan in the state of Hidalgo in Central Mexico. During the relocation, families that could not afford reburial donated the remains of their next of kin to UNAM (Figueroa-Soto 2012). The Xoclán cemetery is located in Mérida, Yucatan, and serves as an overflow cemetery for the main burial ground in the state's capital (Chi-Keb et al. 2013). Plots within this cemetery are leased for a specified amount of time, after which the lease is renegotiated or the interred individual is moved to a mass burial (Chi-Keb et al. 2013). In 2006, the Facultad de Ciencias Antropológicas (School of Anthropological Sciences) of the Universidad Autónoma de Yucatán (UADY) began to curate a portion of these relocated individuals that are positively identified (Chi-Keb et al. 2013).

Secondary reference data was obtained from the FDB for comparison purposes. A reference group of Guatemalans was included in analyses due to the fact that once inside the borders of the U.S., they are considered Hispanic. This group is composed of victims of human right's violations during

Guatemalan's Civil War (Spradley et al. 2008). Data was collected at the Forensic Anthropology Foundation in Guatemala (FAFG) and curated in the FDB. Some of the Guatemalans are positively identified. Positively identified American Blacks and Whites with known demographics are also included because, along with Hispanics, they represent the three largest population groups in the U.S.

B. DATA COLLECTION

Craniometric data was collected using a Microscribe® G2X digitizer in conjunction with the program 3Skull (Ousley 2004). The Microscribe® G2X digitizer collects landmark or coordinate data. 3Skull archives the coordinate data in one table and calculates the inter-landmark distances, archiving these data in another table. The end result is a database containing inter-landmark distances (or traditional craniometric data) and the landmark data. The traditional craniometric data archived includes all the standard craniometric data and additional craniometric data defined by Howells (1973) (Table 17). Most forensic anthropologists utilize traditional, standard craniometric data (Buikstra and Ubelaker 1994; Moore-Jansen et al. 1994). The most popular application of traditional craniometric data by forensic anthropologists is FORDISC 3.0, used for estimation of sex, ancestry, and stature from unknown forensic cases. Although the cranial data collected is coordinate data, the traditional craniometric data is automatically computed by 3Skull and will be archived in both formats. Standard postcranial metric data were also collected (Buikstra and Ubelaker 1994; Moore-Jansen et al. 1994), as were additional postcranial metrics following the definitions outlined in Zobeck (1983) (Table 18). These additional postcranial measurements have shown to differentiate population groups better than the standard measurements (Zobeck 1983). All traditional cranial and postcranial measurements were recorded to the nearest millimeter.

C. METHODS

SEX ESTIMATION

Discriminant Function Analysis

In order to provide new population-specific criteria for sex estimation, a discriminant function analysis (DFA) was employed to generate classification functions for each long bone, clavicle, scapula, and calcaneus. A stepwise discriminant analysis (STEPDISC) was performed in SAS 9.3 (2002-2010) using the Wilks' lambda criterion and an alpha of .05 in order to find the best subset of variables, per individual bone, for discrimination of sex. The stepwise selected variables were then run in a DFA for each bone in order to generate Mahalanobis D^2, cross-validated classification rates, and Fisher's linear discriminant scores. The STEPDISC process was run using the *standard* measurements and the Zobeck measurements in order to determine if the Zobeck measurements provide additional discrimination power.

Sectioning Points

Sectioning points were created for individual measurements from the bones with high Mahalanobis D^2 values and classification rates by taking the average of the male and female means, per measurement, and dividing by two. For each sectioning point, the male and female sample size, mean, and standard deviation of each measurement are provided along with the overall classification rate. All analyses were performed in SAS 9.3 (2002-2010) and used measurements from the left side. In cases where the left side was missing a measurement, the value for the right side was substituted when available.

Table 17. Howells Cranial Measurements and Abbreviations.

Abbreviation	Measurement	Abbreviation	Measurement
GOL	glabella-occipital	PAS	parietal subtense
NOL	nasion-occipital	PAF	parietal fraction
BNL	basion-nasion	OCC	occipital chord
BBH	basion-bregma	OCS	occipital subtense
WFB	minimum frontal breadth	OCF	occipital fraction
XCB	max cran br	FOL	foramen magnum length
XFB	max frontal br	FOB	foramen magnum breadth
ZYB	byzygomatic breadth	NAR	nasion radius
AUB	biauricular breadth	SSR	subspinale radius
ASB	biasterionic breadth	PRR	prosthion radius
BPL	basion-prosthion length	DKR	dacryon radius
NPH	nasion-prosthion height	ZOR	zygoorbitale radius
NLH	nasal height	FMR	frontomalare radius
JUB	bijugal breadth	EKR	ectoconchion radius
NLB	nasal breadth	ZMR	zygomaxillare radius
MAB	external palate breadth	AVR	M1 alveolar radius
MAL	external palate length	BRR	bregma radius
MDH	mastoid height	VRR	vertex radius
OBH	orbital height	LAR	lambda radius
OBB	orbital breadth	OSR	opisthion radius
DKB	interorbital br	BAR	basion radius
NDS	nasion-dacryon subtense	NAA	nasion angle
WNB	simotic chord	PRA	prosthion angle
SIS	simotic subtense	BAA	basion angle, nasion-prosthion
ZMB	bimaxillary br	NBA	nasion angle
SSS	zygo-maxillary subtense	BBA	basion angle, nasion-bregma
FMB	bifrontal breadth	BRA	Bregma angle
NAS	nasio-frontal subtense	SSA	zygomaxillary angle
EKB	bi-orbital breadth	NFA	nasio-frontal angle
DKS	dacryon subtense	DKA	dacryal angle
IML	inferior malar length	NDA	o-dacryal angle
XML	maximum malar length	SIA	simiotic angle
MLS	malar subtense	FRA	frontal angle
WMH	minimum malar height	PAA	parietal angle
SOS	supraorbital projection	OCA	occipital angle
GLS	glabella projection	RFA	radio-frontal angle
STB	bistephanic breadth	RPA	radio-parietal angle
FRC	frontal chord	ROA	radio-occipital angle, lambda-opisthion
FRS	frontal subtense	BSA	basal angle, prosthion-opishtion
FRF	frontal fraction	SBA	sub-bregma angle
PAC	parietal chord	SLA	sub-lambda angle

Table 18. Postcranial Measurements Used in Sex Estimation.

Measurementnt	Source*	Measurement	Source*
1.Clavicle maximum length	1	32.Ulna med/lateral diam of shaft	2
2. Clav. ant/post diameter midshaft	2	33. Ulna least circumf of shaft	1
3. Clav. sup/inf diam midshaft	2	34. Innominate height	2
4. Scapula maximum height	1	35. Iliac breadth	2
5. Scapula maximum breath	1	36. Femur maximum length	1
6. Scapula spine length	1	37. Femur bicondylar length	3
7. Scapula supraspinous length	1	38. Femur trochanteric length	3
8. Scapula infraspinous length	1	39. Fem subtroch ant/post diam	1
9. Scap. glenoid cavity breadth	3	40. Fem subtroch med/lateral diam	1
10. Scap. glenoid cavity height	3	41. Fem ant/post diam midshaft	1
11.Scap. glenoid to inf. angel	3	42. Fem med/lateral diam midshaft	1
12.Humerus maximum length	1	43. Fem max vert diam of head	3
13. Humerus prox epiph breadth	3	44. Femur max horiz diam of head	3
14. Hum max diam midshaft	1	45. Fem ant/post diam of lat condyle	3
15. Hum min diam midshaf	1	46. Fem ant/post diam of med condyle	3
16. Hum max diam of head	1	47. Femur epicondylar breadth	3
17. Humerus epicondylar breadth	3	48. Femur bicondylar breadth	3
18. Hum least circumf of shaft	1	49. Femur min vert diam of neck	3
19. Radius maximum length	1	50. Femur circumference midshaft	2
20. Radius maximum diam of head	3	51. Tibia condylo-malleolar length	3
21. Radius ant/post diam of shaft	2	52. Tibia max breadth of prox epiph	3
22. Radius med/lateral diam of shaft	2	53. Tibia max breadth of distal epiph	3
23. Rad neck shaft circumference	3	54. Tibia ant/post diam nutr. foramen	1
24. Ulna maximum length	1	55. Tibia med/lateral diam nutr. foramen	1
25. Ulna physiological length	1	56. Tibia position of nutr. foramen	3
26. Ulna max breadth olecranon	3	57. Tibia circum at nutr. foramen	1
27. Ulna min breadth olecranon	3	58. Fibula maximum length	1
28. Ulna max width olecranon	3	59. Fibula maximum diam midshaft	2
29. Ulna olec-radial notch	3	60. Calcaneus maximum length	2
30. Ulna olec-coronoid length	3	61. Calcaneus middle breadth	2
31. Ulna ant/post diam of shaft	2		

**Measurements from 1 and 2 are considered standard (Buikstra and Ubelaker 1994)*

1	Bass 1987
2	Moore-Jansen and Jantz 1989
3	Zobeck 1983

ANCESTRY ESTIMATION

With new population-specific craniometric data from Mexico, it is necessary to recognize how the overall craniofacial morphology of this group compares to other reference groups commonly used in anthropological practice. Three questions relating to ancestry estimation are addressed in this report using the reference groups previously outlined in the Reference Samples section:

1. How do the reference groups differ in overall craniofacial morphology?
2. Do standard measurements provide better classification rates for ancestry over Howells measurements?
3. Do traditional linear measurements (e.g. standard or Howells) provide better classification rates than data derived from geometric morphometric analyses?

Geometric Morphometric Analyses

In order to address how the reference groups differ in overall craniofacial morphology, three-dimensional landmark data were imported into MorphoJ (Klingenberg 2011) via the 3Dildout program (Ousley 2013). Data from the PCOME Mexican sample are from forensic cases, and many have incomplete data due to trauma or taphonomic processes. Therefore, landmarks were selected to represent overall craniofacial morphology and to maximize the sample sizes for each group. Table 19 provides a list and definitions of the 3D landmarks used for geometric morphometric analyses.

Prior to any analyses, the "find outlier" function in MorphoJ (Klingenberg 2011) was utilized to detect outliers. This function provides a graphic showing an individual specimen compared to the average of all individuals. Additionally, a plot of the cumulative distribution of individual specimen distances to the sample average shape was also used to assess outliers (Klingenberg 2011). The individuals removed exhibited extreme values and are likely due to instrumentation error (e.g., not zeroing out the digitizer, movement of equipment or crania when collecting landmarks, or calibration issues). After outliers were removed, a principal components analysis (PCA) was performed for each reference group for the purpose of detecting any additional outliers. In each instance, outliers were examined to see if they were true outliers, pathological, or juveniles.

Table 19. Cranial Landmarks Used in Geometric Morphometric Analyses.

No.	Landmark	No.	Landmark
1	Alare L	16	Nasion
2	Alare R	17	Inferior nasal border L
3	Asterion L	18	Inferior nasal border R
4	Asterior R	19	Occipital subtense point
5	Basion	20	Opisthion
6	Bregma	21	Parietal subtense point
7	Dacryon L	22	Prosthion H
8	Dacryon R	23	Minimum frontal breadth point L
9	Ectoconchion L	24	Minimum frontal breadth point R
10	Ectoconchion R	25	Cheek height inferior point L
11	Frontomalar anterior L	26	Cheek height superior point R
12	Frontomalar anterior R	27	Frontotemporale L
13	Glabella	28	Frontotemporale R
14	Lambda	29	Zygion L
15	Metopion	30	Zygion R

An analysis of variance (ANOVA) in SAS 9.3 (SAS 2002-2010) was used to determine if groups exhibit significant differences in centroid size; a Tukey multiple comparison test was used to determine which groups differ significantly. Separate ANOVAs were run on males and females due to sex differences in size. Guatemalan females were omitted from the ANOVA due to the small sample size (n=4). A General Procrustes Analysis (GPA) was used to center, scale, and rotate all individuals into a common coordinate system and eliminate non–shape-related variation (i.e., size) (Mitteroecker and Gunz 2009; Slice 2007). Because size variation is removed in the GPA, males and females were pooled to increase sample sizes. A canonical variates analysis (CVA) was performed in MorphoJ (Klingenberg 2011) to determine the shape features that distinguish the four reference groups. Interpretation of wireframe graphs were used to help assess the morphological shape differences among groups. Principal components and centroid size from the GPA were exported for DFA using SAS 9.3 (SAS 2002-2010) in order to ascertain whether traditional morphometric methods or geometric morphometric methods provide better classification accuracy for ancestry estimation.

Traditional Morphometric Analyses

To address whether standard measurements provide better classification rates for ancestry over Howells' measurements, two DFAs were run. All measurements were imported into FORDISC 3.0 (Jantz and Ousley 2005) using the custom import function. DFA analyses were performed by selecting the “no classify” option. This option allows FORDISC to be used as statistical software that will run a DFA with a variety of options. The first DFA included the standard measurements, while the second used the Howells measurements. Both DFAs included a Forward Wilks stepwise discriminant analysis to determine the variables that best maximize group differences and to maintain appropriate variable numbers relative to sample size.

3 RESULTS

A. SEX ESTIMATION

Discriminant Function Analysis

Standard postcranial measurements

The results of the DFA using the standard postcranial measurements indicate that the scapula provides highest overall classification rate of 95.55%. The femur, tibia, radius, and clavicle also provide classification rates greater than or equal to 90%. The fibula has the lowest classification rate at 80.36%. The stepwise selected measurements are provided in Table 20 along with classification functions. Table 21 provides a list of sample sizes, Mahalanobis D^2, female and male cross-validated classification rates, and the overall classification rates.

The length and breadth measurements for the scapula, clavicle, and calcaneus were selected for use in the DFA. For the long bones, the length measurements were only found significant to include in the DFA for the radius, fibula, and ulna, with the radius exhibiting the most dimorphism and the fibula the least. The femur, tibia, and humerus exhibit the most dimorphism based on joint surfaces rather than length (e.g. epiphyseal breadth and head diameter). Femoral distal epiphyseal breadth, head diameter, and medio-lateral midshaft diameter provide a cross-validated classification rate of 93%. Tibial distal epiphyseal breadth and maximum nutrient foramen provide a classification rate of 91.5%.

Table 20. Classification Functions with Stepwise Selected Variables[†,‡].

Bone	**Classification Function†**
Clavicle	(0.214*maximum length) + (0.586*anterior-posterior diameter) + (-36.980)
Scapula	(0.233*height) + (0.322*breadth) + (-64.974)
Humerus	(0.306*epiphyseal breadth) + (0.385*maximum head diameter) + (0.534*minimum diameter mid-shaft) +(-41.584)
Radius	(0.070* maximum length) + (1.466*anterior-posterior diameter mid-shaft) + (-31.026)
Ulna	(0.104* maximum length) + (0.310*dorso-volor diameter mid-shaft) + (-29.136)
Ulna*	(0.641*ORLL) + (0.417*BOPL) + (0.517*MBOL) + (-40.919)
Femur	(0.153*epiphyseal breadth) + (0.589*maximum head diameter) + (0.355*medio-laterial diameter at mid-shaft) + (-44.912)
Tibia	(0.612*maximum distal epiphyseal breadth) + (0.506*anterior-posterior diameter at nutrient foramen) + (-45.420)
Fibula	(0.067*maximum length) + (-22.302)
Calcaneus	(0.323*maximum length) + (0.349*middle breadth) + (-37.484)

[†] Section point is 0; females are negative and males positive.

[‡] All measurements recorded in mm.

[*] Classification function using Zobeck stepwise selected measurements.

Table 21. Cross-validated Classification Rates from DFA for Mexican Reference Data Using FDB Stepwise Selected Measurements.

Bone	Female n	Male n	D^2	Female %	Male %	Overall %
Clavicle	35	52	5.19	91.43	86.54	88.99
Scapula	31	41	8.30	93.55	97.56	95.55
Humerus	32	60	6.00	90.63	85.00	87.82
Radius	35	53	4.95	94.29	86.79	90.54
Ulna	32	46	3.64	90.63	71.74	81.19
Femur	27	64	6.20	100	85.94	92.97
Tibia	32	65	6.56	96.88	86.15	91.52
Fibula	32	56	2.27	87.5	73.21	80.36
Calcaneus	22	30	4.39	90.91	73.33	82.12

Zobeck measurements

The Zobeck measurements established as significant in the stepwise discriminant analyses are found in the scapula, radius, ulna, and femur (Table 22). For these bones, sex estimation improved for the radius and ulna, however the Mahalanobis D^2 increased for all bones. The radius classification rate improved 1%; however; the ulna classification improved by over 4%, and the femur and scapula rates remained almost the same. Because classification rates increased only for the ulna, classification functions are not provided for the other bones.

Table 22. Cross-validated Classification Rates from DFA for Mexican Reference Data Using Zobeck Stepwise Selected Measurements.

Bone	Female n	Male n	D^2	Female %	Male %	Overall %
Scapula	28	30	9.85	96.55	93.75	95.15
Radius	34	50	5.56	97.06	86.00	91.32
Ulna	26	31	5.86	89.66	81.58	85.62
Femur	25	38	9.19	100.00	86.36	93.18

Sectioning Points

Male and female sample sizes, means, and standard deviations are provided in Table 23, along with the sectioning point and the percentage of the reference sample correctly classified. Clavicle length, scapula height, and radial length provide the highest classification rates; however, with the exception of the femur MTV measurement, all sectioning points provide high classification rates.

Table 23. Sectioning Points and Percent of Reference Sample Correctly Classified for Select Postcranial Measurements.

Measurement	Female			Male			Sectioning Points	
	N	Mean (mm)	Std Dev (mm)	N	Mean (mm)	Std Dev (mm)	Value (mm)	Percent Correctly Classified
Tibia max breadth of distal epiphyses	32	45.06	2.30	65	51.57	3.14	48	0.96
Tibia ant/post diam nut foramen	34	28.88	2.28	78	34.08	2.71	31	0.94
Femur epicondylar breadth	28	69.21	3.87	64	79.58	5.93	74	0.91
Fem max vert diam of head	34	38.71	1.70	78	44.64	2.89	42	0.91
Fem med/lateral diam midshaft	33	23.67	1.80	81	26.78	2.41	25	0.82
Radius maximum length	35	209.89	9.65	53	236.23	17.12	223	0.99
Humerus epicondylar breadth	33	52.21	2.78	64	59.70	4.02	56	0.91
Hum max diam of head	32	39.31	2.91	63	45.29	3.02	42	0.96
Scapula maximum height	32	133.56	7.37	41	153.15	8.12	143	1.00
Scapula maximum breadth	32	92.28	4.35	49	103.31	5.47	98	0.93
Maximum clavicle length	35	134.09	6.37	52	151.44	9.36	143	0.99

B. ANCESTRY ESTIMATION

Geometric Morphometric Analyses

Size

The ANOVA indicates significant differences in size for both males ($p < .0001$) and females ($p < .0001$). The American Black females have the largest values for centroid size, followed by American Whites, although they do not significantly differ from one another (Tables 24 and 25). The Mexican females have the smallest centroid size, and based on the Tukey multiple comparisons, they differ significantly when compared to American Blacks and Whites. The males follow the same pattern as the females. The American Black and White males have the largest values for centroid size, and do not significantly differ from one another. The Guatemalan males have the smallest centroid size, and do not significantly differ from the Mexican males. Significant differences in centroid size are found between American Black and White males when compared to Guatemalan and Mexican males. The individuals that fall outside the standard deviation for centroid size were investigated to determine if they were outliers. No reason could be found to exclude these individuals from further analyses; they remain either larger or smaller on average than other individuals within their group, and no pathologies or error in recording were noted.

Table 24. Female Centroid Size Means and Standard Deviations.

Group	N	Mean	Std Dev
American Black	17	400.16	12.87
American White	134	395.72	10.32
Mexican	29	379.96	11.78

Table 25. Male Centroid Size Means and Standard Deviations.

Group	N	Mean	Std Dev
American Black	61	419.16	11.28
American White	247	418.19	11.24
Mexican	95	403.26	12.80
Guatemalan	71	398.96	8.75
Note: Mexican and Guatemalans are significantly different to both American Whites and Blacks in centroid size, but do not differ between each other.			

Shape

The Mahalanobis distance matrix (Table 26) and associated p-values indicate that all groups are significantly different. The Mexican and Guatemalan groups are more similar to one another than the American Black and White groups. The first canonical variate (CV) explains 69.72% of the total variation, followed by 17.15% and 13.12% for CVs 2 and 3, respectively (Figure 6). The first CV separates the American Whites and Blacks from the Mexican and Guatemalan groups. Shape changes are visualized in wireframe graphs associated with each CV (Figures 7 and 8). The light blue lines represent the average configuration of all individuals and the dark blue lines represent a change in 10 Mahalanobis distance units on the positive axis. The first CV reflects morphological differences between the American White (negative axis) and Guatemalans and Mexicans (positive axis) (see Figure 6A). The morphological shape differences in the positive direction include a more anteriorly positioned prosthion, posteriorly positioned nasion, glabella, posterior-inferiorly positioned metopion, inferiorly positioned bregma, anteriorly positioned parietal subtense, lambda, occipital subtense, and superiorly positioned opisthion and basion (see Figure 7A).

Overall, the sagittal contour of the Guatemalan and Mexican groups is smaller than the average configuration. The anterior view of the wireframe graph for CV 1 (see Figure 8A) also indicates that the left and right zygion are positioned lateral to the average configuration, the points for superior and inferior cheek height suggest that Guatemalans and Mexicans are more projecting superiorly and inferiorly, and the right and left alare project lateral to the average. The American White group displays less prognathism, a more projecting frontal bone, and the landmarks representing the sagittal contour fall outside the average configuration.

The second CV separates American Blacks from other groups (see Figure 6A). Shape changes along the positive axis of CV 2 include a posterior-inferior positioning on prosthion, anterior-superior position of nasion and glabella, posterior-superior position of metopion, superior position of bregma and parietal subtense, anterior position of lambda, interior position of occipital subtense, and inferior position of opisthion (see Figure 7B). The anterior view of the wireframe graph associated with CV 2 (see Figure 8B) indicates that the position of left and right zygion are laterally positioned from the average and that left and right alare are medial and inferior to the average, and the points for nasal height are also positioned inferiorly to the average.

The third CV (see Figure 7B) separates the Guatemalans from all other groups. The most notable differences on this axis are the superior positioning of bregma and parietal subtense with an inferior position of opisthion and basion. Metopion, glabella, and nasion are all positioned posteriorly. Left and right zygion are also positioned lateral to the average. CV 3 is separating Guatemalan from other groups based on vault height.

Table 26. Mahalanobis Distances from Canonical Variates Analysis.

Group	American Black	Guatemalan	Mexican
American Black (n=78)	-	< 0.0001	<0.0001
Guatemalan (n=75)	4.54	-	<0.0001
Mexican (n=124)	4.65	3.42	-
American White (n=381)	3.45	4.86	4.86
*Mahalanobis distances below diagonal, p-values for permutation test of distances above.			

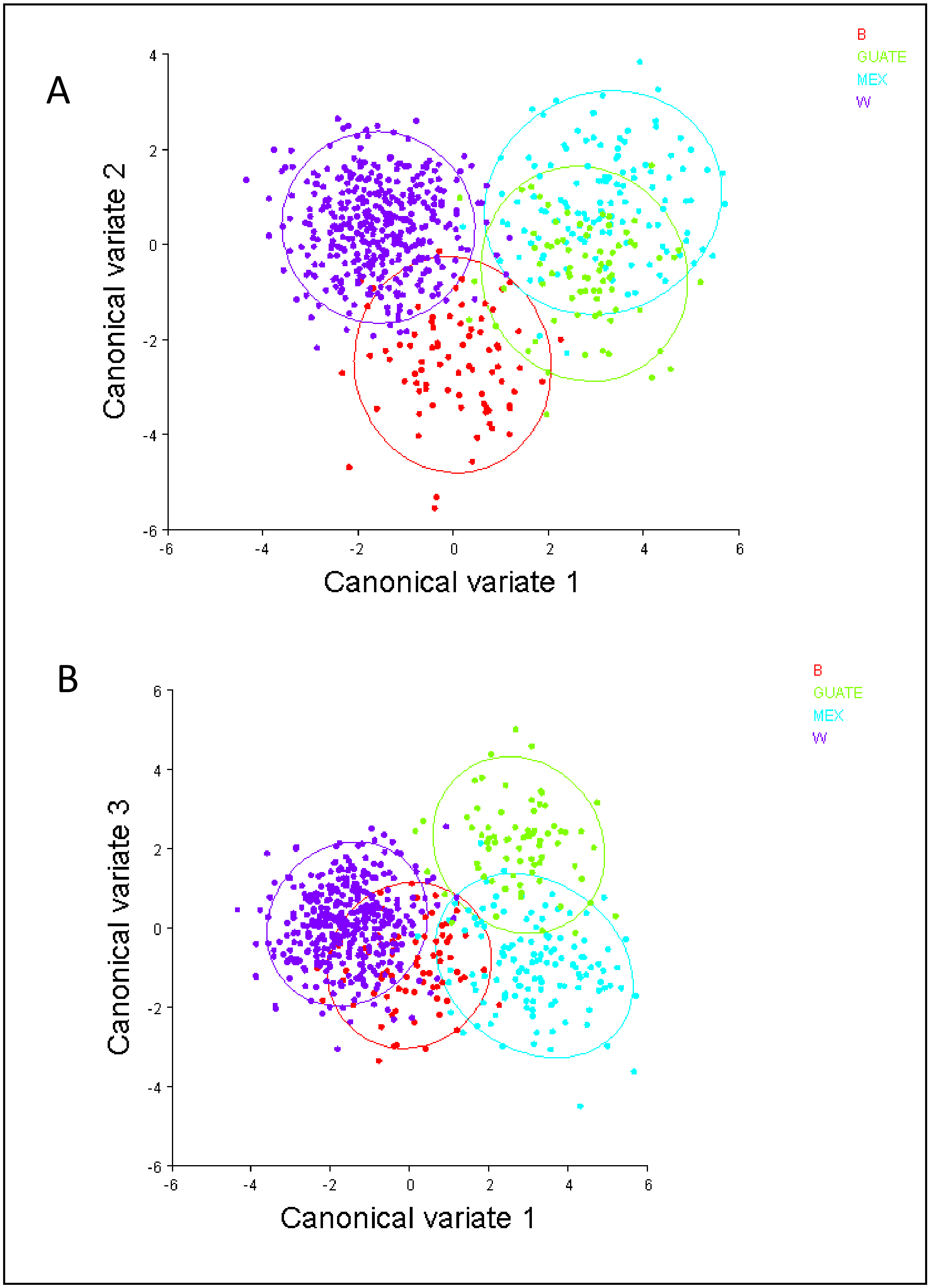

Figure 6. A) Canonical variates 1 (69.72%) and 2 (17.16%) and B) canonical variates 1 (69.72%) and 3 (13.12%).

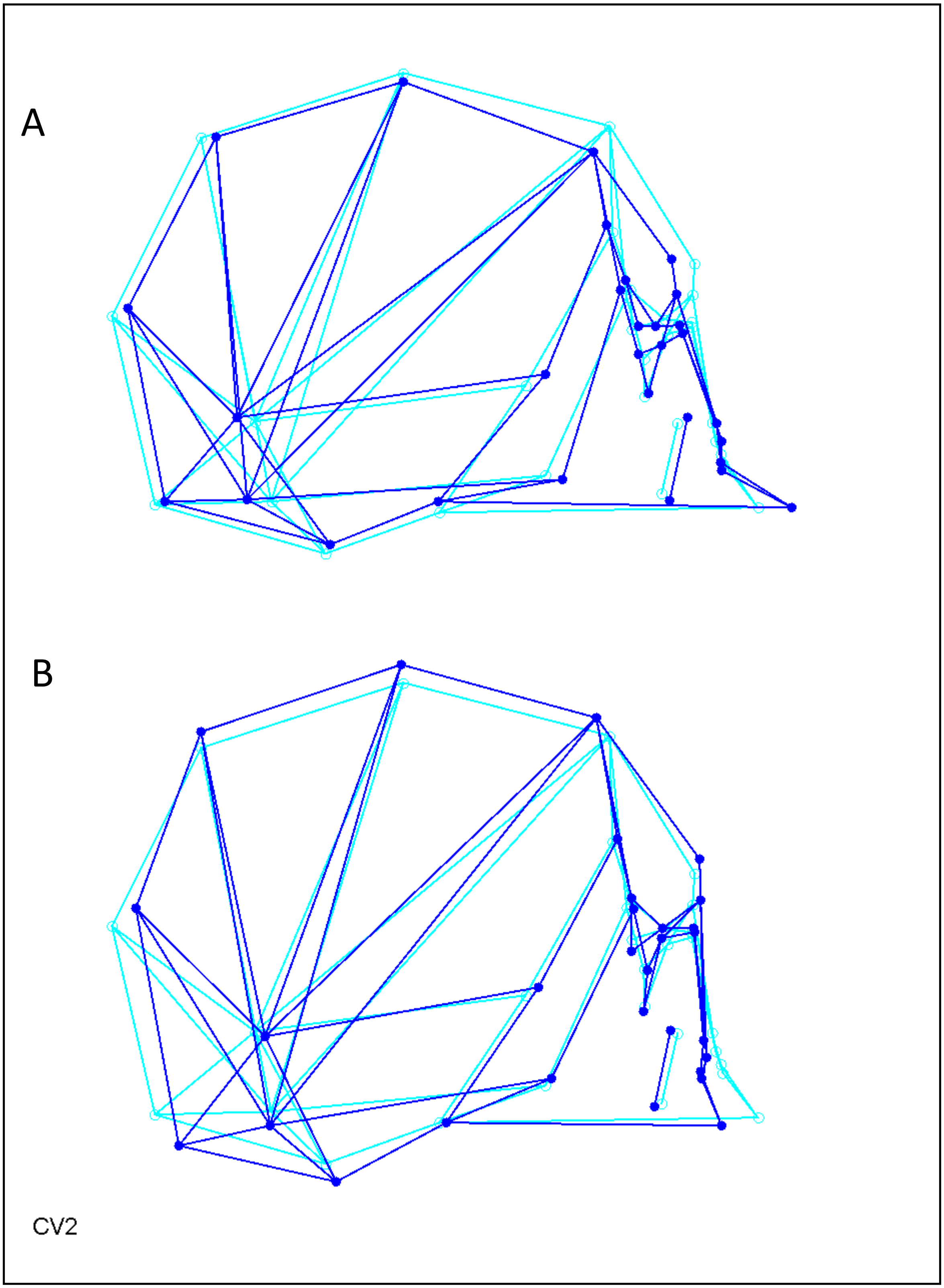

Figure 7. Lateral view of A) shape changes associated with CV 1 and B) shape changes associated with CV 2.

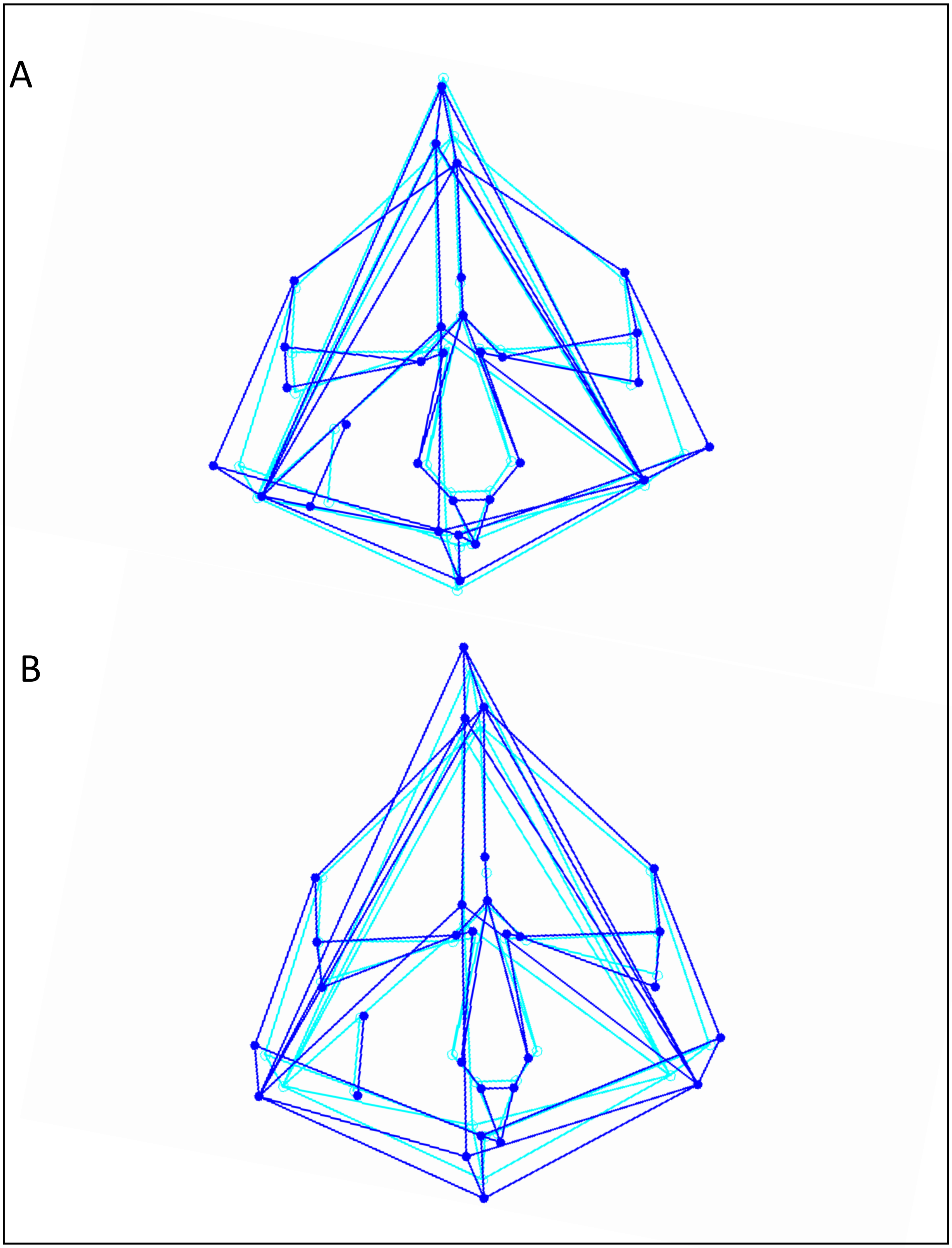

Figure 8. Anterior view of A) shape changes associated with CV 1 and B) shape changes associated with CV 2.

In summary, the Guatemalans and Mexicans on the first axis are separated primarily due to overall smaller cranial vaults, pronounced prognathism, wide zygomatics, and larger values for cheek height and nasal breadth. The second CV is separating the American Blacks from other groups based on a longer and lower cranial vault, more pronounced prognathism, a less pronounced glabellar region, superiorly projecting posterior cranial vault, narrower face and vault, and wide nasal aperture. The third CV separates the Guatemalans from the other groups based on short and high cranial vaults.

Ancestry Estimation

The first ten principal components account for 60.3% of the total variation and were included with centroid size in DFAs. Because the test of homogeneity of the covariance matrices was found to be significant at the 0.1 level, the within-covariance matrices were used in quadratic DFAs. The cross-validated classification rates are provided in Table 27. American Whites have the highest classification rate (84%) and American Blacks the lowest (60%), with the Mexican (61%) and Guatemalan (57%) groups intermediate. The majority of misclassified Guatemalans classified into the Mexican group and vice versa. When Guatemalans are removed from the DFAs, classification rates improve for all groups, especially Mexicans (78%) (Table 28).

Table 27. Cross-validated Classification Rates using Principal Components and Centroid Size, All Groups.

Group	n	Percent Classified Into			
		American Black	Guatemalan	Mexican	American White
American Black	78	**60.26**	7.69	6.41	25.64
Guatemalan	71	5.63	**57.75**	32.39	4.23
Mexican	126	9.68	20.97	**61.29**	8.06
American White	383	11.29	2.89	2.10	**83.73**

Table 28. Cross-validated Classification Rates using Principal Components and Centroid Size, Guatemalans Removed.

Group	n	Percent Classified Into		
		American Black	Mexican	American White
American Black	78	**64.10**	10.26	25.64
Mexican	126	12.90	**78.23**	8.87
American White	383	11.81	2.89	**85.30**

Traditional Morphometric Analyses

Males

DFA results for males using the 12 stepwise selected variables from the standard measurements set provides an overall cross-validated classification rate of 82.2% using the reference groups American Black and White, Guatemalan, and Mexican (Table 29). Using the standard measurement subset, 89% of American Whites, 80% of American Blacks, 74.6% of Guatemalans, and 61.0% of Mexicans correctly classified into their own group. Measurements selected by the stepwise procedure include the cranial vault (length and width), the facial region (inter-orbital breadth, orbit height and width, nasal breadth and facial height), and measures of prognathism.

Table 29. DFA results for Mexican, Guatemalan, American Black, and American White Males Standard vs. Howells Measurements.

Group	DFA Results Using Mexican Reference Group			
	12 Stepwise Selected Standard Measurements[1]		17 Stepwise Selected Howells Measurements[2]	
	N	% Correct	N	% Correct
American Black	70	80	34	91
Guatemalan	71	74.6	59	85
Mexican	41	61	53	76
American White	227	89	149	87

[1] GOL MAB BBH OBH OBB NLB AUB DKB BNL BPL XCB UFHT

[2] GOL PRA DKA DKB OBH XFB MLS AUB EKB BAA JUB FRS BRA FRF MAB MDH PAC

The 17 stepwise selected variables from the Howells measurements provide an overall cross-validated classification rate of 85.8%. Using these measurements, 91% of American Blacks, 85% of Guatemalans, 87% of American Whites, and 76% of Mexicans correctly classified into their own group. Howells measurements selected by the stepwise procedure include 8 standard measurements common between the two measurement sets. The measurements included in the analysis are from the cranial vault (length, frontal width) and include multiple angles involving basion and bregma, and fractions and subtenses involving the frontal bone. The majority of measurements involves the facial region and include prosthion and dacryon angles, inter-orbital breadth, orbital breadth, facial width, palate breadth, and malar projection.

Females

Because the Guatemalan female sample is too small (n=5), it was not included in the female DFAs. DFA results for females using the 12 stepwise selected variables from the standard measurements set provides an overall cross-validated classification rate of 89.1% using the reference groups American Black and White, Guatemalan, and Mexican (Table 30). Using the standard measurement subset, 92% of American Whites, 84% of American Blacks, and 82.0% of Mexicans correctly classified into their own group. Standard measurements selected by the stepwise procedure include the cranial vault (length, height, and width), the facial region (orbit height, nasal breadth, palate length, and facial width), and measures of prognathism. Howells measurements included in the DFAs include 5 out of 10 standard measurements. The included Howells measurements include nasion and dacryal angles, biasterionic breadth, maximum frontal breadth, and zygo-orbitale radius.

Table 30. DFA results for Mexican, American Black, and American White Females Standard vs. Howells Measurements.

Group	DFA Results Using Mexican Reference Group			
	12 Stepwise Selected Standard Measurements[1]		10 Stepwise Selected Howells Measurements[2]	
	N	% Correct	N	% Correct
American Black	37	84	15	93
Mexican	17	82	13	85
American White	102	92	53	98

[1] NLB BBH MAL AUB OBH GOL BPL BNL FOB WFB ZYB XCB
[2] NAA OBH GOL NLB ZYB NDA WFB ASB XFB ZOR

4 CONCLUSIONS

A. DISCUSSION

The first goal of Project IDENTIFICATION was to obtain population-specific cranial and postcranial skeletal measurements from individuals from Mexico to establish a database of available reference data for further research and development by forensic anthropologists. Osteometric data is now available for 215 positively identified individuals from Mexico. Metric data was collected for an additional 318 undocumented border crossers. These remains are not identified at this time, although efforts to are underway for their identification. All data is available through the FDB, curated at The University of Tennessee at Knoxville by Dr. Richard Jantz. As positive identifications are made, the data will be updated.

The second goal of this project was to create sectioning points and classification functions for population-specific sex estimates applicable to the majority of Hispanics within the U.S. Because the majority of Hispanics in the U.S. are of Mexican ancestry, the new sexing criteria provided should be the most appropriate for forensic anthropology practice. The classification functions provided for long bones should be considered more robust than the sectioning points, as multivariate methods are more robust than univariate. The classification rates from postcranial metrics, classification functions, and sectioning points are higher than those presented by Tise et al. (2013). The improved classification rates are likely due to the use of increased sample sizes particularly for females and individuals with known sex rather than estimated. The use of a test sample at this time was not feasible due to small sample sizes, particularly for the females. As more positive identifications are made at the PCOME, males and females will be used as a test sample for provided error rates.

The third goal of this project was to utilize traditional and geometric morphometric methods with the new reference data to explore morphological variation of among Mexicans, American Blacks, and Whites. Within this goal, three main questions were addressed: 1) how do the reference groups differ in overall craniofacial morphology; 2) do standard measurements provide better classification rates for ancestry than Howells measurements; and 3) do traditional linear measurements provide better classification rates than data derived from geometric morphometric data? Geometric morphometric analyses using the new Mexican data and data from Guatemalans, American Blacks, and American Whites was used to explore the biological variation of these groups. Differences in both size and shape are noted for the groups. Although the two groups considered Hispanic (Guatemalan and Mexican) are more similar to each other than American Whites and Blacks, they differ significantly in their overall craniofacial morphology.

Results from DFAs for males and females both suggest that use of additional Howells measurements improves overall classification accuracy in ancestry estimation. Classification rates for the Mexican group were the lowest for both males and females. The female rates were higher; however, that is most likely because no Guatemalan females were included in the analyses. Based on the geometric morphometric results, the Guatemalans and Mexican—although morphological different from one another—are more similar to each other than American Blacks and Whites. Thus, the inclusion of the Guatemalan sample in the male DFA sample lowers the classification rate for the Mexicans, as both groups commonly misclassified as each other. The low sample sizes of the Mexican females could also skew the results. When the DFA results from the data (centroid size and principal components) derived from the geometric morphometric analysis and the traditional linear measurements were used, the latter performed better in ancestry estimation based on classification rates.

The improvement in the classification rates for Mexicans when Guatemalans are removed from the analysis could be due to the fact that the two groups share a geographic border and similar parental population groups. The Guatemalan sample represents several Mayan groups from rural areas. If data from urban areas were available and included in the present analyses, the results may be different as there may be differences in admixture rates between rural and urban Guatemalans. Additionally, based on the primary source of data for the Mexican group, this group represents individuals from rural, low SES areas rather than urban areas. Because of the complex population history of Mexico influencing rural and urban admixture rates, different results may be obtained with different reference data.

B. IMPLICATIONS FOR POLICY AND PRACTICE

This study has investigated the morphological differences between two groups considered Hispanic by the U.S. Although the Guatemalans and Mexicans are more similar to each other than to American Whites and Blacks, they do exhibit significant differences in morphology. These results suggest that population groups considered Hispanic with different geographic origins should not be lumped together when creating new criteria and methods for forensic identification. Furthermore, because most individuals considered Hispanic in the U.S. are Mexican, the Mexican data derived from this project should be the most appropriate reference data for the U.S. However, it should be noted that the data collected from the PCOME represents individuals that died in their attempt to enter the United States.

These individuals most likely represent a portion of the Mexican population that is considered to be of low socioeconomic status. Relethford (1983) previously linked higher percentages of Native American admixture to lower SES among Mexican Americans in Texas. Therefore, the data accumulated through this project represents a unique cross section of Mexico, most likely low SES individuals with high Native American admixture.

Although the positive identifications did not accumulate as rapidly as expected, metric data from 215 positively identified Mexicans are available to further research and development. Additionally, the data collected during this project will be updated when additional positive identifications are made, and all data will be made available to the FDB and subsequently to FORDISC. The female sample size is still relatively small, and as a result, no test sample was pulled from this group to test the classification functions, which would greatly contribute to the findings. As more females become positively identified, the classification functions and sectioning points for sex estimation will be tested.

When using classification statistics for the purpose of ancestry estimation, practitioners should always be cognizant of statistical assumptions and interpretation of any method used in forensic anthropological investigation (SWGANTH statistics document, www.swganth.org). Additionally, familiarity with the populations in a practitioner's geographic area, along with the population history and structure of reference data, is equally important. The present research finds that Guatemalans and Mexicans differ in cranial morphology; however, they are more similar to one another than compared to Blacks and Whites. If an unknown classifies as Mexican over Guatemalan, it does not mean that the unknown is Mexican. Rather, it indicates that the unknown is most similar to the Mexican group, a group with a complex ancestry including varying rates of Native American admixture (Bonilla et al. 2005; Lisker et al. 1986; Rubi-Castellanos et al. 2009).

C. IMPLICATIONS FOR FURTHER RESEARCH

Although the term Hispanic has no precise biological or genetic meaning, it is the terminology used by practitioners within the medico-legal agencies and law enforcement in the U.S., and can be useful in facilitating identifications. However, it is still important for anthropologists to understand that Hispanic groups are not homogenous; rather, they are quite complex. As data become available, the use of multiple national origin groups from Latin America will also assist in finer-grained approaches of ancestry estimation along the U.S.–Mexico border and in regions of the U.S. with high numbers of non-Mexicans (e.g., Florida has a large Cuban population) (Motel and Patten 2012b). Undocumented border-crossing fatalities found on the U.S. side of the U.S.–Mexico border are high, especially for Arizona and more recently Texas (Jimenez 2009; MacCormack 2013). Even if DNA is obtained from these fatalities and submitted to CODIS (as is common practice for unidentified remains in the U.S.), there may be no family reference data available. Therefore, the possibility of narrowing down the specific region of a border-crosser decedent will be helpful. As the positive identifications accumulate for data collected during this project, data will be available to explore regional variation within Mexico, and if possible other Latin American countries. The reported higher rates of European admixture in North Mexico (Rubi-Castellanos et al. 2009) and decreasing rates in the South may be reflected in cranial morphology, allowing for regional classification of unknowns within Mexico and, if data allows, other areas in Latin America.

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Dissemination of Research Findings

1 PUBLICATIONS

1. Spradley, MK. In Press. Ancestry estimation from the postcranial skeleton. In Berg G, Ta'ala S, editors. Biological affinity in forensic identification of human skeletal remains: beyond black and white. ISBN-10: 1439815755.
2. Hefner JT, Spradley MK, Anderson BE. In Press. Assessment using random forest modeling. J Forensic Sci.
3. Tise ML, Spradley MK. 2012. Postcranial sex estimation of individuals considered Hispanic. J Forensic Sci. Early View: doi: 10.1111/1556-4029.12006.

2 PRESENTATIONS

1. Spradley MK. 2012. Cranial secular change in Hispanics. Presented at the American Association of Physical Anthropology Annual Meetings. April 11-14, 2012.
2. Figueroa-Soto C, Spradley MK. 2012. Sexual dimorphism: a comparison of migrant and non-migrant Mexican populations. American Association of Physical Anthropology Annual Meeting. Portland, Oregon.
3. Spradley MK. 2012. Identifying the Dead along the U.S. Mexico Border. Tejas Foco Regional Conference of that National Association of Chicano and Chicana Studies. March 1-3, 2012.
4. Figueroa-Soto C, Spradley MK. 2012. Cranial variation among three regional groups in Mexico. Texas Academy of Science 115th Annual Meeting. Alpine, TX.
5. Spradley MK, Figueroa-Soto C. 2011. Demographic change and ancestry estimation in the United States: the need for reference data from Mexico. Presented at the XVI Coloquio internacional de antropologia Fisica Juan Comas November 13-19. Oaxaca, Oax. Mexico.
6. Spradley MK. 2011. Forensic identification of individuals involved in U.S./Mexico border crossing fatalities. Presented at the Seminaro Internacional de Antropologia Forense. Hosted by the UniversidadNacional Autónomade México Instituto de Investigaciones Antropológicas. March 28 – April 1 2011.
7. Tise ML, Spradley MK. 2010. Postcranial sex estimation for individuals considered Hispanic. Presented at the 60th annual meeting of the American Academy of Forensic Sciences, February 22 – 26, 2010.
8. Tise ML, Spradley MK. 2010. A metric analysis of the postcranial skeleton of Hispanic individuals to improve the estimation of sex. Texas Association of Biological Anthropologists Annual Meeting, November 12-13, 2009 in Austin, Texas.

3 INVITED PRESENTATIONS

1. Project IDENTIFICATION: Developing Accurate Identification Criteria for Hispanic Individuals (May 10 and 23, 2012), National Institute of Justice Webinar online.
2. Improving Forensic Anthropological Methods of Identification (April 2012), Michigan State University.
3. Project IDENTIFICATION: Developing Accurate Identification Criteria for Hispanic Individuals (February 2012), NIJ Grantees Meeting: How NIJ funded Research Impacts the World, Atlanta, Georgia.
4. Demographic Change and Forensic Identification: Methods for sex and ancestry estimation for individuals considered Hispanic (April 2011), University of Arizona.
5. Forensic Identification of U.S. Mexico Border Crossing Fatalities (April 2010), California State Chico.
6. Forensic Identification of U.S. Mexico Border Crossing Fatalities (October 2010). Baylor University.
7. Forensic Identification of U.S. Mexico Border Crossing Fatalities (November 2010). San Diego State University.
8. Project IDENTIFICATION (December 6 – 7, 2009). The National Institute of Justice Forensic Anthropology Grantees Meeting in Washington D.C.

4 TECHNOLOGY TRANSFER

1. Traditional craniometric data from positively identified individuals resulting from this project have been
    a. submitted to the Forensic Anthropology Data Bank.
    b. provided to the programmers of FORDISC.
2. Landmark data from positively identified individuals has been provided to the programmers of 3D-ID.