

CRANIOMETRIC VARIATION OF MODERN ASIAN AND HISPANIC
INDIVIDUALS USING MULTIVARIATE ANALYSIS

by

Nandar Yukyi, B.A.

A thesis submitted to the Graduate Council of
Texas State University in partial fulfillment
of the requirements for the degree of
Master of Arts
with a Major in Anthropology
August 2017

Committee Members:

M. Katherine Spradley, Chair

Daniel J. Wescott

Ashley H. McKeown

COPYRIGHT

by

Nandar Yukyi

2017

FAIR USE AND AUTHOR'S PERMISSION STATEMENT

Fair Use

This work is protected by the Copyright Laws of the United States (Public Law 94-553, section 107). Consistent with fair use as defined in the Copyright Laws, brief quotations from this material are allowed with proper acknowledgment. Use of this material for financial gain without the author's express written permission is not allowed.

Duplication Permission

As the copyright holder of this work I, Nandar Yukyi, authorize duplication of this work, in whole or in part, for educational or scholarly purposes only.

DEDICATION

To Papa and Mama,
for all your sacrifices.

ACKNOWLEDGEMENTS

First, I would like to thank my advisor, Dr. Kate Spradley, for her continuous guidance and support throughout my time at Texas State, and for graciously sharing her data with me. Thank you for teaching me how to be independent and confident, and for your encouragement especially during my times of self-doubt. I would also like to thank my committee members. Dr. Danny Wescott, you have amazingly taught me a lot of things that may or may not be related to my thesis, just by saying only a few words at a time. Dr. Ashley McKeown, your expertise and comments have been most helpful. Thank you Dr. Nick Herrmann for your brilliant ideas that kept being added to my thesis and other projects, despite not being on my committee. I also promise you that one day, I will learn to love R as much as you do. I am extremely thankful to Dr. Michael Pietrusewsky for kindly sharing his craniometric data on Asian individuals. This thesis project would have been impossible without your generosity.

I would like to thank my parents and my older sister for cheering me on every step of the way and offering nothing but love through my ups and downs. Thank you Kenny Kao for his friendship, patience, humor, and love for me while I pursue my dream. Last but not least, thank you to my friends in cohorts above and below mine, and especially those in my cohort/fam. Thank you for keeping me grounded, inspired, and sane. Thank you for not judging me for my tremendous love for food, for patiently teaching me about American pop culture, and for being my solid support system through this rollercoaster ride called grad school. I couldn't have done it without y'all.

TABLE OF CONTENTS

	Page
ACKNOWLEDGEMENTS	v
LIST OF TABLES	viii
LIST OF FIGURES.....	ix
LIST OF ABBREVIATIONS	x
 CHAPTER	
I. INTRODUCTION	1
Research Problem and Objective	1
Cranioetrics	3
Asian and Hispanic Groups.....	4
Population History.....	6
Research Questions	7
II. MATERIALS AND METHODS	9
Reference Samples	9
Asian Samples	9
Hispanic Samples	11
Forensic Anthropology Data Bank Samples	13
Data Collection.....	14
Cranioetric Landmarks.....	14
Statistical Analyses	14
Discriminant Function Analysis.....	14
Canonical Variates Analysis	16
Mahalanobis Distance (D^2)	16
Comparison to FORDISC Analysis	17

III. RESULTS.....	19
Asian and Mexican Groups Only	19
Classification Rates	19
Mahalanobis Squared Distance	20
Class Means on Canonical Variates	21
Females (Asian and Mexican only).....	21
Males (Asian and Mexican only)	24
Asian and Mexicans with Other Groups	27
Classification Rates	27
Females (All Groups).....	27
Males (All Groups).....	29
Mahalanobis Squared Distance	31
Class Means on Canonical Variates	31
Females (All Groups).....	31
Males (All Groups).....	32
Analysis of Initial Asian and Mexican Samples in FORDISC	35
IV. DISCUSSION	36
Analysis of Asian and Mexican Groups Only.....	36
Analysis of Asians and Mexicans with Other Groups	40
Analysis of Initial Asian and Mexican Samples in FORDISC	43
Future Research.....	43
V. CONCLUSION	46
APPENDIX SECTION	50
LITERATURE CITED	54

LIST OF TABLES

Table	Page
1. Summary of reference samples	12
2. Cranial measurements used for analysis and their abbreviations.....	15
3. Classification matrix for three female sample groups.....	21
4. Classification matrix for 11 male sample groups.....	22
5. Mahalanobis squared distance matrix among three female sample groups	23
6. Mahalanobis squared distance matrix among 11 male sample groups	23
7. Between canonical structure values for three female sample groups.....	25
8. Between canonical structure values for 11 male sample groups.....	25
9. Cross-validated classification matrix for five female sample groups	27
10. Cross-validated classification matrix for 14 male sample groups.....	28
11. Mahalanobis squared distance matrix among five female sample groups	29
12. Mahalanobis squared distance matrix among 14 male sample groups	30
13. Between canonical structure values for five female sample groups	33
14. Between canonical structure values for 14 male sample groups.....	33
15. Measurements currently utilized for Asian Hispanic groups on FORDISC 3.1	45

LIST OF FIGURES

Figure	Page
1. Plotted class means for three female sample groups.....	26
2. Plotted class means for 11 male sample groups.....	26
3. Plotted class means for five female sample groups.....	34
4. Plotted class means for 14 male sample groups.....	34
5. Map depicting the geographical origins of the Asian sample groups	39

LIST OF ABBREVIATIONS

Abbreviation	Description
ASB	Biasterionic breadth
AUB	Biauricular breadth
BBH	Basion-bregma height
BNL	Cranial base length
BPL	Basion-prosthion length
CT	Computerized tomography
CV1	First canonical variate
CV2	Second canonical variate
CVA	Canonical Variates Analysis
DFA	Discriminant Function Analysis
EKB	Biorbital breadth
FACTS	Forensic Anthropology Center at Texas State
FDB	Forensic Anthropology Databank
FMB	Bifrontal breadth
FOL	Foramen magnum length
FRC	Frontal chord
GOL	Maximum cranial length
ILD	Interlandmark distance
IBD	Isolation by distance model
IRB	Institutional Review Board
JUB	Bijugular breadth
MANOVA	Multivariate analysis of variance
NamUs	National Missing and Unidentified Persons Systems
NAS	Nasio-frontal subtense
NLB	Nasal breadth
NLH	Nasal height
NOL	Nasio-occipital length
OBB	Orbital breadth
OBH	Orbital height
OCC	Occipital chord
OpID	Operation Identification
ORPL	Osteological Research and Processing Laboratory
PAC	Parietal chord
PCOME	Pima County Office of the Medical Examiner
SES	Socioeconomic status
SSS	Zygomaxillary subtense

Abbreviation	Description
STB	Bistephanic breadth
UADY	Universidad Autónoma de Yucatán
UNAM	Universidad Nacional Autónoma de México
WMH	Cheek height, minimum
XCB	Maximum cranial breadth
XFB	Maximum frontal breadth
XML	Malar length, maximum
ZMB	Bimaxillary breadth
ZYB	Bizygomatic breadth

I. INTRODUCTION

Research Problem and Objective

When dealing with cases in which human remains are heavily decomposed or are mostly skeletal, forensic anthropologists have to generate biological profiles that include sex, age, ancestry, and stature. Through this process, forensic anthropologists narrow down a list of possible matches between identified persons and records of missing persons (Spradley, 2013). Online databases such as the National Missing and Unidentified Persons Systems (NamUs) allow experts to enter information about unidentified and missing persons, which is publicly available. Biological profiles are extremely important for NamUs and other databases because sex, age, and ancestry are the main criteria utilized searching for missing persons. Out of these criteria, sex and ancestry are the most important aspects. Without the correct sex or ancestry estimation, the remains will not be correctly identified (Spradley, 2013). Biological sex estimation narrows down only fifty percent of the possible population due to the dichotomous nature of biological sex. On the other hand, ancestry estimation can further narrow the list of possible matches, thereby increasing the chances of a positive identification. Thus, correct ancestry estimation is crucial for building an accurate biological profile.

Forensic anthropologists can establish population-specific standards only with an adequate collection of data from reference groups, which can represent a variety of groups originating from various geographic origins. In forensic cases, it is important to compare data from an unidentified individual against data from different reference groups in order to examine to which group(s) the unknown may belong. Therefore, in order to

accurately represent a wide variety of reference groups, it is crucial to collect data on a diverse array of population groups. Data collected on different reference groups can be used to generate population-specific standards. The importance of these population-specific standards is that they are the basis of any accurate ancestry estimation, which ultimately aids with building correct biological profiles in forensic cases.

Currently, the majority of the skeletal collections that are accessible to forensic anthropologists for research consist mostly of American Black and White individuals (Shirley et al. 2011; Spradley, 2013; White et al., 2012). Even now in the 21st century, an era in which demographics of minority groups are changing in the United States, research data for these groups are still lacking. Among these groups, two ancestral groups that have been growing steadily in the United States are Asians and Hispanics. From 2000 to 2010, the Asian population in the United States has increased by 43% in the “Asian alone” category and 59.8% in the “Asian in combination [with other races]” category. Likewise, the Hispanic population has also increased by 43% during the same time period (U.S. Census Bureau). As rapidly growing populations, it is important for the Asian and Hispanic groups to be represented in forensic anthropological reference data. For instance, areas such as San Francisco, Los Angeles, Seattle, or New York City have considerable immigrant populations, particularly Asians and Hispanics (U.S. Census Bureau). For forensic cases or missing person’s cases in these urban cities with high immigrant populations, it is beneficial for forensic anthropologists to have established population-specific reference data for comparison. In cases that involve individuals of Asian or Hispanic ancestry, it would be inaccurate to use standards that are based on American Black or White populations.

Further, according to Dudzik (2015) and Dudzik and Jantz (2016), there have been high numbers of misclassifications between Hispanic and Asian populations in the ancestry estimation software FORDISC, as reported by various forensic anthropologists. Therefore, in order to avoid mistaking an unknown Asian individual as Hispanic, or vice versa, it is beneficial to conduct further research on cranial morphological comparisons between these two groups with shared ancestry. Thus, the purpose of this thesis is to examine if and how modern Asian and Hispanic individuals are morphologically distinguishable from each other using multivariate statistics.

Craniometrics

Qualitative and quantitative analyses of cranial morphology are the most common methods employed by forensic anthropologists for ancestry estimation. Cranial morphology plays a significant factor in ancestry estimation because of its moderate to high heritability (Sjøvold, 1984; Devor, 1987; Relethford, 1994; Carson, 2006). Comparative studies have been conducted to test for connections between cranial shape and size and genetic relationships (Smith, 2008). Results of these studies show that overall, cranial measurements of various geographic groups correlate to their mitochondrial, nuclear, as well as Y DNA (Relethford and Harpending, 1994; Smith, 2008; Harvati and Weaver, 2006). Therefore, the use of cranial morphology is effective in the estimation of an unknown individual's ancestry.

Traditionally, anthropologists have applied a typological approach on human crania in order to estimate ancestry. The typological approach is a visual- and experience-based method through which ancestry is estimated. This approach depends on a list of

morphoscopic or nonmetric traits, which are assessed on a binary scale by marking either the presence or absence of a given trait. However, not only does the subjective nature of the typological approach increase the chances of inter-observer error, but the approach also lacks standardization (Hefner, 2009). In contrast, craniometric analysis, which is based on measurements taken from landmarks on the cranium, is more reliable than the typological approach. Thus, by analyzing metric data from the crania of individuals of known populations, anthropologists can narrow down the list of possible matches in forensic cases that involve unidentified human remains.

Asian and Hispanic Groups

The term “Hispanic” is used to refer to individuals who originate from any Spanish-speaking region, as defined by the U.S. Census Bureau. In the first part of this thesis, Mexico is the only group that represents the Hispanic component of the population groups used, due to the small sample sizes available of identified individuals in other Hispanic groups. However, it is important to note that general terms such as “Hispanic” and “Asian” do not accurately represent the diverse array of populations that originate from various geographic regions. Although commonly used, these terms merely undermine the actual diversity within and between populations that form these groups (Spradley, 2013; Dudzik and Jantz, 2016).

There is great diversity within the Asian population, as represented by differences in physical appearance and morphological structure between individuals from various geographical regions in Asia. For instance, Southeast Asians exhibit expansive distribution of DNA patterns, due to different population histories of the diverse groups

(Schurr and Wallace, 2002). These DNA patterns manifest as different physical appearances and morphological structures. Specifically, cranial morphology is highly heritable based on its genetic components, but it can also be influenced by environmental factors (Sjøvold, 1984; Devor, 1987; Relethford, 1994; Carson, 2006). In addition, Asian populations occupy a wide range of geographic regions with varying environmental conditions, which also contributes to differences in cranial morphology. Thus, individuals inhabiting various parts of the same country may have different cranial morphologies. For instance, individuals from North Japan and South Japan exhibit differences in cranial morphology because of their unique population histories (Pietrusewsky, 2010). Likewise, Hispanics in Mexico, which include both Mestizos and Mexican Amerindian ethnic groups, are extremely diverse as well, (Rangel-Villalobos et al., 2008). Thus, it is extremely important to account for the amount of diversity within and between these groups.

Further, it is likely that there will be cranial morphological differences between Asian or Hispanic individuals born and raised in their native countries and American-born Asians or Hispanics, since migrating to a new environment has an effect on cranial morphology (Gravlee et al., 2003a, 2003b; Relethford, 2004a). Disparities in the environment and available dietary resources between the United States and Asian or Hispanic countries may explain these differences in morphology. Therefore, it is imperative that these differences are accounted for in future research. However, current records show low numbers of Asian American and Hispanic American individuals in skeletal collections (Weiss, 2015). Thus, it would be beneficial for forensic

anthropologists to focus on including more Asian American and Hispanic American individuals in future research.

Population History

Common ancestry and morphological similarities between Asian and Hispanic populations have been studied due to the dispersion of Asian populations in the New World (de Azevedo et al., 2011). In a genetic study of over 300,000 Native American nucleotide variations, Reich et al. (2012) state that the Native American people are genetically linked to Asians. Another interdisciplinary study that utilized both genetic and craniometric data also proposes migration models that support geographic dispersion to the New World originating from Asia (Hubbe et al., 2010). According to Hubbe et al. (2010), geographic dispersion from Asia to the New World came in two different waves via the Bering Strait.

Further, there is also evidence that Hispanics inherited genomic segments from their Native American ancestors (Bryc et al., 2010; Wall et al., 2011). However, it is important to note that not all Hispanics have the same amount of Native American genetic components. The Hispanic population is a highly admixed group due to the complex population histories of different countries or geographic regions. Specifically, Mexicans have greater Native American genetic components because of the high occupancy of Native Americans in the region in pre-Columbian times. Later, after European settlers arrived, admixture between the indigenous groups and the Europeans began to occur. In areas such as Mexico, in which Native American populations were large, populations in later generations exhibit elevated amounts of Native American

components admixed with European components. On the contrary, in countries such as the Dominican Republic or Puerto Rico, in which the trans-African slave trade took place, populations in later generations have higher African genetic components admixed with European components (Bryc et al., 2010). Ultimately, European colonization of Latin America created diverse hybrid and tri-hybrid populations that are currently referred to as Hispanic. In addition, Mexicans are expected to have higher indigenous components (Bryc et al., 2010; Wall et al., 2011). In turn, this connects Hispanic individuals with high Native American genetic components, such as Mexicans, with their ancestors that dispersed to the New World from Asia.

Research Questions

This thesis project will focus on craniometric similarities and differences between modern Asian and Hispanic individuals. The primary research question of this thesis will explore if these two populations are statistically significantly different in terms of craniometrics. In other words, can the two groups be distinguished from one another through craniometric analysis? If they can be distinguished, how are they morphologically different from one another? If they are misclassifying as each other, what are the patterns of misclassification?

Further, how do classifications of Asians and Hispanics differ when only these two groups are analyzed, compared to when they are analyzed after being combined with other groups? This research question is especially important because in a forensic case, it would only be realistic to analyze using all available reference groups due to the ambiguous nature of unidentified persons cases. Thus, even if Asians and Hispanics can

be distinguished when only two groups are analyzed, can they still be distinguished when analyzed with other groups, due to their shared population histories? In addition, how do these samples classify when they are run with reference sample groups currently available on ancestry estimation programs such as FORDISC 3.1? Finally, are the sample groups from this thesis misclassifying in FORDISC 3.1. If so, into which groups are they misclassifying? This research will benefit the field of forensic anthropology, and biological anthropology at large, by contributing a deeper understanding of how Asian and Hispanic groups relate to each other through craniometric analysis.

II. MATERIALS AND METHODS

Reference Samples

Most of the craniometric data utilized in this study were graciously provided by Dr. Michael Pietrusewsky (Asian craniometric data), and Dr. Kate Spradley (Hispanic craniometric data). Some Asian craniometric data collected by Dr. W. W. Howells (Konigsberg), were also utilized in this study. The sample consists of modern adult Asian and Hispanic individuals who were born in or around the 20th century or later. Table 1 shows a detailed summary of the sample size based on their geographical origins.

Asian Samples

The Asian samples utilized for craniometric analysis in this project are comprised of nine different groups from East and Southeast Asia: 1) Ba Chúc, Vietnam; 2) Thailand; 3) Hong Kong; 4) Taiwan; 5) Kanto, Japan; 6) Tohoku, Japan; 7) Kyushu, Japan; 8) Hokkaido, North Japan; and 9) Philippines. Data from the samples numbered 1 through 7 were collected by Dr. Pietrusewsky, while the latter two were obtained from the Howells craniometric database.

The Ba Chúc Vietnamese sample group is made up of 51 males, who were victims of the 1978 Khmer rouge massacre in a village called Ba Chúc located in the western Angiang Province in Vietnam. The Thai sample group encompasses 50 males, who were dissecting room specimens in Bangkok. The Hong Kong sample group includes 50 males who died in Hong Kong between 1978 and 1979. The Taiwan sample group is comprised of 47 males who are of Chinese descent, living in modern-day

Taiwan. Their origins can be traced back to Fujian and Guangdong Provinces in Mainland China. The Kanto Japanese group includes 50 modern male individuals from a dissecting room in the Kanto District on eastern Honshu Island. Most of these individuals were born in the Meiji Period (1868-1911) and died before 1940. The Tohoku Japanese sample group is also made up of 50 modern males from a dissecting room in the Tohoku District of northern Honshu Island. The Kyushu Japanese sample group is comprised of 51 modern male individuals mainly from the Fukuoka Prefecture, but also from Yamaguchi, Saga, Nagasaki, and nearby Prefectures on Kyushu Island (Pietrusewsky, 2005, 2008a, 2008b, 2010, 2013).

The Hokkaido, North Japan sample group originates from Hokkaido University, Sapporo, Japan (Howells, 1989). This group is made up of 55 modern males and 32 modern females from the dissecting room collection at the university. This group of individuals does not represent a specific regional population, because Japanese immigration to Hokkaido did not start until about the 1800s, a century before Dr. Howells collected craniometric data on these samples. Finally, the Philippines sample group is comprised of 50 males, who were inmates at the Manila prison that were not claimed for burial by next of kin. The crania of these individuals were consequently stored in the Anatomy Department at the medical school in Manila, and then measured by Dr. Howells. In addition to the Asian data from above nine groups, craniometric data of the Ainu group from the Howells database was also added. The purpose of this addition is to examine where the Ainu, which is an indigenous group in Japan, would fall in relation to the Hispanic and other Asian groups. The Ainu sample group consists of 48 males and 38

females who were chosen based on their lack of Japanese admixture in order to be studied as a separate population from the Japanese (Howells, 1989).

Hispanic Samples

The Hispanic samples utilized for craniometric analysis in this study originate exclusively from Mexico. Craniometric data of the Hispanic samples came from four different sources: 1) identified Operation Identification (OpID) individuals; 2) identified border crossers at the Pima County Office of the Medical Examiner (PCOME); 3) Xoclán cemetery collection from Mexico; and 4) Zimapan cemetery collection from Mexico. All craniometric data were provided by Dr. Spradley.

The OpID sample group is comprised of individuals who died while crossing the U.S.-Mexico border in Texas. Their remains were retained at the Osteology Research and Processing Laboratory (ORPL) at the Forensic Anthropology Center at Texas State (FACTS) as part of the OpID project. OpID is a project led by Dr. Spradley, in efforts to positively identify and repatriate the remains of presumed Hispanic migrants exhumed in Brooks County, Texas. In this thesis project, only craniometric data of positively identified OpID individuals were used. Although the positively identified OpID individuals came from various geographic origins in Central and South America, only individuals originating from Mexico were utilized. This is due to the fact that there are not enough identified samples from the OpID group that could be compared to the other populations at a significant level. Craniometric data of two identified OpID males and one female from Mexico were combined with the rest of the Mexico sample groups from other institutions.

The PCOME samples came from presumed Hispanic individuals who died during their attempt to cross the U.S.-Mexico border at the Pima County Office of the Medical Examiner (PCOME) in Tucson, Arizona. Similarly to OpID individuals, craniometric data of positively identified individuals were utilized. Of the identified individuals, data from 68 males and nine females from various regions of Mexico were utilized because the sample size for identified migrants from other geographic origins was too small. The Xoclán sample group consists of individuals from a documented cemetery collection in Mérida, Yucatán, Mexico (Chi-Keb et al., 2013). The remains of these individuals, whose birth years span from the early 19th century to 1980, are held at the Universidad Autónoma de Yucatán (UADY). Lastly, the Zimapan sample group includes individuals from a cemetery collection in Zimapan, Hidalgo, Mexico. These individuals were born around early to mid-20th century, and their remains are curated at the Universidad Nacional Autónoma de México (UNAM).

Table 1. Summary of reference samples

Asian			Hispanic		
	Male	Female		Male	Female
Southeast Asia			OpID (identified)		
Vietnam	51	0			
Thailand	50	0			
Philippines	50	0	PCOME (identified)		
North and East Asia					
Hong Kong	50	0			
Taiwan	47	0	UADY (Xoclan)		
Kanto	50	0			
Tohoku	53	0			
Kyushu	51	0	UNAM (Zimapan)		
North Japan	55	32			
Ainu	48	38			
Total Crania	505	70	Total Crania	83	31
	575			114	

Forensic Anthropology Data Bank Samples

In addition to the original three female and 11 male Asian and Hispanic groups (n=689), additional samples from the Forensic Anthropology Data Bank (FDB) were added to the sample pool. Additional samples include: 117 American White females, 23 American Black females, as well as 265 American White males, 53 American Black males, and 66 Guatemalan males. These samples originate from a variety of forensic cases in various regions across the United States. The purpose of this data addition is to investigate how well the Asian and Hispanic samples would classify when other ancestral groups are added to these two groups for analysis. Including all the possible ancestral groups in an analysis would be more representative of a forensic case. Using this pooled data (n=1213), a second statistical analysis was performed. This analysis serves to examine if there would be a difference in classification rates when other ancestral groups were added to the original Asian and Hispanic groups. This second analysis is necessary because including all the possible ancestral groups in an analysis would be more representative of a forensic case. Even if Asians and Hispanics can be distinguished from one another when only two groups are analyzed, it is important that they can still be distinguished if they are analyzed with other groups.

Data Collection

Craniometric Landmarks

This thesis utilizes a total of 27 cranial interlandmark distances (ILDs) (Table 2), some of which are not the standards distances used on FORDISC 3.1. However, they were chosen due to their overall representation of cranial morphology, as well as their presence in all the data sets provided by different recorders. Craniometric data of the Asian sample group were taken with traditional calipers, while those of the Hispanic sample group were taken using a Microscribe G2 3D digitizer in conjunction with the program 3Skull (Ousley, 2004). Despite the two different techniques used to collect craniometric data, the precision of measurements by a 3D digitizer is highly comparable to that by a traditional caliper (Hildebolt and Vannier, 1988). Therefore, traditional and digitized data were used interchangeably in this thesis.

Statistical Analyses

Discriminant Function Analysis

The craniometric measurements were analyzed using discriminant function analysis (DFA) on SAS 9.3 (SAS Institute Inc.). The purpose of DFA is to predict group membership by utilizing a set of data (Christensen et al., 2014). In this thesis, DFA was utilized to examine how each Asian or Hispanic group classifies. Males and females were analyzed separately. For each individual, a discriminant function score can be calculated, which can then be compared to the mean DFA score of each reference group. The group whose mean is closest to the unknown individual's discriminant function score is the group to which the individual is classified (Ousley, 2012; Ousley and Jantz, 2013). Not

only does DFA examine which groups these Asians and Hispanics will classify into, but it provides their classification rates as well. In addition, misclassification rates were also calculated, which pinpoints which particular groups are misclassifying as each other.

Table 2. Cranial measurements used for analysis and their abbreviations

	Measurement	Abbreviation
1	Maximum Cranial Length	GOL
2	Nasio-Occipital Length	NOL
3	Cranial Base Length	BNL
4	Basion-Bregma Height	BBH
5	Maximum Cranial Breadth	XCB
6	Maximum Frontal Breadth	XFB
7	Bistephanic Breadth	STB
8	Bizygomatic Breadth	ZYB
9	Biauricular Breadth	AUB
10	Biasterionic Breadth	ASB
11	Basion-Prosthion Length	BPL
12	Nasal Height	NLH
13	Nasal Breadth	NLB
14	Orbital Height	OBH
15	Orbital Breadth	OBB
16	Bijugal Breadth	JUB
17	Bimaxillary Breadth	ZMB
18	Bifrontal Breadth	FMB
19	Biorbital Breadth	EKB
20	Malar Length, Maximum	XML
21	Cheek Height, Minimum	WMH
22	Foramen Magnum Length	FOL
23	Frontal Chord	FRC
24	Parietal Chord	PAC
25	Occipital Chord	OCC
26	Zygomaxillary Subtense	SSS
27	Nasio-Frontal Subtense	NAS

Canonical Variates Analysis

Because there are more than two groups of samples in this thesis, more than one axis or dimension is involved in the process of determining group assignment for an individual of an unknown group membership. Each of the multiple dimensions involved in this process has a group mean score, called the centroid. Ultimately, group membership is determined based on the shortest distance of the individual score to the centroid. This type of analysis, which is known as the canonical variates analysis (CVA), was utilized in this thesis (Ousley, 2012). A canonical discriminant analysis was run on SAS 9.3 (SAS Institute Inc.) using the CANDISC procedure on the samples (n=689) after separating the males and females. The CANDISC procedure calculated between canonical structures and the proportions of their effect on variance. The purpose of this procedure is to examine which particular ILDs are weighing the canonical variates values, and ultimately assigning where groups would fall in relation to each other.

Mahalanobis Distance (D^2)

In addition to the canonical structures, the CANDISC procedure on SAS 9.3 (SAS Institute Inc.) also calculated Mahalanobis distances (D^2) between the sample groups. In this case, the D^2 value for each group indicates a measure of the multivariate distance between different population groups that have been converted from univariate differences (Ousley, 2012).

Comparison to FORDISC Analyses

Currently, FORDISC 3.1 is the most commonly used ancestry estimation program in the field of forensic anthropology. However, it includes only 17 cranial interlandmark distances (ILDs) out of 23 for the analysis of both Asian and Hispanic individuals. This is because the Asian samples do not have all of the standard ILDs included in FORDISC 3.1 due to the fact that data collectors utilized different protocols (Dudzik and Jantz, 2016). Not all the 27 ILDs utilized in this research are the standard ILDs used in FORDISC 3.1. However, these nonstandard ILDs could possibly help distinguish the Asian and Hispanic individuals better than the standard ones. Further, the sample size for Asian and Hispanic groups on FORDISC 3.1 is 386 individuals, compared to 588 individuals in the current research. Therefore, a discriminant function analysis was run on the reference samples in FORDISC 3.1. The purpose of this step is to examine how differently the Asian and Hispanic samples in FORDISC 3.1 would classify in comparison to the samples in the current research project.

Lastly, 20 male samples were chosen randomly out of the original 11 Asian and Hispanic groups (n=588) and run in FORDISC 3.1. Out of the 27 ILDs used in this thesis, 18 measurements could be entered on FORDISC 3.1. Further, because not all the standard ILDs are available for Asian groups, three measurements were eliminated for analysis: EKB, FOL, and ASB. Thus, the 15 measurements utilized for analysis of the 20 random samples in FORDISC 3.1 include: GOL, XCB, ZYB, BBH, BNL, BPL, AUB, ASB, ZMB, NLH, NLB, OBB, OBH, EKB, FRC, PAC, OCC, and FOL. The purpose of this step is to investigate how the samples from this thesis would classify when run with the Asian and Hispanic reference groups that are currently available to forensic

anthropologists. Further, this analysis also serves to examine if Asian and Hispanic samples from the current research are misclassifying in FORDISC 3.1, which groups are misclassifying as each other, and to what degree.

In FORDISC 3.1, the options for Asian and Hispanic groups are: Japanese, Vietnamese, Chinese, Hispanic, and Guatemalan. The samples utilized in this thesis are categorized into more specific geographic regions, such as Kanto, Kyushu, Tohoku, and North Japan. However, these groups correspond to the overall Japanese group in FORDISC. Likewise, the Hong Kong and Taiwan groups correspond to the FORDISC Chinese group, since individuals from these two groups are of Chinese descent. Thus, the classification rates in this analysis were based on the number of correct overall ancestry and are not based on specific geographic regions.

The analysis was run three times with different combinations of reference groups. First, all three Asian groups and both Hispanic and Guatemalan groups were utilized. Then, the Guatemalan group was taken out of the second time because it was not included in the initial analysis. Lastly, all five Asian and Hispanic groups as well as American Whites and Blacks were included in the third time in order to examine how well Asians and Hispanics would classify with the presence of other ancestral groups.

III. RESULTS

Asian and Mexican Groups Only

Classification Rates

The female sample size was significantly smaller than the male. Data for only three sample population groups (n=101) were available for analysis for females: Ainu, North Japan, and Mexico. For males, 11 sample population groups (n=588) were analyzed: Ainu, Hong Kong, Kanto (Japan), Kyushu (Japan), North Japan, Philippines, Taiwan, Thailand, Tohoku (Japan), Vietnam, and Mexico. Results from the canonical variate analysis MANOVA (stepwise Wilks' Lambda) indicate that there is a statistical significant difference between the sample groups for both females and males.

In order to address the initial problem addressed by Dudzik and Jantz (2016) that Hispanics are misclassifying as Asians, it is important to first examine the classification rates of the sample groups utilized. Further, to answer the research question of how Asians and Hispanics are misclassifying, correct classification rates must be established first. The correct classification rate for the three female groups is 96.0%. Out of 101 individuals, 97 classified correctly, and four misclassified (Table 3). Two individuals from the Ainu group misclassified as North Japan, while two individuals from North Japan misclassified as Ainu. All Mexican females were correctly classified. Further, the correct classification rate for the 11 male groups is 78.6%. Out of 588 individuals, 462 classified correctly, while 126 misclassified (Table 4). Unsurprisingly, most of the individuals that misclassified into another group mostly did as groups with which they cluster. For instance, the three Japanese groups that cluster together (Kanto, Kyushu, and

Tohoku) misclassified as each other for the most part. The Japanese also misclassified as other East Asian groups (Taiwan and Hong Kong), as well as the mainland Southeast Asians (Thailand and Vietnam), all of which clustered together on the lower end of CV1 values. Moreover, both North Japan and Ainu misclassified as each other, or as Philippines. Some misclassifications were observed between Philippines and Mexico. This is the only instance in which an Asian group misclassified as Hispanic, and vice versa. One individual in the Philippines group misclassified as Mexican, while three individuals in the Mexico group misclassified as Filipino. Further, two individuals from the Mexico group misclassified as North Japanese. However, none of the individuals from North Japan misclassified as Mexican.

Mahalanobis Squared Distances

For females, the largest Mahalanobis distance is 12.14 between Mexico and Ainu (Table 5). The larger the distance between two groups, the more dissimilar they are to each other. Out of the three sample groups assessed, Mexico is the farthest to the other two groups (Ainu and North Japan). The smallest squared distance is 10.36 between Ainu and North Japan. For males, the largest Mahalanobis distance is 85.50 between Taiwan and Ainu (Table 6). Ainu has the highest distances from the rest of the groups. The closest group to Ainu is North Japan. The smallest distance is 1.96 between Tohoku and Kyushu, both Japanese groups.

Table 3. Classification matrix for three female sample groups

From Population	Actual	Predicted			% Correct
		AINU	MEXICO	N JAPAN	
AINU	38	36	0	2	94.7%
MEXICO	31	0	31	0	100%
N JAPAN	32	2	0	30	93.8%

Class Means on Canonical Variates

Females (Asian and Mexican only)

In Figure 1, the first canonical variate (CV1) for females is expressed on the x-axis and contributes to 76% of the variation. Subsequently, the second canonical variate (CV2) for the same group is represented on the y-axis and contributes to 24% of the variation. The plotted class means for the three female groups show that there is a clear separation among all three groups, since none of the groups clustered together.

CV1 for females is most heavily loaded by 17 measurements: GOL, NOL, BNL, BBH, XFB, STB, ZYB, BPL, NLB, OBB, JUB, ZMB, EKB, WMH, FRC, PAC, and OCC. Further, CV2 is loaded highest by NLH, OBH, and XML (Table 7). Compared to Mexico and Ainu groups, North Japan females display features such as wider nasal breadths, taller cranial vaults, longer cranial base lengths, and taller cheek heights. Further, compared to North Japan and Ainu groups, Mexico females have smaller maximum malar lengths, nasal heights, and orbital heights.

Table 4. Classification matrix for 11 male sample groups

From Pop	Actual	Predicted											% Correct
		VIET	HK	KAN	KYU	TW	THAI	TOHO	NJ	PHIL	AINU	MEX	
VIET	51	40	2	1	2	0	6	0	0	0	0	0	78.4%
HK	50	2	41	0	1	3	3	0	0	0	0	0	82%
KAN	50	0	3	25	5	2	4	11	0	0	0	0	50%
KYU	51	0	4	5	29	4	2	7	0	0	0	0	56.9%
TW	47	3	0	0	1	38	2	3	0	0	0	0	80.9%
THAI	50	3	1	5	2	2	37	0	0	0	0	0	74%
TOHO	53	1	1	3	8	1	0	39	0	0	0	0	73.6%
NJ	55	0	0	0	0	0	0	0	47	5	3	0	85.5%
PHIL	50	0	0	0	0	0	0	0	3	45	1	1	90%
AINU	48	0	0	0	0	0	0	0	4	1	43	0	89.6%
MEX	83	0	0	0	0	0	0	0	2	3	0	78	94%

Squared Mahalanobis distance matrix among three female sample groups				
Squared Distance to Population				
From Population	AINU	MEXICO	NJAPAN	
AINU	0			
MEXICO	12.14354	0		
NJAPAN	4.89653	6.98331		0

Table 5. Squared Mahalanobis distance matrix among three female sample groups

Squared Mahalanobis distance matrix among 11 male groups											
Squared Distance to Population											
From Population	AINU	HONG KONG	KANTO	KYUSHU	MEXICO	NJAPAN	PHILLIPI	TAIWAN	THAI-LAND	TOHOKU	VIET
AINU	0										
HONGKONG	77.18266	0									
KANTO	64.29723	5.90448	0								
KYUSHU	73.81817	6.85542	2.46809	0							
MEXICO	28.53335	56.51502	48.94527	62.65396	0						
NJAPAN	7.63021	67.12882	54.94877	65.0313	18.46692	0					
PHILLIPI	11.75113	61.33729	53.84417	63.38847	15.20097	5.92161	0				
TAIWAN	85.49712	8.99023	8.18827	8.1477	65.22032	73.08556	64.31034	0			
THAILAND	73.61408	5.20336	5.03005	8.39246	48.4393	61.59755	53.53204	8.36632	0		
TOHOKU	67.7213	10.06543	3.09287	1.95901	56.30627	57.71872	58.39444	8.25293	10.963	0	
VIET	73.86625	9.14619	10.50824	12.78584	49.61146	61.63933	48.59183	9.03247	3.47042	15.60788	0

Table 6. Squared Mahalanobis distance matrix among 11 male groups

Males (Asian and Mexican only)

Similarly to the female groups, CV1 for the 11 male sample groups is represented on the x-axis in Figure 2 and accounts for 77% of the variation. CV2 is also expressed on the y-axis and contributes to 9.8% of the variation. For males, the plotted class means show some clustering of sample population groups. Seven out of 11 groups (Vietnam, Thailand, Hong Kong, Taiwan, Kanto, Kyushu, and Tohoku) clustered toward lower CV1 values, while the other four groups (Mexico, Philippines, North Japan, and Ainu) fall toward higher CV1 values. This type of clustering shows that CV1 divides the mainland Northeast and Southeast Asian groups (except for Kyushu) from island Northeast and Southeast Asian groups and Mexico. CV2 does not have a separation that is as distinct as that of CV1. However, all of the five Japanese groups (Kanto, Kyushu, Tohoku, North Japan, and Ainu) fall on the lower end of CV2, specifically in the negative values, while the rest of the groups fall on the positive side of the axis.

For males, CV1 is greatly loaded by ASB, NLB, JUB, EKB, and FOL, while CV2 is loaded highest by NLH and NAS (Table 8). Vietnam, Thailand, Taiwan, Hong Kong, Kanto, Kyushu, and Tohoku, which are on the lower end of CV1 in Figure 2, exhibit features such as narrower breadths across the left and right orbits (EKB), narrower nasal apertures (NLB), and shorter foramina magna (FOL). Compared to these seven groups, the three Asian island groups (Philippines, North Japan, and Ainu) and Mexico have higher values for the aforementioned measurements. Moreover, compared to the five Japanese groups, the other six groups display taller nasal heights and greater nasio-frontal subtenses. However, compared to CV1 and CV2 values for the measurements in females, those of males seem much lower. The highest CV value for males is 0.911841 for FOL,

whereas for females, there are multiple CV values that are at or around 0.99 (Tables 7 and 8).

Table 7. Between canonical structure values for three female sample groups

Variable	Can1	Can2
GOL	0.932161	-0.362045
NOL	0.938181	-0.346146
BNL	0.975131	-0.221627
BBH	0.997758	-0.066928
XCB	0.710894	-0.703299
XFB	0.815838	-0.578281
STB	0.876898	-0.480677
ZYB	0.864278	-0.503015
AUB	-0.339462	-0.94062
ASB	0.560687	-0.828028
BPL	0.807026	-0.590516
NLH	0.164544	0.98637
NLB	0.999982	0.00597
OBH	0.408306	0.912845
OBB	0.787537	-0.616268
JUB	0.913754	-0.406267
ZMB	0.849303	-0.527906
FMB	0.66277	-0.748823
EKB	0.951777	-0.306791
XML	-0.011081	0.999939
WMH	0.950721	0.310049
FOL	0.66068	0.750668
FRC	0.872503	-0.488609
PAC	0.924584	-0.380979
OCC	0.986916	0.161235
SSS	-0.998855	0.047841
NAS	-0.1371	-0.990557

Table 8. Between canonical structure values for 11 male samples groups

Variable	Can1	Can2
GOL	0.288189	-0.901202
NOL	0.252085	-0.90907
BNL	0.325863	-0.83585
BBH	-0.528769	-0.541479
XCB	0.510433	0.240007
XFB	-0.208816	-0.002698
STB	0.267329	0.180166
ZYB	0.473165	-0.737344
AUB	0.397371	0.040137
ASB	0.687894	-0.098159
BPL	0.551123	-0.560212
NLH	-0.269495	0.627788
NLB	0.6866	0.23598
OBH	0.457666	0.132264
OBB	-0.234297	-0.402947
JUB	0.798984	-0.458605
ZMB	-0.364217	-0.395148
FMB	-0.928714	-0.198924
EKB	0.864512	-0.27411
XML	0.525748	-0.35441
WMH	-0.599527	0.037788
FOL	0.911841	-0.166264
FRC	-0.34573	-0.255297
PAC	-0.021541	-0.735613
OCC	0.011124	-0.849781
SSS	0.383906	0.274039
NAS	0.37777	0.583636

Note: Measurements with highest loadings are bolded.

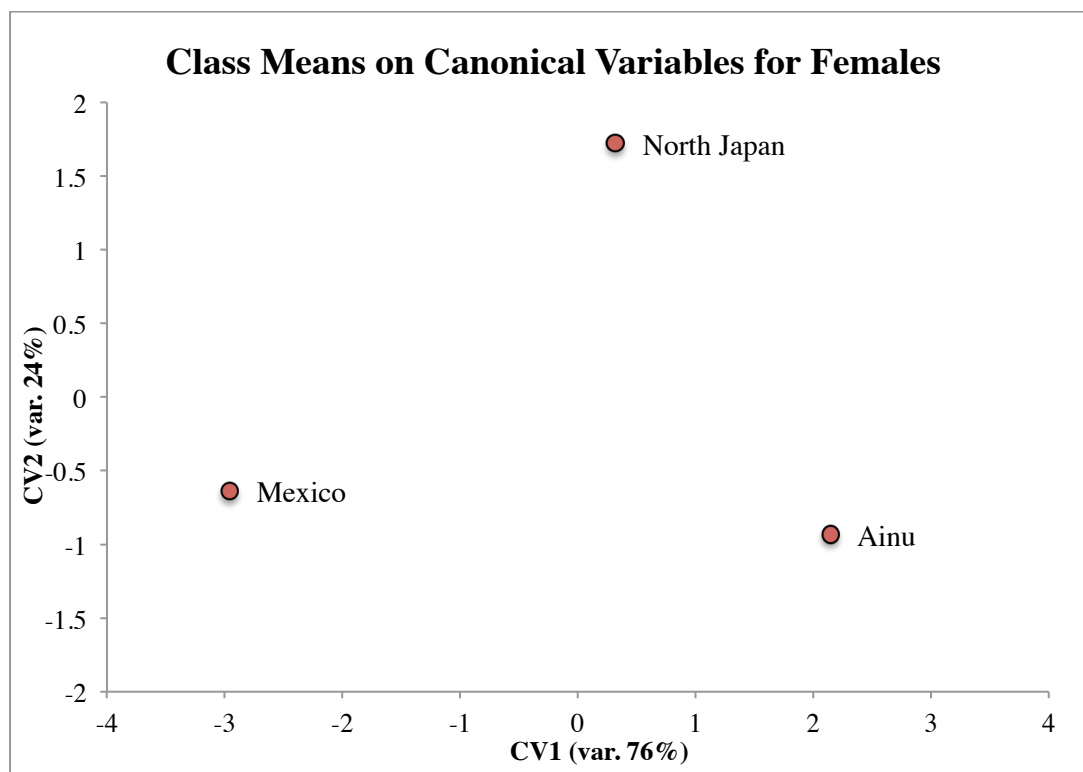


Figure 1. Plotted class means for three female sample groups

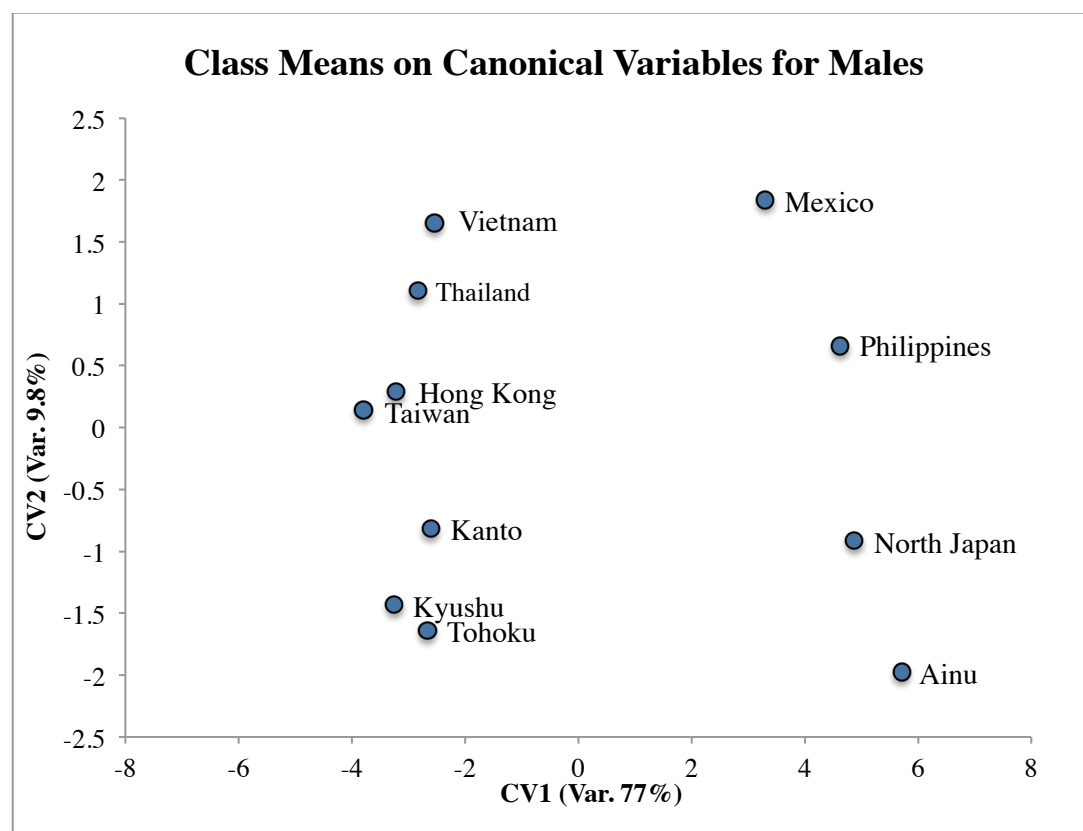


Figure 2. Plotted class means for 11 male sample groups

Asians and Mexicans with Other Groups

Classification Rates

Females (All groups)

A second analysis conducted after combining the original Asian and Mexican groups with American Blacks and Whites, and Guatemalans (for males). The correct classification rate for the five female groups (Ainu, North Japan, Mexico, American Black, and American White) based on the cross validation is 85.1%. Out of 241 individuals, 205 classified correctly, while 36 misclassified (Table 9). The two most common misclassifications were between North Japan and Ainu, and between American White and American Black. In this analysis, Mexican females misclassified as American Black, North Japan, and White females. Compared to the analysis run without American Black and White individuals (correct classification rate 96.0%), this analysis yielded lower correct classification rates.

Table 9. Cross-validated classification matrix for five female sample groups.
Classification rate for each group is bolded

From Population	AINU	BLACK	MEXICO	N JAPAN	WHITE	Total
AINU	31	0	1	6	0	38
	81.58	0	2.63	15.79	0	100
BLACK	0	17	2	2	2	23
	0	73.91	8.7	8.7	8.7	100
MEXICO	0	3	25	2	1	31
	0	9.68	80.65	6.45	3.23	100
NJAPAN	4	1	2	25	0	32
	12.5	3.13	6.25	78.13	0	100
WHITE	1	6	3	0	107	117
	0.85	5.13	2.56	0	91.45	100
Total	36	27	33	35	110	241
	14.94	11.2	13.69	14.52	45.64	100

Table 10. Cross-validated classification matrix for 14 male sample groups. Classification rate for each group is bolded

From Pop	AINU	BLACK	GUAT	HK	KAN	KYU	MEX	NJ	PHIL	TW	THAI	TOHO	VIET	WHITE	Total
AINU	40	3	1	0	0	0	0	4	0	0	0	0	0	0	48
	83.33	6.25	2.08	0	0	0	0	8.33	0	0	0	0	0	0	100
BLACK	0	40	2	0	0	0	6	0	1	0	0	0	0	4	53
	0	75.47	3.77	0	0	0	11.32	0	1.89	0	0	0	0	7.55	100
GUAT	0	0	51	0	0	0	8	1	6	0	0	0	0	0	66
	0	0	77.27	0	0	0	12.12	1.52	9.09	0	0	0	0	0	100
HK	0	0	0	34	3	1	0	0	0	4	6	0	2	0	50
	0	0	0	68	6	2	0	0	0	8	12	0	4	0	100
KAN	0	0	0	3	16	11	0	0	0	2	6	11	1	0	50
	0	0	0	6	32	22	0	0	0	4	12	22	2	0	100
KYU	0	0	0	6	11	17	0	0	0	3	1	13	0	0	51
	0	0	0	11.76	21.57	33.33	0	0	0	5.88	1.96	25.49	0	0	100
MEX	0	3	18	0	0	0	53	1	3	0	0	0	0	5	83
	0	3.61	21.69	0	0	0	63.86	1.2	3.61	0	0	0	0	6.02	100
NJ	4	1	1	0	0	0	0	43	6	0	0	0	0	0	55
	7.27	1.82	1.82	0	0	0	0	78.18	10.91	0	0	0	0	0	100
PHIL	1	0	3	0	0	0	1	5	40	0	0	0	0	0	50
	2	0	6	0	0	0	2	10	80	0	0	0	0	0	100
TW	0	0	0	1	2	2	0	0	0	31	3	4	4	0	47
	0	0	0	2.13	4.26	4.26	0	0	0	65.96	6.38	8.51	8.51	0	100
THAI	0	0	0	4	6	2	0	0	0	3	26	0	9	0	50
	0	0	0	8	12	4	0	0	0	6	52	0	18	0	100
TOHO	0	0	0	2	5	12	0	0	0	2	0	31	1	0	53
	0	0	0	3.77	9.43	22.64	0	0	0	3.77	0	58.49	1.89	0	100
VIET	0	0	0	3	1	2	0	0	0	0	11	0	34	0	51
	0	0	0	5.88	1.96	3.92	0	0	0	0	21.57	0	66.67	0	100
WHITE	0	9	2	0	0	0	9	1	1	0	0	0	0	243	265
	0	3.4	0.75	0	0	0	3.4	0.38	0.38	0	0	0	0	91.7	100
Total	45	56	78	53	44	47	77	55	57	45	53	59	51	252	972
	4.63	5.76	8.02	5.45	4.53	4.84	7.92	5.66	5.86	4.63	5.45	6.07	5.25	25.93	100

Males (All groups)

Further, the correct classification rate for the 11 male groups is 71.9%. Out of 972 individuals, 699 classified correctly, while 273 misclassified (Table 10). Compared to the analysis run without American Black and White individuals (correct classification rate 78.6%), this analysis yielded lower correct classification rates. However, this correct classification rate is still much higher than random chance. Further, similar to the misclassifications in the first analysis, misclassifications in this analysis were observed mostly among groups that have geographic proximity. For instance, the three Japanese groups that clustered together (Kanto, Kyushu, and Tohoku) also misclassified as each other. However, there were higher misclassifications between East and Southeast Asian groups compared to results from the first analysis. Additionally, Guatemalan males and Mexican males mostly misclassified as each other. However, both groups misclassified as Filipino males as well, similar to the misclassifications between Mexican and Filipino males in the first analysis. Overall, the classification patterns from the second analysis were similar to those from the first analysis.

Table 11. Mahalanobis squared distance matrix among five female sample groups

Squared Distance to Population					
From Population	AINU	BLACK	MEXICO	NJAPAN	WHITE
AINU	0				
BLACK	9.33741	0			
MEXICO	9.72785	5.12788	0		
NJAPAN	4.53147	6.97898	5.26222	0	
WHITE	29.13595	8.46518	15.7537	20.03162	0

Table 12. Mahalanobis squared distance matrix among 14 male sample groups

Squared Distance to Population														
From Pop.	AINU	BLACK	GUAT	HK	KAN	KYU	MEX	NJ	PHIL	TW	THAI	TOHO	VIET	WHITE
AINU	0													
BLACK	19,395	0												
GUAT	24,090	13,476	0											
HK	81,755	58,777	66,969	0										
KAN	66,799	48,794	56,901	5,7487	0									
KYU	78,485	61,736	69,272	6,6781	2,6407	0								
MEX	28,953	12,457	7,4113	60,279	50,275	66,522	0							
NJ	7,6400	14,786	13,803	70,259	55,657	67,949	17,714	0						
PHIL	12,240	14,440	9,7519	61,397	52,139	63,334	13,403	5,7289	0					
TW	91,224	70,667	72,735	8,2474	8,1787	7,7717	69,024	76,309	65,185	0				
THAI	78,113	55,557	60,128	4,5225	4,4784	7,3397	52,001	64,137	54,046	7,3733	0			
TOH	71,129	56,374	60,614	9,5077	2,9742	1,9695	57,833	59,228	57,018	8,1271	9,5297	0		
VIET	80,658	57,451	58,198	8,4291	10,033	11,950	54,495	65,947	50,979	8,1616	3,3420	14,319	0	
WHITE	43,283	14,162	37,738	98,750	77,228	100,29	27,566	35,102	39,175	111,94	89,083	91,638	97,630	0

Mahalanobis Squared Distance

For females, the largest Mahalanobis squared distance is 29.14 between Ainu and White (Table 11). The larger the distance between two groups, the more dissimilar they are to each other. Out of the five sample groups assessed, North Japan and Ainu are most similar to each other with the smallest squared distance, 4.53. The Mahalanobis distances also showed that Mexican females similar to North Japanese (squared distance = 5.26) and American Black (squared distance = 5.13) females. For males, the largest squared Mahalanobis distance is 111.94 between Taiwan and American White (Table 12). The smallest distance is 1.97 between Kanto and Tohoku, both of which are Japanese groups.

Class Means on Canonical Variates

Females (All groups)

Figure 3 shows that CV1 for the five female groups is expressed on the x-axis and contributes to 70% of the variation. Subsequently, CV2 for the same group is represented on the y-axis and contributes to 15% of the variation. The plotted class means for the five female groups indicate clear separations among all five groups, since none of the groups clustered together. CV1 for females is most heavily loaded by SSS, NAS, ASB, FOL, and PAC, while CV2 is loaded highest by nine measurements: GOL, NOL, BNL, BBH, XCB, XFB, STB, OBB, and OCC (Table 13). The ILDs that weigh the CV values influence how the different groups compare and relate to each other in terms of cranial morphology. Groups with high CV1 and CV2 values such as American White females generally have larger facial and cranial vault features than the rest of the groups. American Black females have exhibit CV1 values, but lower CV2 values. This indicates

that American Black females have broader faces as characterized by wider nasio-frontal subtenses (NAS) and bimaxillary subtenses (SSS), as well as broader cranial vaults at the base, at the asterion level. In contrast, Ainu, North Japanese and Mexican females exhibit lower CV1 values, indicating that they have narrower faces and cranial bases compared to American White and Black females.

Males (All groups)

CV1 for the 14 male sample groups is also represented on the x-axis in Figure 4 and accounts for 71% of the variation. CV2 is also expressed on the y-axis and contributes to 14% of the variation. For males, the plotted class means show clear clustering patterns of sample groups. Similar to results from the first analysis, seven out of 14 groups (Vietnam, Thailand, Hong Kong, Taiwan, Kanto, Kyushu, and Tohoku) clustered toward lower CV1 values, while the other seven groups (Mexico, Philippines, North Japan, Ainu, American Black, and American White) fall toward higher CV1 values.

For males, CV1 is greatly loaded by FOL, EKB, ASB, SSS, and NAS, while CV2 is loaded highest by FRC, BBH, SSS, and NAS (Table 14). Vietnam, Thailand, Taiwan, Hong Kong, Kanto, Kyushu, and Tohoku, which are on the lower end of CV1 in Figure 4 exhibit features as shorter foramen magnum lengths (FOL) and narrower faces characterized by the biorbital breadth (EKB). Further, compared to the results from the first analysis, these seven groups clustered even closer together with the addition of Guatemalan, American Black, and American White males. Compared to the remaining 13 groups, American White males display features that have the largest values for both CV1

and CV2, indicating that American Whites likely have greater values for the measurements that most heavily load the canonical variates.

Table 13. Between canonical structure values for five female sample groups

Variable	Can1	Can2
GOL	0.287743	0.752523
NOL	0.227593	0.765862
BNL	0.339274	0.839119
BBH	0.639895	0.730475
XCB	0.148368	0.772993
XFB	0.382254	0.817407
STB	0.382617	0.765558
ZYB	-0.939895	0.255056
AUB	-0.470175	-0.147442
ASB	0.887349	0.383556
BPL	-0.677451	0.134338
NLH	0.135405	0.148296
NLB	-0.963281	0.123757
OBH	-0.775933	-0.304114
OBB	0.183832	0.762505
JUB	-0.922614	0.313364
ZMB	-0.993895	-0.046809
FMB	0.064774	0.387733
EKB	-0.667063	0.543326
XML	0.603901	-0.124792
WMH	-0.851607	0.39279
FOL	0.814725	0.366882
FRC	0.597363	0.656377
PAC	0.695367	0.587999
OCC	0.245048	0.850305
SSS	0.934853	-0.311744
NAS	0.889011	0.06497

Table 14. Between canonical structure values for 14 male sample groups

Variable	Can1	Can2
GOL	0.439728	0.458767
NOL	0.41148	0.439811
BNL	0.522185	0.542347
BBH	-0.011675	0.707033
XCB	0.179033	0.06136
XFB	-0.153006	0.459409
STB	0.367328	0.421252
ZYB	-0.133883	-0.682087
AUB	0.012443	-0.166793
ASB	0.759243	0.573866
BPL	0.311735	-0.399981
NLH	-0.026143	0.515095
NLB	0.228369	-0.757272
OBH	0.541718	-0.056233
OBB	0.0971	0.634269
JUB	0.252181	-0.833505
ZMB	-0.627837	-0.735493
FMB	-0.901706	0.117114
EKB	0.779776	-0.160335
XML	0.535158	0.464072
WMH	-0.770369	-0.475745
FOL	0.90274	0.315581
FRC	0.147229	0.709814
PAC	0.403326	0.556601
OCC	0.257286	0.513524
SSS	0.668668	0.660791
NAS	0.644663	0.699852

Note: Measurements with highest loadings are bolded.

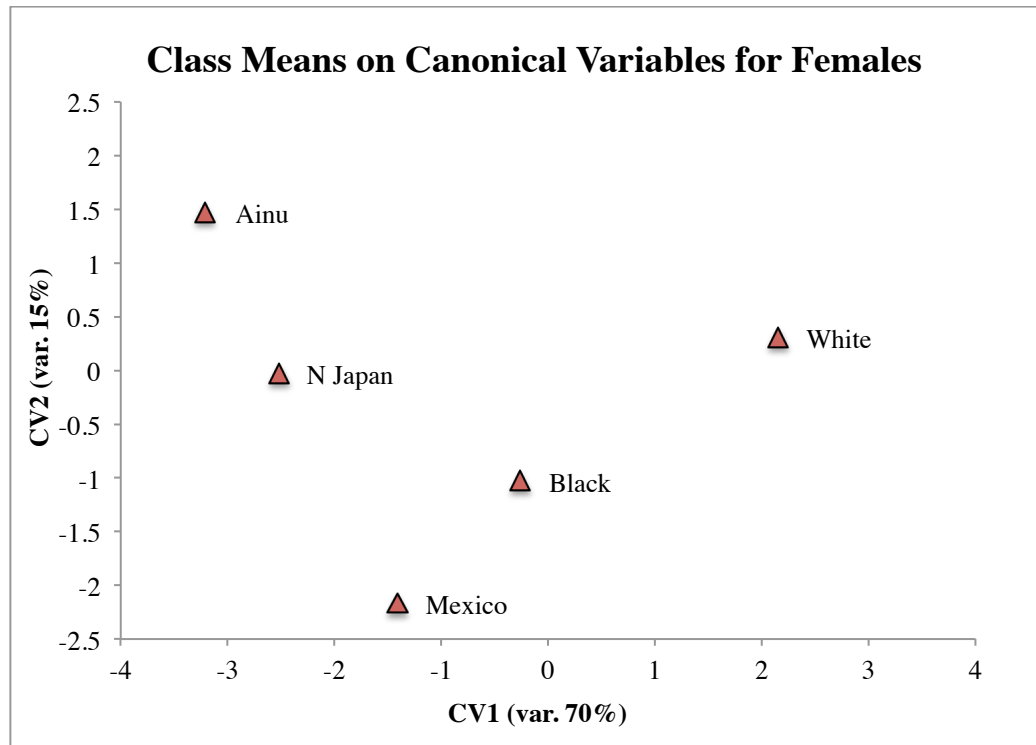


Figure 3. Plotted class means for five female sample groups

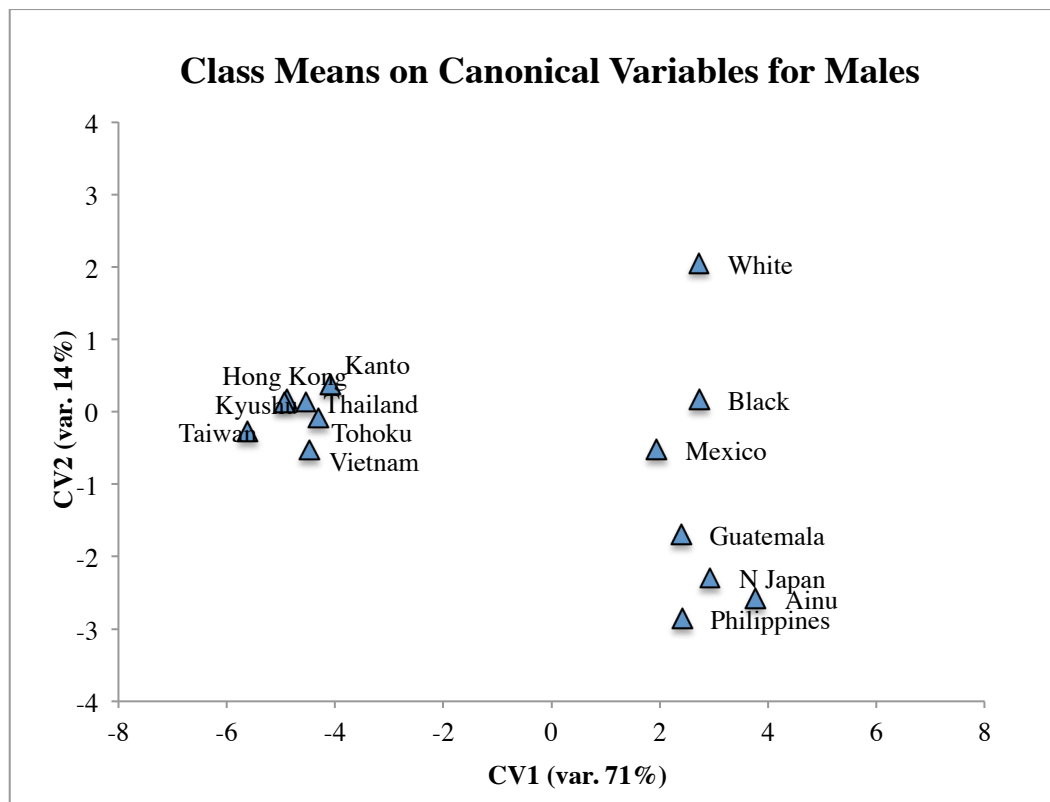


Figure 4. Plotted class means for 14 male sample groups

Analysis of Initial Asian and Mexican Samples in FORDISC

A sample of 20 male individuals from the Asian and Mexican groups from the first analysis was chosen at random and analyzed in FORDISC 3.1 using 15 measurements. The purpose of this analysis is to test whether the Asian and Hispanic samples utilized in this thesis research would also misclassify in FORDISC 3.1 as reported in Dudzik and Jantz (2016). According to the results of FORDISC analyses of 20 male individuals, the correct classification rate is 35%. Seven out of 20 Asian and Hispanic males from the current thesis sample pool classified correctly into their corresponding ancestral groups.

Eight Asian groups misclassified as another Asian group. Further, one Mexican individual misclassified as Guatemalan when the Guatemalan reference group was utilized. However, when it was reanalyzed without the Guatemalan group, the same individual classified as Hispanic. There were three cases of misclassifications between Asians and Hispanics. First, a Taiwanese individual and a Kanto (South Japanese) individual misclassified as Hispanic. In addition, one Mexican individual misclassified as Japanese.

IV. DISCUSSION

Analysis of Asian and Mexican Groups Only

The first research question in this thesis addresses if modern Asian and Hispanic individuals can be differentiated from each other on a statistically significant level using cranial morphology. According to the results, modern Hispanic individuals who were represented only by individuals from Mexico in this study can be differentiated from modern Asian individuals.

The second research question examines how cranial morphologies of modern Asian and Hispanic individuals are different from each other, if they are significantly distinct. When the sample is separated by sex, a difference in the clustering pattern was observed between Hispanic females and males in relation to the Ainu and North Japan groups. Moreover, only individuals from Mexico are utilized for the first analysis in this study. However, because individuals from Mexico alone cannot represent the Hispanic demography, it is crucial to add data from a larger sample of positively identified Hispanic individuals from a diverse array of geographic origins.

Further, according to the Mahalanobis squared distances, the Ainu and North Japan groups are most similar to each other in both males and females. This can be explained by the proximity in geography between the Ainu and North Japan individuals. Modern Japanese are a hybrid population with a mix of indigenous Jomon people and Yayoi migrants from Northeast Asia, and admixture between these groups still occurs today (Hanihara, 1991; Nakagome et al., 2015; Dudzik and Jantz, 2016). In this analysis, both male and female North Japan groups exhibit morphological similarity to the Ainu

group, despite the Ainu samples' antiquity, which could contribute to secular change. This could be explained by the fact that Ainu people inhabited Hokkaido, which is located in North Japan. In this case, morphological similarity follows geographic proximity. This pattern is consistent with the Isolation by Distance (IBD) model, which suggests that the likelihood of individuals sharing genes decreases as geographic distance increases. Thus, the cranial morphologies of two population groups that are geographically distant will be less similar to each other (Relethford 2004b, 2009).

Further, three out of the five Japanese groups (Kanto, Kyushu, Tohoku) cluster closely together most likely based on the distribution of Yayoi migrants around these areas. The Yayoi came through South Japan through the Korean Peninsula and possibly made their way to Kanto and Tohoku regions. Further, the Jomon are the indigenous group in Japan, who are related to the Ainu, who primarily inhabited Hokkaido in North Japan (Hanihara, 2009; Ishida, 2009; Nakagome et al., 2015; Dudzik and Jantz, 2016). This explains the morphological similarity between Ainu and North Japan, as well as the dissimilarity between the North Japan (Ainu and North Japan) and South Japan (Kanto, Kyushu, and Tohoku) groups.

In addition, other trends observed in the male samples' class means distribution follow a geographic pattern as well. For instance, the two mainland Southeast Asian groups (Vietnam and Thailand) cluster together, most likely due to their geographical proximity, following the IBD model (Figure 5). Moreover, the two East Asian island groups (Hong Kong and Taiwan) cluster together, indicating morphological similarity. It is important to note, however, that although Taiwan and Hong Kong are islands, the

majority of its inhabitants are of Han Chinese descent (Executive Yuan). This explains the similarity in cranial morphology between Taiwan and Hong Kong sample groups.

Moreover, results showed that the Mexico group clustered with three other Asian groups: Philippines, North Japan, and Ainu on the higher end of CV1 values. Although Mexico alone does not represent the entire Hispanic demographic, it is worthwhile to discuss its similarity in morphology to some Asian groups through the population history of Mexico. Hispanics are in fact a highly admixed group that is comprised of genetic components from various ancestry groups, including Native American, European, and African. Among various Hispanic groups, Mexico is one of the groups with the highest Native American genetic components (Bryc et al., 2010). Further, Native Americans have ancestors that dispersed to the New World from Asia thousands of years ago (Hubbe et al., 2010; de Azevedo et al., 2011; Reich et al. 2012). Thus, Hispanic groups with high indigenous genetic components, such as Mexicans, are most likely genetically linked to Asians. This connection could then explain the morphological similarities between Mexicans and some Asian groups. In the first analysis of this thesis, the Hispanic group examined is represented solely by individuals from Mexico. Thus, some misclassifications between individuals from the Mexico group and some Asian groups, such as Philippines and North Japan, were observed. These three groups, in addition to the Ainu group, exhibit features such as wider faces and nasal apertures.

It is interesting to note that individuals from the Mexico group most commonly misclassified as belonging to the Philippines group (3.6%), followed by North Japan (2.4%). Dudzik and Jantz (2016) noted that Hispanics from the Southwest and Mexico usually misclassify as Japanese. This is consistent with the findings of this research, but

Dudzik and Jantz (2016) did not include Philippines among the examined groups. A possible explanation for this similarity is the Spanish colonization of both the Philippines and Mexico. Thus, it would be worthwhile to further explore any morphological similarities between Filipino and Mexican individuals.

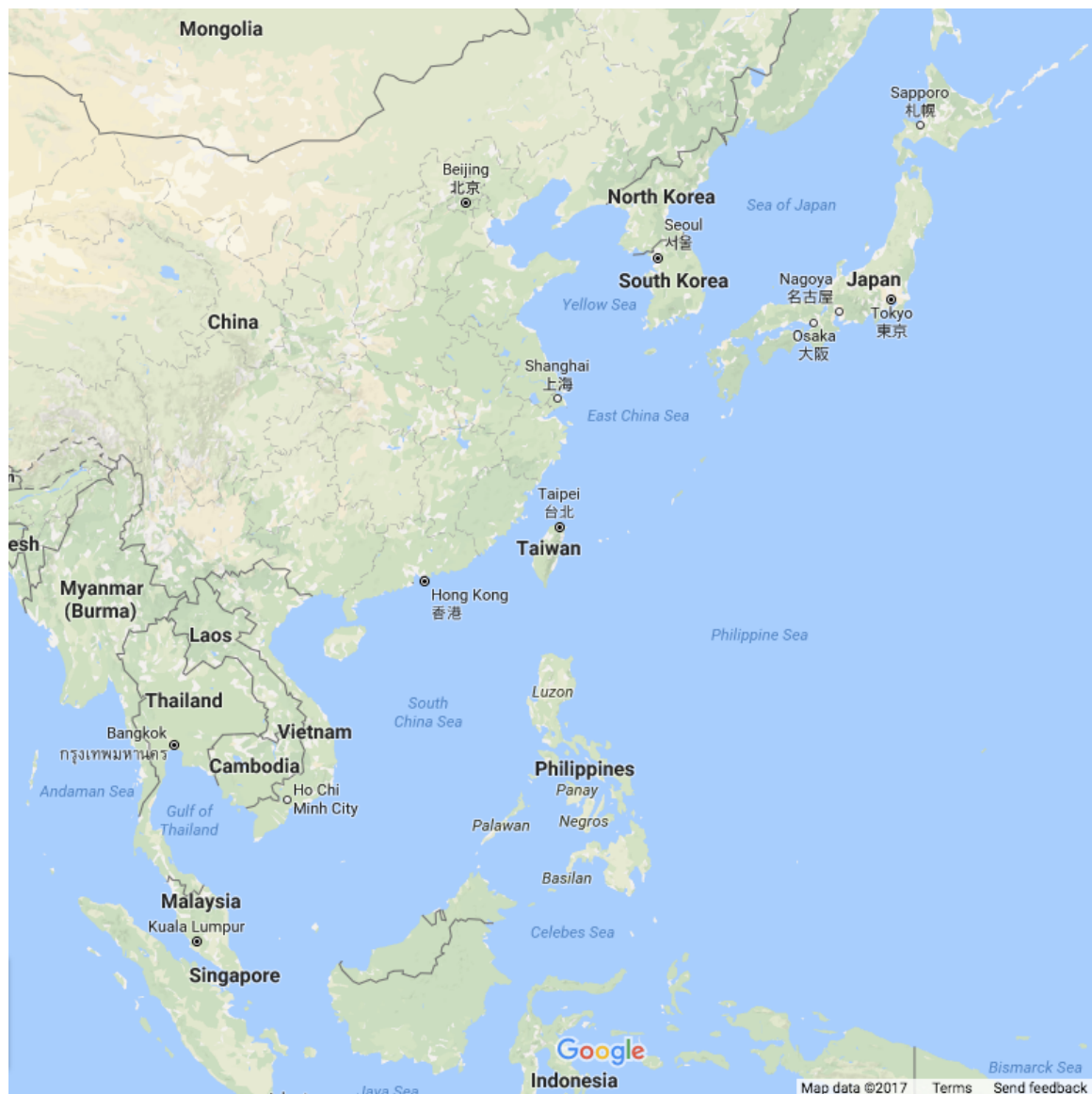


Figure 5. Map depicting the geographic origins of the Asian sample groups

Analysis of Asians and Mexicans with Other Groups

A second analysis performed with additional groups (American Black and White) to the original three female groups (Ainu, North Japan, and Mexico) yielded five separate groups. Generally, Mexican females clustered more closely to North Japan and Ainu groups on the lower first canonical variates (CV1) values when American Black and White individuals were added (Figure 3). Misclassifications between Mexican and North Japanese females were observed in this second analysis, which was not observed in the first. This indicates that adding American Black and White individuals to the female sample pool lowered the correct classification rate for Mexicans.

Moreover, when the three new groups (American Black, American White, and Guatemalan) were added to the original 11 male sample groups, the seven Asian groups on the lower end of the CV1 axis (Vietnam, Thailand, Taiwan, Hong Kong, Kanto, Kyushu, and Tohoku) grouped even closer together (Figure 4). Additionally, the correct classification rates for these seven groups decreased as well. Moreover, the Asian male group that both Mexican and Guatemalan males most misclassify as is Philippines.

As shown in the results, major dissimilarities in cranial morphology exist between some individuals from the same country but different regions. For instance, both analyses for males (with or without American Blacks, Whites, and Guatemalans) indicate that the two North Japan groups (Ainu and North Japan) are clearly distinguishable from the three South Japan groups (Kanto, Kyushu, and Tohoku) based on their cranial morphology. North Japan males generally exhibit wider faces compared to South Japan males. In both analyses, the cranial morphology of North and South Japanese individuals follows the IBD model.

Compared to Dudzik and Jantz (2016)'s results, results from this research had higher classification rates for Hispanics (Mexican and Guatemalan males), even with American White and Black individuals added in the analysis. Further, results from current research showed that Hispanics are more similar to American Blacks and Whites than they are to most Asian groups, except for Ainu, North Japan, and Philippines. These results contradict the findings of Dudzik and Jantz (2016), which stated that Hispanics are more similar to all Asian groups that they used, except for Ainu. This may be attributed by the difference in the amount and types of interlandmark distances (ILDs) used by Dudzik and Jantz (2016) and the current research. Dudzik and Jantz (2016) utilized 21 ILDs, compared to the 27 ILDs used in this research. The ILDs utilized in Dudzik and Jantz (2016) are more consistent with the standard ILDs in FORDISC 3.1. In contrast, only 18 out of 27 ILDs in this thesis research are listed in the standard FORDISC measurements. The remaining nine nonstandard ILDs include subtenses, as well as measurements that encompass the morphology of the cheek area, such as minimum cheek height (WMH), maximum malar length (XML), and bimaxillary breadth (ZMB). This is consistent with the findings of Spradley and Jantz (2016) that nonstandard ILDs yield more accurate ancestry estimations than the standard ones.

Further, the difference in results could also be attributed by the fact that Dudzik and Jantz (2016) pooled their Hispanic samples of various origins into one Hispanic group, whereas this thesis grouped Mexicans and Guatemalans separately. Dudzik and Jantz (2016)'s Hispanic sample group consisted mostly of Mexican individuals, but also had individuals from Guatemala, El Salvador, Nicaragua, and Panama pooled into the

group. Thus, for future research, it would be interesting to obtain more data from the non-Mexican Hispanic groups and analyze them separately from the Mexicans.

With increasing immigrant populations in the United States, individuals belonging to groups such as Asians and Hispanics should be accounted for when dealing with forensic cases that involve unidentified persons. More importantly, it would only be accurate to refer to an individual specifically based on their geographic origin, rather than using umbrella terms such as “Asian” and “Hispanic.” A great amount of diversity exists within and between Asian groups, or Hispanic groups, due to the various genetic makeups of individuals inhabiting a vast array of geographic origins. These diverse genetic structures are attributed by unique population histories behind these differing population groups. The genetic portion is one part of cranial morphology; the other part is environmental conditions. A combination of genetic and environment factors contribute to the overall cranial morphology of these individuals.

One confounding factor that can affect cranial morphology is the socioeconomic status (SES) of an individual. Cranial morphology of individuals with lower SES may be influenced by environmental factors that are related to inadequate nutrition and healthcare, which can lead to developmental stress. For instance, Mexican samples from the Pima County Office of the Medical Examiner (PCOME) utilized in this research exhibit some evidence of developmental stress (Birkby et al., 2008; Beatrice and Soler, 2016). Further, Filipino male samples utilized in this research were inmates that were not claimed by their next of kin (Howells, 1989). Although this is not a direct indicator of low SES, it is likely that these individuals were not of high SES, since they did not have a proper burial by their families. Thus, the SES of groups such as the PCOME border

crossers or Filipino inmates may have somehow influenced the cranial morphology of these individuals.

Analysis of Initial Asian and Mexican Samples in FORDISC

When a sample of 20 Asian and Mexican males from the initial 11 male groups was chosen at random and entered in FORDISC 3.1 using 15 ILDs, results showed that the correct classification rate was 35%. This indicates that the misclassification rate is higher than the correct classification rate. In the first analysis using Japanese, Vietnamese, Chinese, Hispanic, and Guatemalan, most of the misclassifications occurred between different Asian groups. However, there were some instances of misclassifications between Asians and Hispanics. In particular, two Asian males (Taiwan and Kanto) misclassified as Hispanic, while one Mexican male misclassified as Japanese. Further, there was no classification assigned when an analysis using 15 ILDs was performed on an Ainu individual. This result is consistent with what is expected when an individual from an older time period, such as Ainu, is compared against modern reference groups. Overall, the correct classification rate is low, possibly due to the low number of variables or ILDs and sample sizes available for Asian groups on FORDISC 3.1.

Future Research

As the Asian and Hispanic population sizes increase in the United States, forensic anthropologists should work toward collecting data on larger sample sizes of reference groups in order to include the morphological variation within each group. Further, collecting more data on Asian and Hispanic populations will help increase sample sizes,

and thus better represent the diversity in morphology that each ancestral group embodies. Currently, there are not as many craniometric measurements on Asian and Hispanic groups as American Whites and Blacks. For instance on the FORDISC program, only 17 cranial interlandmark distances (ILDs) out of 23 are available for analysis when both Asian and Hispanic reference groups are included to compare measurements with an unknown individual (Table 15). However, when running FORDISC, it is important to have as many ILDs as possible, because the more variables utilized, the better the accuracy of classification will be (Ousley et al., 2009). Nonetheless, caution must be used when using many variables, since complexity can lead to overfitting.

Further, current records also show that there are significantly smaller Asian and Hispanic samples in skeletal collections, compared to American Black and White sample sizes (Shirley et al. 2011; Spradley, 2013; White et al., 2012). In addition, even lower numbers of Asian American individuals are observed in skeletal collections across the United States (Weiss, 2015). This may be due to certain cultural prescriptions that could prevent Asians in the United States from donating their bodies to science, or decomposition facilities. Moreover, it may also be that there is a lack of knowledge or access to skeletal donation facilities in the Asian American community. Thus, future efforts to increase awareness about skeletal donation facilities should be emphasized in order to create more inclusive skeletal reference samples that represent Asian Americans. Further, an alternative way to include skeletal data from Asian Americans is to collect computerized tomography (CT) data on living patients from hospitals after going through an Institutional Review Board (IRB) process. Through these methods, the sample sizes of these reference groups could be improved.

Table 15. Measurements currently utilized for Asian and Hispanic groups on FORDISC 3.1.

	Measurement	Abbreviation
1	Biauricular Breadth	AUB
2	Basion-Bregma Height	BBH
3	Cranial Base Length	BNL
4	Basion-Prosthion Length	BPL
5	Frontal Chord	FRC
6	Maximum Cranial Length	GOL
7	External Palate Breadth	MAB
8	Nasal Height	NLH
9	Nasal Breadth	NLB
10	Orbital Height	OBH
11	Orbital Breadth	OBB
12	Occipital Chord	OCC
13	Parietal Chord	PAC
14	Upper Facial Height	UFHT
15	Minimum Frontal Breadth	WFB
16	Maximum Cranial Breadth	XCB
17	Bizygomatic Breadth	ZYB

V. CONCLUSION

As the Asian and Hispanic population sizes grow steadily in the United States, the need for suitable reference samples and data banks arises. Especially in urban areas in which immigrant populations continue to grow, the chances of forensic cases involving individuals from these demographics increase as well. In such cases, it would be difficult to compare the data collected on an unknown Asian or Hispanic individual if their reference groups were not represented by a diverse array of individuals within the groups. Currently, not only are there not enough craniometric measurements collected on Asian and Hispanic individuals, but their sample sizes are also very small compared to those of American Whites and Blacks. This eventually leads to problems such as Hispanic individuals being misclassified as Asian, or vice versa, on ancestry estimation programs such as FORDISC 3.1.

Currently, FORDISC 3.1 only includes 17 out of 23 total cranial interlandmark distances for Asian and Hispanic reference groups. Further, the classification rate when Asian and Hispanic male groups on FORDISC 3.1 (Chinese, Japanese, Vietnamese, and Hispanic) are run together with 17 measurements is 59.3% (251 correct out of 386). In comparison, the classification rate for Asian and Hispanic (various Chinese and Japanese groups, Vietnamese, Thai, Filipino, and Mexican) males in this thesis research run with 27 measurements is 78.6% (462 correct out of 588 for 11 male groups). The classification rate for female groups (Japanese and Hispanic) on FORDISC is 94.2% (98 correct out of 104), while the classification rate for female samples (North Japanese, Ainu, and Mexican) in the first analysis of this thesis is 96.0% (97 out of 101 for three female

groups). However, because the female sample sizes are small and do not have as many different groups as males, the classification rate may be higher than expected.

Overall, compared to the data currently available for Asian and Hispanic individuals in FORDISC, data and results from the current research exhibits promising classification rates. Thus, adding larger sample sizes and more ILDs to existing data sets for Asians and Hispanics on ancestry estimation programs such as FORDISC 3.1 (Jantz and Ousley, 2005) would greatly benefit the field of forensic anthropology. This will not only help improve the accuracy of ancestry classifications, but also will help build more accurate biological profiles. Ultimately, this will lead to higher rates of positive identifications for forensic cases involving unidentified human remains.

Further, when dealing with unidentified individuals of Asian or Hispanic descent, it is important to recognize the population histories behind these ancestral groups. Dudzik and Jantz (2016) identified a problem within forensic anthropology: Hispanics misclassifying as Asians, particularly Japanese in FORDISC. However, it is impossible to understand this problem without understanding the population histories behind Asians and Hispanics and how they may be connected. Currently, it is widely accepted that the first groups of individuals that populated the New World migrated from East Asia through Beringia (Hubbe et al., 2010). In addition, there is also evidence that some Hispanic groups, such as Mexicans, are admixed populations with high Native American components. During the pre-Columbian times, Mexico had large populations of Native Americans. After the Europeans' arrival, admixture occurred between Native Americans and Europeans (Bryc et al., 2010). Although the admixture led to changes in cranial morphology in later generations, Mexicans still retained indigenous components. Thus,

similarities in cranial morphology between modern Mexicans and some Asians were observed.

This study examines whether cranial morphologies of Asian and Hispanic individuals can be distinguished or not, and if they are distinctive, how are the morphologies different? The results indeed showed that the cranial morphology of these two groups are distinguishable. Hispanics represented by individuals originating from Mexico generally exhibit wider faces and nasal apertures compared to most East and Southeast Asians. Some Asian groups such as North Japan, Ainu, and Philippines also exhibit similar features to the Mexico group. However, the Mexico group also displays taller nasal apertures compared to North Japan, Ainu and Philippines. Overall, Mexicans exhibit wider faces and larger nasal apertures than Asians. Differences in these cranial features help distinguish Asians and Hispanics from one another. Quantifying the influence that different cranial ILDs have on ancestral group assignment helps understand which facial and cranial features are important to differentiate Asians from Hispanics.

A probable reason for Asians and Hispanics misclassifying as each other in FORDISC is that the current sample sizes of their reference groups are not large enough compared to those of American White and Black. Further, another reason is that there are not enough cranial interlandmark distances being utilized to analyze Asian and Hispanic crania. As a result, the variation in cranial morphology within these groups is currently not being represented well enough. For instance, most of the identified OpID individuals originated from South and Central American countries other than Mexico. However, the sample sizes for reference samples for identified non-Mexican Hispanics are still very

small. Therefore, it is extremely important to continue collecting and adding more data on known and/or positively identified Asian and Hispanic populations.

APPENDIX SECTION

	Page
A. Craniometric Landmark Definitions	51

APPENDIX A: CRANIOMETRIC LANDMARK DEFINITIONS

Landmark	Abbrev.	R/L/Midline	Measurements Used	Definition
Asterion	as	R/L	ASB	“The common meeting point of the temporal, parietal, and occipital bones, on either side” (Howells, 1973)
Auriculare	au	R/L	AUB	"The point vertically above the center of the external acoustic meatus at the root of the zygomatic process, a few millimeters above porion" (White, 2012)
Basion	ba	Midline	BNL, BBH	“On the anterior border of the foramen magnum, in the midline, at the position pointed to by the apex of the triangular surface at the base of either condyle, i.e., the average position from the crests bordering this area. Mark carefully with a pencil” (Howells, 1973)
Bregma	br	Midline	BBH, FRC, PAC	"The posterior border of the frontal bone in the median plane" (Howells, 1973)
Cheek height, superior point	-	R/L	WMH	The superior point on the "minimum distance, in any direction, from the lower border of the orbit to the lower margin of the maxilla, mesial to the masseter attachment" (Howells, 1973)
Cheek height, inferior point	-	R/L	WMH	The inferior point on the "minimum distance, in any direction, from the lower border of the orbit to the lower margin of the maxilla, mesial to the masseter attachment" (Howells, 1973)
Dacryon	dk	R/L	OBB	"The apex of the lacrimal fossa, as it impinges on the frontal bone. Mark with a pencil point on both sides" (Howells, 1973)

Ectoconchion	ek	R/L	EKB	"The intersection of the most anterior surface of the lateral border of the orbit and a line bisecting the orbit along its long axis. Mark both sides with a pencil" (Howells, 1973)
Eurion	eu	R/L	XCB	"The instrumentally determined ectocranial point of greatest cranial breadth" (White, 2012)
Frontomale anterior	fm:a	R/L	FMB, NAS	"The most anterior point on the fronto-malar suture. It may be found with the side of a pencil lead held in the transverse plane" (Howells, 1973)
Glabella	g	Midline	GOL	"The most anterior midline point on the frontal bone, usually above the frontonasal suture" (White, 2012)
Jugale	ju	R/L	JUB	"The point in the depth of the notch between the temporal and frontal processes of the zygomatic" (White, 2012)
Lambda	la	Midline	PAC, OCC	"The apex of the occipital bone at its junction with the parietals, in the midline" (Howells, 1973)
Lower orbital border	-	R/L	OBH	The inferior point on the orbit height, "perpendicular to the long axis of the orbit and bisecting it" (Howells, 1973)
Maximum frontal point	-	R/L	XFB	The points at "the maximum breadth at the coronal suture, perpendicular to the median plane" (Howells, 1973)
Most inferior nasal border	-	R/L	NLH	"The lowest point on the border of the nasal aperture on either side" (Howells, 1973)
Nasion	na	Midline	NOL	"The intersection of the fronto-nasal suture and the median plane. Mark with a pencil" (Howells, 1973)
Opisthion	os	Midline	FOL, OCC	"The inferior edge of the posterior border of the foramen magnum in the midline" (Howells, 1973)

Opisthocranium	op	Midline	GOL	"Instrumentally determined point at the rear of the cranium defined as the midline ectocranial point at the farthest chord length from glabella" (White, 2012)
Prosthion	pr	Midline	BPL	"The most anteriorly prominent point, in the midline, on the alveolar border, above the septum between the central incisors. Mark with a pencil" (Howells, 1973)
Stephanion	st	R/L	STB	"The intersection of the coronal suture and the limit of the temporal muscle (the inferior temporal line). Mark with a pencil on both sides" (Howells, 1973)
Subspinale	ss	Midline	SSS	"The deepest point seen in the profile below the anterior nasal spine" (Howells, 1973)
Upper orbital border	-	R/L	OBH	The superior point on the orbit height, "perpendicular to the long axis of the orbit and bisecting it" (Howells, 1973)
Zygion	zy	R/L	ZYB	"Instrumentally determined point of maximum lateral extent of the lateral surface of the zygomatic arch" (White, 2012)
Zygomaxillare	zm	R/L	ZMB	"The most inferior point on the zygomaticomaxillary suture" (White, 2012)
Zygoorbitale	zo	R/L	XML	"The intersection of the orbital margin and the zygomatic suture. Mark with a pencil" (Howells, 1973)

LITERATURE CITED

- de Azevedo S, Nocera A, Paschetta C, Castillo L, González M, González-José R. 2011. Evaluating microevolutionary models for the early settlement of the New World: The importance of recurrent gene flow with Asia. *Am J Phys Anthropol* 146:539–552.
- Beatrice JS, Soler A. 2016. Skeletal Indicators of Stress: A Component of the Biocultural Profile of Undocumented Migrants in Southern Arizona. *J Forensic Sci* 61(5):1164-72.
- Birkby WH, Fenton TW, Anderson BE. 2008. Identifying Southwest Hispanics using nonmetric traits and the cultural profile. *J Forensic Sci* 53(1):29–33.
- Bryc K, Velez C, Karafet T, Moreno-Estrada A, Reynolds A, Auton A, Hammer M, Bustamante CD, Ostrer H. 2010. Genome-wide patterns of population structure and admixture among Hispanic/Latino populations. *Proc Natl Acad Sci USA* 107(2):8954-61.
- Carson EA. 2006. Maximum likelihood estimation of human craniometric heritabilities. *Am J Phys Anthropol* 131:169-180.
- Chi-Keb JR, Albertos-González VM, Ortega-Muñoz A, Tiesler VG. 2013. HOMO - Journal of Comparative Human Biology 64:366–376.
- Devor EJ. 1987. Transmission of human craniofacial dimensions. *J Craniofac Genet Dev Biol* 7:95–106.
- Dudzik B. February 2015. *Comparing Cranial Morphology in Asian and Hispanic Populations: Exploring Why Misclassifications Can Occur When Using Discriminant Function Analysis (Abstract)*. Paper presented at the 67th Annual Meeting of the American Association of Forensic Sciences, Orlando, FL.
- Dudzik B, Jantz RL. 2016. Misclassifications of Hispanics using Fordisc 3.1: comparing cranial morphology in Asian and Hispanic populations. *J Forensic Sci* 61(5):1311-1318.
- Executive Yuan, Republic of China (Taiwan) [cited 2017 March 9]. Available from: <http://english.ey.gov.tw/>
- Gravlee CC, Bernard HR, Leonard WR. 2003a. Boas's Changes in bodily form: the immigrant study, cranial plasticity, and Boas's physical anthropology. *Am Anthropol* 105:326-332.
- Gravlee CC, Bernard HR, Leonard WR. 2003b. Heredity, environment, and cranial form: a reanalysis of Boas's immigrant data. *Am Anthropol* 105:125-138.
- Hanihara K. 1991. Dual structure model for the population history of the Japanese. *Nichibunken. Jpn Rev* 2:1-33.

- Hanihara T, Ishida H. 2009. Regional differences in craniofacial diversity and the population history of Jomon Japan. *Am J Phys Anthropol* 139(3):311-22.
- Harvati K, Weaver TD. 2006. Human cranial anatomy and the differential preservation of population history and climate signatures. *Anat Rec A Discov Mol Cell Evol Biol* 288A:1225-1233.
- Hefner JT. 2009. Cranial nonmetric variation and estimating ancestry. *J Forensic Sci* 54(5):985-995.
- Hildebolt CF, Vannier MW. 1988. Three-dimensional measurement accuracy of skull surface landmarks. *Am J Phys Anthropol* 76(4):497-503.
- Howells WW. 1973. Cranial variation in man. A Study by Multivariate Analysis of Patterns of Differences among Recent Human Populations. *Papers of the Peabody Museum of Archaeology and Ethnology*, vol. 67, pp 259. Cambridge, Mass.: Peabody Museum.
- Howells WW. 1989. Skull Shapes and the Map: Craniometric Analyses in the Dispersion of Modern Homo. *Papers of the Peabody Museum of Archaeology and Ethnology*, vol. 79, pp. 189. Cambridge, Mass.: Peabody Museum.
- Hubbe M, Neves W, Harvati K. 2010. Testing Evolutionary and Dispersion Scenarios for the Settlement of the New World. *PLoS One* 5(6):1-9.
- Ishida H, Hanihara T, Kondo O, Fukumine T. 2009. Craniometric divergence history of the Japanese populations. *Anthrop Sci* 117(3):147-56.
- Jantz RL, Ousley SD. 2005. Fordisc, version 3.0. Knoxville, TN: University of Tennessee.
- JMP®, Version <x>. SAS Institute Inc., Cary, NC, 1989-2007.
- Konigsberg LW. <http://konig.la.utk.edu/>
- Nakagome S, Sato T, Ishida H, Hanihara T, Yamaguchi T, Kimura R, Mano S, Oota H, The Asian DNA Repository Consortium. 2015. Model-Based Verification of Hypotheses on the Origin of Modern Japanese Revisited by Bayesian Inference Based on Genome-Wide SNP Data. *Mol Biol Evol* 32(6):1533-1543.
- Ousley SD. 2004. ThreeSkull. Version 1.76
- Ousley SD. 2012. Fordisc Help File Version 1.35; [cited 2015 December 7]. Available from: <http://math.mercyhurst.edu/~sousley/Fordisc>
- Ousley SD, Jantz RL, Fried D. 2009. Understanding race and human variation: why forensic anthropologists are good at identifying race. *Am J Phys Anthropol* 139:68-76.

Ousley SD, Jantz RL. 2013. Fordisc 3 - Third generation of computer-aided forensic anthropology. *Rechtsmedizin* 23(2):97-99.

Pietrusewsky, M. 2005. The Physical Anthropology of the Pacific, East Asia, and Southeast Asia: A Multivariate Craniometric Analysis. In Sargat, L., R. Blench and A. Sanchez-Mazas (eds.) *The Peopling of East Asia: Putting Together Archaeology, Linguistics, and Genetics*. pp.203-231. Routledge Curzon, London.

Pietrusewsky, M. 2008a. Craniometric variation in Southeast Asia and neighboring regions: a multivariate analysis of cranial measurements, *Human Evolution* 23 (1-2):49-86.

Pietrusewsky, M. 2008b. The modern inhabitants of Island Southeast Asia: a craniometric perspective. In E. Indriati (ed.) *Proceedings of the International Seminar on Southeast Asian Paleoanthropology: Recent Advances on Southeast Asian Paleoanthropology and Archaeology*, pp.185-201. Laboratory of Bioanthropology and Paleoanthropology, Faculty of Medicine Gadjah Mada University, Yogyakarta, Indonesia.

Pietrusewsky M. 2010. A multivariate analysis of measurements recorded in early and more modern crania from East Asia and Southeast Asia. *Quaternary International* 211: 42-54.

Pietrusewsky M. 2013. Biological connections across the Sea of Japan: a multivariate comparison of ancient and more modern crania from Japan, China, Korea, and Southeast Asia. In: Pechenkina E, Oxenham, MF, editors. *Bioarchaeology of East Asia: Movement, Contact, Health*. Gainesville: University Press of Florida. p. 144-178.

Rangel-Villalobos H, Muñoz-Valle JF, González-Martín A, Gorostiza A, Magaña MT, Páez-Riberos LA. 2008. Genetic admixture, relatedness, and structure patterns among Mexican populations revealed by the Y-chromosome. *Am J Phys Anthropol* 135:448-461.

Relethford JH. 1994. Craniometric variation among modern human populations. *Am J Phys Anthropol* 95:53-62.

Relethford JH. 2004a. Boas and beyond: migration and craniometric variation. *Am J Hum Biol* 16:379-386.

Relethford JH. 2004b. Global patterns of isolation by distance based on genetic and morphological data. *Hum Biol* 76:499-513.

Relethford JH. 2009. Race and global patterns of phenotypic variation. *Am J Phys Anthropol* 139:6-22.

Relethford JH, Harpending HC. 1994. Craniometric variation, genetic theory, and modern human origins. *Am J Phys Anthropol* 95:249-470.

SAS Institute Inc., SAS 9.1.3 Help and Documentation, Cary, NC: SAS Institute Inc., 2002-2004.

Shirley NR, Wilson RJ, Jantz LM. 2011. Cadaver use at the University of Tennessee's Anthropological Research Facility. *Clin Anat* 24(3):372-380.

Sjøvold T. 1984. A report on the heritability of some cranial measurements and non-metric traits. In: van Vark GN, Howells WW, editors. *Multivariate statistical methods in physical anthropology*. Dordrecht: D. Reidel Publishing Co. p223-246.

Smith HF. 2008. An evaluation of the association between three-dimensional cranial morphology and molecular distances in humans. PhD Dissertation. Arizona State University.

Spradley MK. 2013. Project IDENTIFICATION: Developing Accurate Identification Criteria for Hispanics. (National Institute of Justice Grant No. 2008-DN-BXK464). Washington, DC: U. S. Department of Justice.
<https://www.ncjrs.gov/App/Publications/abstract.aspx?ID=266273>

Spradley MK, Jantz RL. 2016. Ancestry estimation in forensic anthropology: geometric morphometric versus standard and nonstandard interlandmark distances. *J Forensic Sci* 61(4):892-897.

U.S. Census Bureau [cited 2016 February 16]. Available from:
<http://www.census.gov/en.html/>

Wall JD, et al. 2011. Genetic Variation in Native Americans, Inferred from Latino SNP and Resequencing Data. *Mol Biol Evol* 28(8):2231-2237.

Weiss E. 2015. Can we create ethnically diverse skeletal collection from donated bodies? *Anthropol Anz* 72(1):43-53

White TD, Black MT, Folkens PA. 2012. *Human Osteology*. 3rd edition. San Diego (CA): Academic Press.