GEOGRAPHIC ORIGIN ESTIMATION OF LATIN AMERICAN

INDIVIDUALS USING CRANIOMETRIC DATA

by

Kari E. Helgeson, B.S.

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 Biological Anthropology
August 2019

Committee Members:

M. Kate Spradley, Chair

Daniel J. Wescott

Nicholas P. Herrmann

**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 acknowledgement. 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, Kari E. Helgeson, authorize duplication of this work, in whole or in part, for educational or scholarly purposes only.

**ACKNOWLEDGEMENTS**

# TABLE OF CONTENTS

# LIST OF TABLES

# LIST OF FIGURES

# LIST OF ABBREVIATIONS

| Abbreviation | Description |
| --- | --- |
| CVA | Canonical variates analysis |
| DFA | Discriminant function analysis |
| FAFG | Forensic Anthropology Foundation of Guatemala |
| ILDs | Inter-landmark distances |
| OpID | Operation Identification |
| PCOME | Pima County Office of the Medical Examiner |
| PP | Posterior Probability |
| SES | Socioeconomic status |
| UADY | School of Anthropological Sciences of the Autonomous University of Yucatán, at Mérida |
| USCPB | United States Customs and Border Patrol |
| U.S. | United States |

# ABSTRACT

Since 2011, regions in South Texas have experienced a significant increase in migrant deaths and increased apprehensions of non-Mexicans (Isacson & Meyer, 2013). As migrants from countries other than Mexico cross the Texas-Mexico border, it becomes increasingly difficult to determine country of origin as well as identify and repatriate these individuals. The purpose of the present research is to examine craniometric variation among Central American populations to ultimately improve geographic origin estimation for migrants that die crossing the Texas-Mexico border by looking at variation between Mexico and Guatemala, between the regions of Mexico, and how unknown migrant individuals are classifying. In addition, this study will aid in our understanding of the biological variation of Mexican and Guatemalan populations which may facilitate and potentially expedite the identification and repatriation of unidentified migrants. The study sample consists of different geographic population groups including positively identified Guatemalan and Mexican individuals (North/West, Southeast, and Central regions), as well as unidentified and identified OpID remains. Howells, (1973) inter-landmark distances were collected from each cranium using a Microscribe digitizer and the program *ThreeSkull* (Ousley, 2004). A discriminant function analysis, stepwise function, and canonical variates analysis were performed to look at the variation and classify the individuals. 75.25% of the time Guatemalans can be correctly classified when compared to Mexicans. The cross-validation rate suggests that when the three Mexican regions are compared (Central, Southeast, and North/West) they can be differentiated

x

77.8% of the time. The Mahalanobis Distance matrix indicates the Southeast group is statistically different from the Central and Northwest groups (p=<0.001). When looking strictly at identified OpID individuals, 68% classified as Guatemalan and 32% as Mexican.

Geographic patterns of morphology are beginning to be observed within Mexico and between Mexico and Guatemala. If Guatemala is used as a proxy for Central America, further exploration with other countries is needed. Considering these patterns, this research indicates geographic origin estimation can be used in lieu of broad ancestry estimation in forensic casework and reference samples need to be reassessed to narrow down the missing persons list and help facilitate identifications of unidentified remains.

## I. INTRODUCTION

**Humanitarian Crisis in Texas**

The humanitarian and human rights crisis along the U.S. Mexico border has resulted in 7,216 deaths over the past 20 years. More than 3,000 of those deaths have occurred in Texas and the majority remain unidentified (U.S. Customs and Border Patrol, 2017a; U.S. Customs and Border Patrol, 2018). The purpose of the present research is to examine craniometric variation among Central American populations to ultimately improve geographic origin estimation for migrants that die crossing the Texas-Mexico border.

Undocumented migration in the United States began in 1965 after the U.S. created more stringent policies regarding passage through the U.S.-Mexico border. Before strict border control, Mexican individuals were allowed temporary access into the United States under labor agreements (Massey, Durand, & Pren, 2014). In 1986, Congress passed the Immigration Reform and Control Act which led to militarization of the border, higher penalties for hiring undocumented migrants, and increased funding for border patrol. In the past few decades, most undocumented individuals have migrated from Mexico (Massey et al., 2014) but since 2014 larger numbers of Central Americans have migrated to the U.S. (U.S. Customs and Border Patrol, 2017b). Undocumented migrants from Mexico have been migrating primarily for economic reasons (Chávez, Flores, & López-Garza, 1989), but recent migrants from Central America are fleeing increasing violence and extortion due to growing presence of gangs and drug cartels (Berk-Seligson & Seligson, 2016; Vogt, 2013). Today, gang violence is the leading reason for Central

Americans to migrate to the United States, followed by poor economic conditions (Vogt, 2013).

Since 2011, regions in South Texas have experienced a significant increase in migrant deaths and increased apprehensions of non-Mexicans (Isacson & Meyer, 2013). The term "other than Mexican" is used in all reported United States Customs and Border Patrol (USCBP) statistics for apprehensions regarding country of origin. USCBP does not differentiate country of origin for migrants in terms besides "Mexican" and "other than Mexican". The USCBP statistics depicts that over the last 17 years, apprehensions of individuals "other than Mexican" are significantly increasing. In the 2017 fiscal year, 140,496 individuals were documented as "other than Mexican" in the Texas Rio Grande Valley and only 29,653 were documented as being from Mexico (U.S. Customs and Border Patrol, 2017b). As migrants from countries other than Mexico cross the Texas-Mexico border, it becomes increasingly difficult to determine country of origin as well as identify and repatriate these individuals.

Many of the unidentified remains found north of the U.S. Mexico border are skeletonized or in advanced states of decomposition and any associated identification documents and personal effects may be severely degraded (Anderson, 2008) making traditional methods of identification utilizing soft tissue nearly impossible (fingerprints, facial features, scars, and tattoos) (Anderson, 2008; Leo, O'Connor, & McNulty, 2013). In remote areas along the border, remains are subjected to taphonomic damage, including weathering and scavenging (Anderson, 2008; Galloway, Birkby, Jones, Henry, & Parks, 1989). When locating scavenged remains, the elements recovered vary; however, the cranium is almost always recovered (Moraitis & Spiliopoulou, 2010). Therefore,

craniometric measurements can be used as an indicator of geographic origin thus narrowing the list of missing persons reports. Within forensic anthropology, biodistance measures can be used to estimate the geographic origin of unknown individuals. If individuals can be correctly classified into regional groups, the potential for identifications of unidentified migrants increase. Specifically, with the migrant population in Texas, biodistance measures can be used to estimate whether unknown individuals are morphologically closer to Mexican or Central American populations.

The goal of the present research is to use new craniometric data collected from Guatemalan populations, in combination with previously collected data from Mexico, to improve geographic origin estimation through biological distance analysis. In addition, this study will aid in our understanding of the biological variation of Mexican and Guatemalan populations which may ultimately aid in the identification of future border fatalities.

**Biodistance**

Biological distance or biodistance uses multivariate statistics to analyze population differences and similarities through craniometric data (Hefner, Pilloud, Buikstra, & Vogelsberg, 2016). Population structure looks at relationships between individuals, while population history looks at external factors such as migration and invasions (Mielke, Konigsberg, & Relethford, 2011). Because it is a proxy for genetic data and demonstrates heritability (Carson, 2006; Sherwood, Duren, Demerath, Czerwinski, Siervogel, & Towne, 2008), craniometric data can highlight regional population structure and reconstruct genetic relationships among populations (Relethford, 2004a; Relethford, 2004b; Strauss & Hubbe, 2010).

3

I will explore biological variation in Guatemalan and Mexican samples through craniometric data using biodistance measures. Analysis of craniometric data will demonstrate whether individuals from Guatemala and Mexico vary enough to accurately estimate geographic origin. The comparative data includes skeletal samples from Guatemalan Mayans and individuals migrating from Central, Southeast, and North/West Mexico, and Guatemala. Considering the lack of information regarding biological variation within Central America, this study will begin to provide insight into the geographic distribution of population structure in Central America.

Throughout this research I choose not to use the term ancestry but rather geographic origin estimation. Ancestry estimation as typically used in forensic anthropology is the estimation of an individual's socially perceived race through skeletal measurements. This estimation can be obtained through skeletal measurements due to the geographical variation of genes and their phenotypic expressions (Hefner & Spradley, 2018). So instead of estimating broad ancestry, I look at specific geographical regions in Guatemala and Mexico and the morphological features present in those regions.

Guatemala historically contains a large indigenous Mayan population, but also individuals with non-indigenous genetic ancestry, or Ladinos (Logan & Qirko, 1990). Ladino is a term used in Guatemala and other Central American countries to describe an individual with "non-Indian" genetic ancestry (Adams, 1994). The Mayan population has been decreasing due to Ladinoization which is when the indigenous Mayan population publicly alters their ethnic culture to appear more like the Ladinos to increase their reproductive fitness. Individuals of Mayan decent are choosing this new lifestyle to gain political and economic freedom as well as escape violence and oppression which in turn

4

increases their reproductive success (Logan & Qirko, 1990). It would be expected that indigenous individuals based on ethnic separation are morphologically different from each other and may contribute to the separation between Mexico and Guatemala. This study does not look at morphological differences between Ladinos and Mayans, but it may contribute to confounding results.

Linguistically, Mexico is very complex with thirteen different languages spoken throughout the country (Eberhard, Simons, & Fennig, 2019). Based on a linguistic map of Mexico, the Mayans are concentrated mostly in the Southeastern region with a small pocket near San Luis Potosí. Central Mexico is the most linguistically complex, potentially suggesting this area is the most ethnically and culturally diverse (Eberhard et al., 2019). With Mayan individuals in both Guatemala and Southeast Mexico, I expect there to be more genetic similarity between the indigenous Mayans when compared to the Ladinos or other regions of Mexico.

Central America and Mexico underwent five centuries of admixture from three primary groups including Native Americans with Asian influence, Europeans with Spanish and Portuguese influence, and Africans (Sans, 2000). With the influx of European colonizers to Central America, native and indigenous populations exchanged genes with the Europeans leading to genetic admixture (Bedoya et al., 2006).

Admixture with Mexico's indigenous population is consistent with the tri-hybrid model that began in the 16th century with the arrival of Spanish conquistadors' African slaves (Hughes, Tise, Trammell, & Anderson, 2013; Kirkwood, 2000). Today 60% of Mexico is composed of Mestizos which is a term used for genetic blending of European

5

and Native American blood (Kirkwood, 2000). Rubi-Castellanos et al. (2009) found that African ancestry was low, but constant throughout Mexico.

Multiple studies have analyzed the population history of Mexico using genetic signatures still present in current populations. Rubi-Castellaos et al. (2009) found two distinct clusters in Mexico, the North/West and the Central/Southeast regions. They discovered an increase in Native American and a decrease in European genetic relatedness in a North to South direction through Mexico.

A study by Rangel-Villalobos et al. (2009) looked at Y-STR profiles from five Mexican populations (Aguascalientes, Jalisco, Guanajuato, Chiapas, and Yucatán) and found results similar with Rubi-Castellanos et al. (2009). Rangel-Villalobos et al. (2009) also found that the Y-STR profiles from these five groups had decreasing European ancestry as well as increasing Native American ancestry from North to South Mexico. Although the results of these studies show minimal contributions by African American genes, it should be noted that the presence of these genes were still observed.

Hughes et al. (2013) performed a similar study but instead of using genetic data, tested to see if craniometric data showed the same pattern Rubi-Castellanos et al. (2009) and Rangel-Villalobos et al. (2009) discovered. Hughes et al. (2013) demonstrated very similar results, also finding a gradient of increasing North to South Native American ancestry and decreasing European ancestry. Humphries, Maxwell, Ross, & Ubelaker (2015) found using craniometric data that Mexican populations from Merida, Chihuahua, Chichen Itza, Michocán, and Oloriz are distinguishable from one another based on geographic region. This study also found that the Mexican populations are more similar

to one another than Spanish or African groups, with African groups being the most dissimilar.

Unlike Mexico, Guatemala experienced less European influence (Pearcy, 2005). Prior to the sixteenth century, most Central American individuals were influenced by Mayan culture and had Native American ancestry. In the late fifteenth century, Europeans began to explore Central America but quickly lost interest which allowed for Spanish control to begin in the early sixteenth century. Spanish domination over Central America, specifically Guatemala and Nicaragua, further controlled and isolated indigenous Guatemalan Mayan populations (Pearcy, 2005).

Multiple studies have demonstrated that it is possible to distinguish Mexican populations from other Central American countries. Spradley (2014) analyzed cranial variation between Mexicans, indigenous Guatemalan Mayan populations, and unidentified migrants from Texas and Arizona. The results demonstrate that with the present Texas and Arizona groups it is possible to estimate geographic origin. Spradley, (2014) points out that the Guatemalan sample being used as a reference group is an indigenous population and most likely does not represent the overall variation in the country of Guatemala. Therefore, more Guatemalan data is needed to accurately assess the genetic variation present between these reference groups. A study conducted by Tise, Kimmerlee, & Spradley (2014) explored the biological variation of multiple Hispanic populations that comprise the undocumented migrants in Florida. The reference samples analyzed included Mexico, Guatemala, Puerto Rico, Cuba, American White, and American Black. Using a canonical variates analysis, Tise et al. (2014) found the Guatemalan sample and the Mexican sample to be the most similar to each other,

whereas the Guatemalan sample and the Cuban sample were the most dissimilar. In their analysis, Tise et al. (2014) also utilized an indigenous Guatemalan population for comparison. These studies demonstrate a need for a more representative sample of the variation present in Guatemala to further assess the genetic variation between other Central American countries and Mexico.

In this research, I will use new data from identified Guatemalan migrants in conjunction with Guatemalan Mayans to further explore biological variation within Guatemala and between Guatemala and Mexico. Information regarding biodistance studies, population history, and previous research suggest Mexican and Guatemalan individuals can be distinguished from one another as well as individuals from different regions of Mexico (Spradley, 2013; Spradley 2014). By using these new data, we can begin to bridge a disconnect of missing data and further explore the human variation within Central America.

Based on the previous research above (Tise et al., 2014; Spradley, 2014; Hughes et al., 2013; Humphries et al., 2015; Rubi-Castellanos et al., 2009; Rangel-Villalobos et al., 2009), I believe it will be possible to distinguish a mixed indigenous and Ladino Guatemalan population group from a Mexican population, as well as differentiate between the three regions of Mexico (Southeast, Central, and North/West). If these geographic groups are distinguishable from each other, a comparison of OpID individuals to known Central American and Mexican groups could provide useful information pertaining to narrowing down the country of origin for Texas migrants.

**Research Questions**

1. Can a mixed Ladino and indigenous Guatemalan population, used as a proxy for Central America, be distinguished from Mexican individuals via cranial morphology?

2. Can Central, Southeast, and North/West Mexican groups be distinguished from each other via cranial morphology? What percent of OpID individuals of Mexican origin classify as either Southeast, Central, or North/West Mexican?

3. What percent of OpID individuals classify as Guatemalan or Mexican?

**Impact Statement**

The lack of information surrounding the term "Hispanic" creates difficulties when attempting to estimate geographic origin due to the wide variety of ancestry encompassed by this term. By looking at the biological variation between Mexican and Guatemalan populations, it will allow for investigation regarding better ways to identify migrants crossing the U.S.-Mexico border. If geographic origin can be estimated based on craniometric measurements, it could potentially narrow down a missing persons list, as well as facilitate and potentially expedite the identification and repatriation of unidentified migrants.

## II. MATERIALS AND METHODS

**Reference Groups and Materials**

The study sample consists of different geographic population groups including

positively identified Guatemalan and Mexican individuals (North/West, Southeast, and

Central regions), as well as unidentified and identified OpID remains. All individuals

used in the present research were collected from four different institutions including the

Pima County Office of the Medical Examiner, Operation Identification at Texas State

University, the School of Anthropological Sciences of the Autonomous University of

Yucatán, at Mérida, and the Forensic Anthropology Foundation of Guatemala. Each of

the institutions and sample compositions available for the following research are

described below. For each research question a different selection of individuals were

utilized, and this selection is stated in the results section.

### *Pima County Office of the Medical Examiner*

The Pima County Office of the Medical Examiner (PCOME), located in Arizona,

collaborates with multiple humanitarian organizations in order to disseminate information

regarding undocumented border crossers to help facilitate positive identifications

(Anderson & Spradley, 2016). The PCOME sample is composed of migrants that have

died crossing the U.S.-Mexico Border during the years 2003-2016. Most individuals are

positively identified from Mexico, Guatemala, El Salvador, and Honduras, with eighty-

three percent originating from Mexico (Martínez, Reineke, Rubio-Goldsmith, & Parks,

2014).

The identified individuals from the PCOME are used as a reference sample in the

Mexico and Guatemalan comparison for the present research. Eighty-four percent of the

identified migrants from the PCOME are male with a mean age of 31 years (PCOME

Annual Report, 2017; Martínez et al., 2014). All individuals are presumed to have birth

dates in the 20$^{th}$ century due to the age distribution and active forensic cases status. Of the

identified migrants, 38% of females and 40% of males fall within the age range of 20-29

years; 33% of females and 32% of males fall within the 30-39-year range (Martínez et al.,

2014). Most migrants (45%) associated with the PCOME have an undetermined cause of

death, and 40% as exposure to the elements (PCOME Annual Report, 2017; Martínez et

al., 2014). According to the PCOME Annual Report, (2017) 83% of the identified

migrants are from Mexico, 10% from Guatemala, 3% from El Salvador since 2000. The

Mexico sample with available craniometric data consists of two hundred and thirty

individuals, nineteen of which are females and two hundred and eleven males. The

Guatemala sample is made up of forty-two individuals with seventeen females and

twenty-five males.

### Operation Identification

The Operation Identification (OpID) project is located at Texas State University

and works to identify human remains found on or near the South Texas border through

community outreach, forensic anthropological analysis, and collaboration with

governmental and non-governmental organizations (Gocha, Spradley, & Strand, 2018).

The individuals are presumed to be unidentified migrants who died crossing the Texas-

Mexico border and have been exhumed from counties in south Texas, predominantly

Brooks County. The OpID sample consists of two hundred and seventy-eight remains,

but only one hundred and eighty-nine individuals will be used in this study due to the

availability and condition of the crania. All individuals are estimated to have a birth date

in the 20th century. The countries of origin are unknown for most individuals but currently twenty-four individuals have been identified through DNA. When the identified individuals are compiled, 58% are males and 42% are females with an average age of 32.55 years. 71% of the positively identified migrants are from Central America (Guatemala, El Salvador, Nicaragua, and Honduras) and 22.6% are from Mexico.

*School of Anthropological Sciences of the Autonomous University of Yucatán, at Mérida*

The Xoclán cemetery was originally used as an overflow plot for the Cementerio General burial grounds in Yucatán. In 2005 an agreement was made between the Autonomous University of Yucatán, at Mérida and the municipal government of Mérida to create a skeletal sample of identified individuals (Chi-Keb, Albertos-González, & Ortega-Muñoz, 2013). The curated Mexican reference sample collected from the Xoclán cemetery is housed at the School of Anthropological Sciences of the Autonomous University of Yucatán, at Mérida (UADY). The individuals are mainly of Mayan decent from rural parts of Mexico with birth years in the late 1900s (Chi-Keb et al., 2013). This sample is composed of sixty-five individuals with twenty-one females and forty-four males. All individuals from the Xoclán sample are categorized as Southeast Mexico because most documentation suggests these individuals are from rural areas in the Yucatan peninsula (Chi-Keb et al., 2013).

*Forensic Anthropology Foundation of Guatemala*

This sample is composed of indigenous Guatemalan Mayans who were genocide victims of human rights violations during the Guatemalan Civil War from 1960-1969 (Spradley, 2014). These individuals were recovered by the Forensic Anthropology

Foundation of Guatemala (FAFG) from mass graves with an anthropological estimation of sex performed to attempt identification (Spradley, Jantz, Robinson, & Peccerelli, 2008). It is likely that these indigenous individuals have very little European ancestry and is composed of mostly modern males from Rabinal and Comalapa, Guatemala (Spradley, 2014; Spradley et al., 2008). In the present study, eighty-seven indigenous Guatemalan Mayan males are included in the sample.

This research was initially intended to include data from Honduras and El Salvador, but due to the limited availability of cranial data these groups could not be included. More data needs to be collected to include other Central American countries in the analysis to further estimate if all Central American countries can be distinguished from each other via cranial morphology.

*Sample Size*

Sample sizes for each institution are shown in Figure 1 along with the breakdown of males and females in each sample. In summary, one hundred and twenty-nine individuals from Guatemala, two-hundred and ninety-five individuals from Mexico, one hundred and eighty-nine unidentified individuals and twenty-four identified individuals from OpID are available. Of the Mexican sample: one hundred and fifteen are from documented states that have been divided into three regions: North/West, Southeast, and Central Mexico. Seventeen are from the North/West region, sixty-seven are from the Southeast region, and twenty-six are documented to be from the Central region.
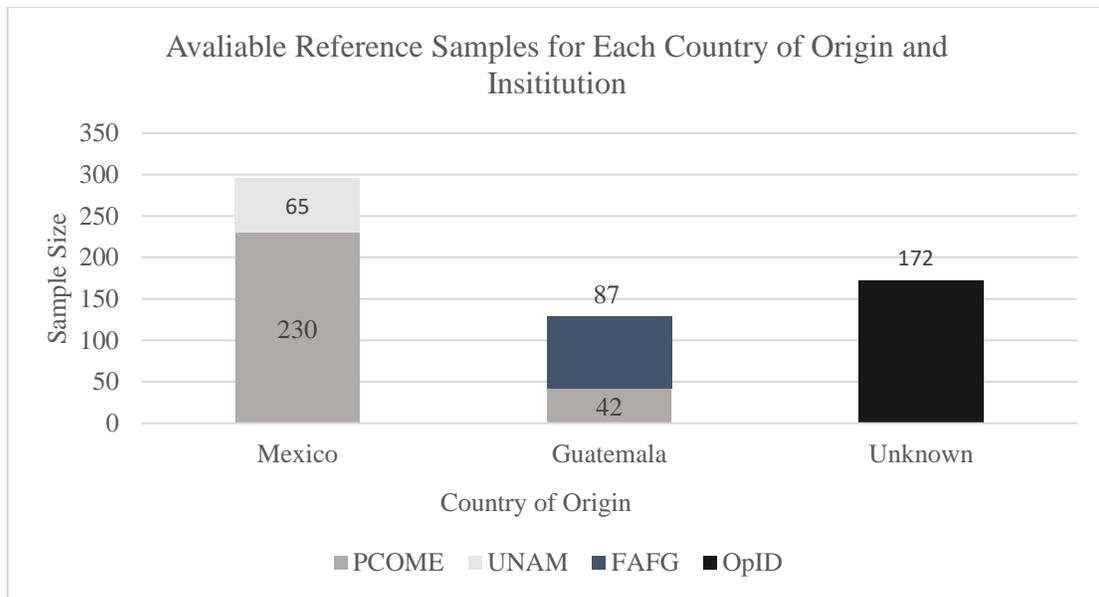
**Figure 1. Available Reference Samples for Each Country of Origin and Institution**.
Each number displays the total number of individuals for each country of origin and each
institution.

## Data Collection

Anatomical landmarks are defined as biologically meaningful loci that can be

located and identified with precision and accuracy on anatomical features (Richtsmeier,

Paik, Elfert, Cole III, Dahlman, 1995). Landmarks are collected and used to understand

and explain biological processes and epigenetics (Bookstein, 1991). Howells (1973)

outlines eighty-two inter-landmark distances to be collected on each cranium which are

designed to represent overall cranial variation. These measurements and their

abbreviations are listed in appendix 1. As many of Howells (1973) inter-landmark

distances as possible including fractions, angles, radii, and subtenses, were collected from

each cranium using a Microscribe digitizer and the program *ThreeSkull* (Ousley, 2004).

*ThreeSkull* calculates the inter-landmark distances (ILDs) between the craniometric

landmarks (Humphries et al., 2015) and stores the measurements and coordinates

digitally. If the skull was damaged, the landmark missing, or a feature was obliterated, the measurement was not collected. Dr. Kate Spradley collected the UADY and FAFG data. Additionally, Dr. Spradley collected PCOME data as well as other researchers from University of Tennessee and researchers at the PCOME trained by Dr. Kate Spradley, including myself.

**Statistical Analysis**

*Comparison of Guatemala and Mexico*

To assess if Guatemalan individuals can be distinguished from Mexican individuals a stepwise function and discriminant function analysis (DFA) were performed using one hundred and eighty-nine individuals. Prior to the DFA, outliers were assessed through calculation of means, minimum and maximum values, and standard deviations. Three individuals with extreme angle measurements were removed, most likely due to instrumentation error. To increase sample size, males and females were pooled by setting the mean equal to zero for both country and sex in SAS 9.3. Next a stepwise discriminant analysis was performed in FORDISC 3.1 (Jantz & Ousley, 2005) to reduce the number of variables and maximize the variation for both groups. The inter-landmark distances (ILDs) were imported using the custom data file feature, the "no classify" option was deselected, and a Forward Wilk's stepwise function was chosen to select the most appropriate variables. The stepwise analysis selected thirty ILDs which are shown in Table 1. Using the selected variables, a DFA was then performed with the thirty ILDs in SAS 9.3 to classify the individuals as either Guatemalan or Mexican. The DFA calculated Mahalanobis $D^2$, posterior probabilities, and cross-validated classifications.

**Table 1. Selected ILDs for Comparison of Guatemala and Mexico.**

| | | |
|---|---|---|
| Interorbital Breadth (DKB) | Nasion-Subtense Fraction (FRF) | Naso-Dacryal Angle (NDA) |
| Simotic Subtense (SIS) | Bregma-Lambda Chord (PAC) | Mastoid Height (MDH) |
| Prosthion Radius (PRR) | Subspinale Radius (SSR) | External Palate Length (MAL) |
| Orbital Height (OBH) | Glabella Occipital Length (GOL) | Lambda-Opisthion Subtense (OCS) |
| Occipital Angle (OCA) | Nasal Height (NLH) | Basion Bregma Height (BBH) |
| Foramen Magnum Length (FOL) | Nasion-Bregma Chord (FRC) | Basion Angle (BBA) |
| Basion Nasion Length (BNL) | Bregma Angle (BRA) | Lambda-Subtense Fraction (OCF) |
| Occipital Chord (OCC) | Malar Length Inferior (IML) | Minimum Frontal Breadth (WFB) |
| Naso-Dacryal Subtesne (NDS) | Glabella Projection (GLS) | Nasio-Frontal Angle (NFA) |
| Nasio-Frontal Subtense (NAS) | Bifrontal Breadth (FMB) | Bizygomatic Breadth (ZYB) |

*Mexico Regional Comparison*

All individuals listed with a documented birth state in Mexico were assigned to

one of the three regions of Mexico. Mexico in this study was originally divided following

the breaks presented in Hughes et al. (2013), but the regional break between Southeast

and Central Mexico was redefined based on the Mayan presence assessed using a linguist

map (Eberhard et al., 2019). A map of Mexico with the regional divisions and Central

America is documented in Figure 2. The sample size from each state is numerically

displayed within the state and states with no numeric represents no available data. The

other Central American countries are included on the map but only data from Guatemala

and Mexico were used in the study.

The data could not be standardized for size prior to analysis because females were

not present in all regional groups. To account for size, females were removed from the

North/West and Central Mexico groups. The Southeast group had twenty-one females

and were therefore separated into their own group and run in a four-group model

(North/West Mexico, Central Mexico, Southeast Mexico females, and Southeast Mexico

males). The inter-landmark data for eighty-four individuals were imported into

FORDISC 3.1 (Jantz & Ousley, 2005) as a custom data file, the "no classify" option was

deselected, and a Forward Wilk's stepwise discriminant analysis was performed. All

three regions (Central, Southeast, North/West) were selected along with all inter-

landmark distances that were not missing large amounts of data. A Forward Wilk's

stepwise function was performed to select the variables that best classified the reference

groups. Seven variables were selected that produced the highest classification rate and are

listed in Table 2. Following the Forward Wilk's stepwise function, two outliers were

reported by FORDISC 3.1 (Jantz & Ousley, 2005). For both individuals each ILD was

visually assessed and determined to fall within the range of normal human variation. The

DFA generated canonical variates scores, cross-validated classification rates, and a

Mahalanobis D² matrix.

After the initial analysis was performed, the individuals from the OpID sample

positively identified to be from Mexico were compared to the reference sample. This

comparison was done by inputting the individuals' ILDs into the custom database

function of FORDISC 3.1 (Jantz & Ousley, 2005). and compared using the same ILDs

selected by the stepwise function. Five individuals in the OpID sample are documented to

be from Mexico, but only four were used in this analysis because one of the individuals

was a female and females were removed from the reference sample.

**Table 2. Seven Selected Variables for Comparison of Mexico Regions**

| Basion Bregma Height (BBH) | Biorbital Breadth (EKB) |
|---|---|
| Basion Angle (BAA) | Minimum Frontal Breadth (WFB) |
| Nasion Angle (NAA) | Bizygomatic Breadth (ZYB) |
| Orbital Breadth (OBB) ||

**Figure 2. Map of Mexico and Central America.** Each region of Mexico is color coded as well as Guatemala and the remainder of Central America. See page 17 for description on how the regions of Mexico were divided. Each state or country with a number represents the number of samples available. Any state or region with no numerical value indicates no data were available.

*OpID Classification*

To compare the OpID individuals to the Mexican and Guatemalan reference sample the OpID sample was standardized by sex and then assessed for outliers. Nine outliers were identified through FORDISC 3.1 (Jantz & Ousley, 2005), visually assessed, and removed which increased the classification rates for Mexico and Guatemala. After the groups were standardized and outliers removed, Guatemala and Mexico were used as reference groups for the unknown OpID individuals. A Forward Wilk's stepwise function was performed in FORDISC 3.1 (Jantz &Ousley, 2005), to maximize the sample size and select the variables that best classified the reference group, which initially selected twenty-five variables. The initial twenty-five variables selected excluded six identified OpID individuals. Four ILDs, palate breadth, naso-dacryal subtense, simotic subtense, and simotic angle, were causing the OpID individuals to be excluded. These four measurements were manually removed, leaving twenty-one ILDs (Table 3) to be used in the discriminant function analysis.

**Table 3. Twenty-One ILDs used for Comparison of OpID Individuals to Guatemala and Mexico.**

| | | |
|---|---|---|
| Interorbital Breadth (DKB) | Nasion-Substense Fraction (FRF) | Mastoid Height (MDH) |
| Bifrontal Breadth (FMB) | Zygomaxillary Subtense (SSS) | Subspinale Radius (SSR) |
| Prosthion Radius (PRR) | Biasterionic Breadth (ASB) | Prosthion Angle (PRA) |
| Zygomaxillary Radius (ZMR) | Bregma-Lambda Chord (PAC) | Nasal Height (NLH) |
| Minimum Frontal Breadth (WFB) | Nasio-Frontal Angle (NFA) | Dacryon Subtense (DKS) |
| Maximum Frontal Breadth (XFB) | Nasio-Frontal Subtense (NAS) | Dacryon Angle (DKA) |
| Orbital Breadth (OBB) | Nasion-Bregma Subtense (FRS) | Bizygomatic Breadth (ZYB) |

## III. RESULTS

**Comparison of Guatemala and Mexico**

The cross-validation summary from the linear discriminant function demonstrated that 75.95% of Guatemalans and 74.55% of Mexicans classified correctly with an average classification rate of 75.25% as shown in Table 4. The cross-validation summary indicates that classification rates for Guatemalans and Mexicans are higher than random chance implying that Guatemalan individuals can be distinguished from Mexican individuals via cranial morphology. One hundred and ten individuals from the Mexico sample and seventy-nine individuals from the Guatemala sample were selected for comparison due to ILD availability as shown in Figure 3. Forty-nine of the Mexican individuals are from UADY, with thirty-two males and seventeen females. The remaining sixty individuals from the Mexican sample are from PCOME with fifty-seven males and four females. Sixty-four individuals from the Guatemalan sample are from FAFG (all males), ten are from the PCOME with eight males and two females and the remaining six are from OpID with three males and three females. Because the Guatemalan sample is much smaller, all identified OpID individuals from Guatemala were included in this comparison to maximize the sample size.

Using a canonical variates analysis, Guatemalans have larger cranial vaults than Mexicans. The ILDs that separate the groups include mastoid height (MDH), nasion angle (NBA), nasio-frontal angle (NFA), occipital angle (OCA), and bregma-lambda chord (PAC).

22
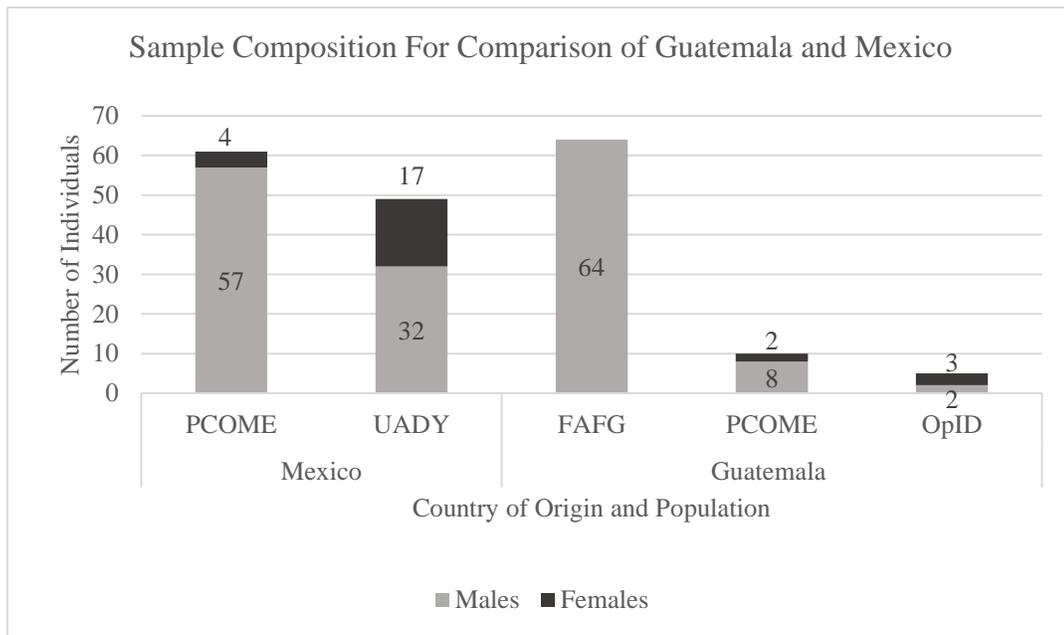
**Figure 3. Sample Composition for Comparison of Guatemala and Mexico.**

**Table 4. Cross-Validation Summary for the Comparison of Guatemala and Mexico.**

| From Country | Guatemala | Mexico | Total |
|---|---|---|---|
| | 60 | 19 | 79 |
| **Guatemala** | 75.95 | 24.05 | 100 |
| | 28 | 82 | 110 |
| **Mexico** | 25.45 | 74.55 | 100 |
| | 88 | 101 | 189 |
| **Total** | 46.56 | 53.44 | 100 |
| **Priors** | 0.5 | 0.5 | |

**Mexico Regional Comparison**

 The cross-validation rate suggests that when the three Mexican regions are compared (Central, Southeast, and North/West) they can be differentiated 75% of the time. 70.8% of Central Mexicans, 62.5% of North/West Mexicans, and 81.8% of Southeast Mexicans were correctly classified. The cross-validation rate is higher than random chance implying the three regions of Mexico can be distinguished from each other via cranial morphology.

 Forty individuals are from the PCOME and forty-four individuals are from UADY. The Central Mexico sample includes twenty-four individuals all from the PCOME, the North/West sample included sixteen individuals, all from the PCOME, and the Southeast sample included forty-four individuals with forty-two from UADY and two from the PCOME as shown in Figure 4.

 The Mahalanobis Distance matrix scores are shown in Table 5. The Mahalanobis Distance matrix indicates the Southeast group is statistically different from the Central and Northwest groups (p=<0.001). The canonical variates analysis (CVA) demonstrates in Figure 5 that the Southeast region is separated on the first axis from the Central and North/West groups by the basion angle (BAA), nasion angle (NAA) and biorbital breadth (EKB), indicating that the Southeast group has a wider upper face and larger values for basion and nasion angles. The major difference between groups as demonstrated by the CVA and Mahalanobis Distance matrix is that the Southeast group is different from the North/West and Central groups.
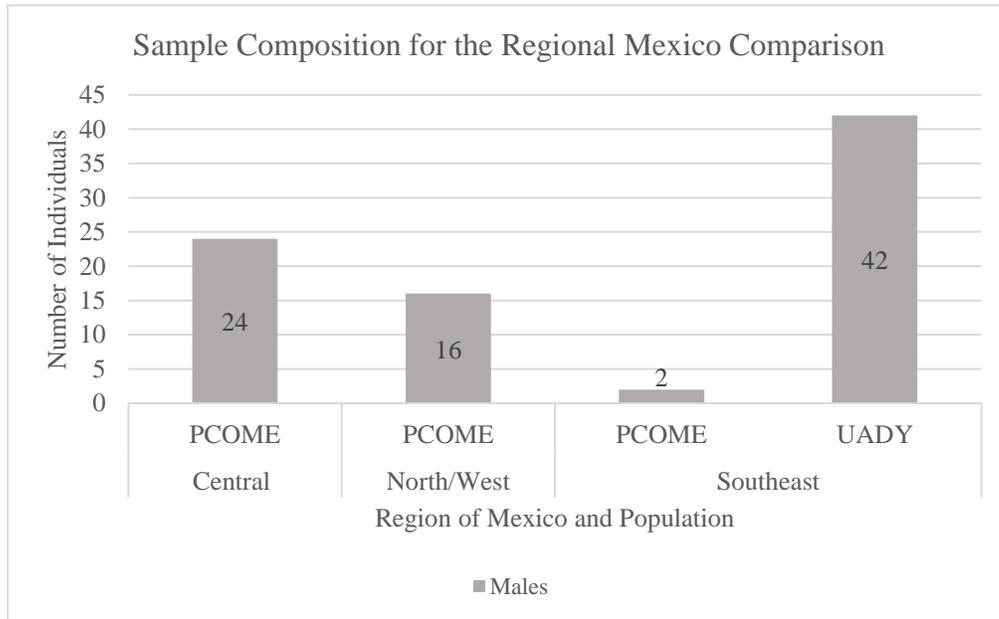
**Figure 4. Sample Size and Composition for the Regional Mexico Comparison.**
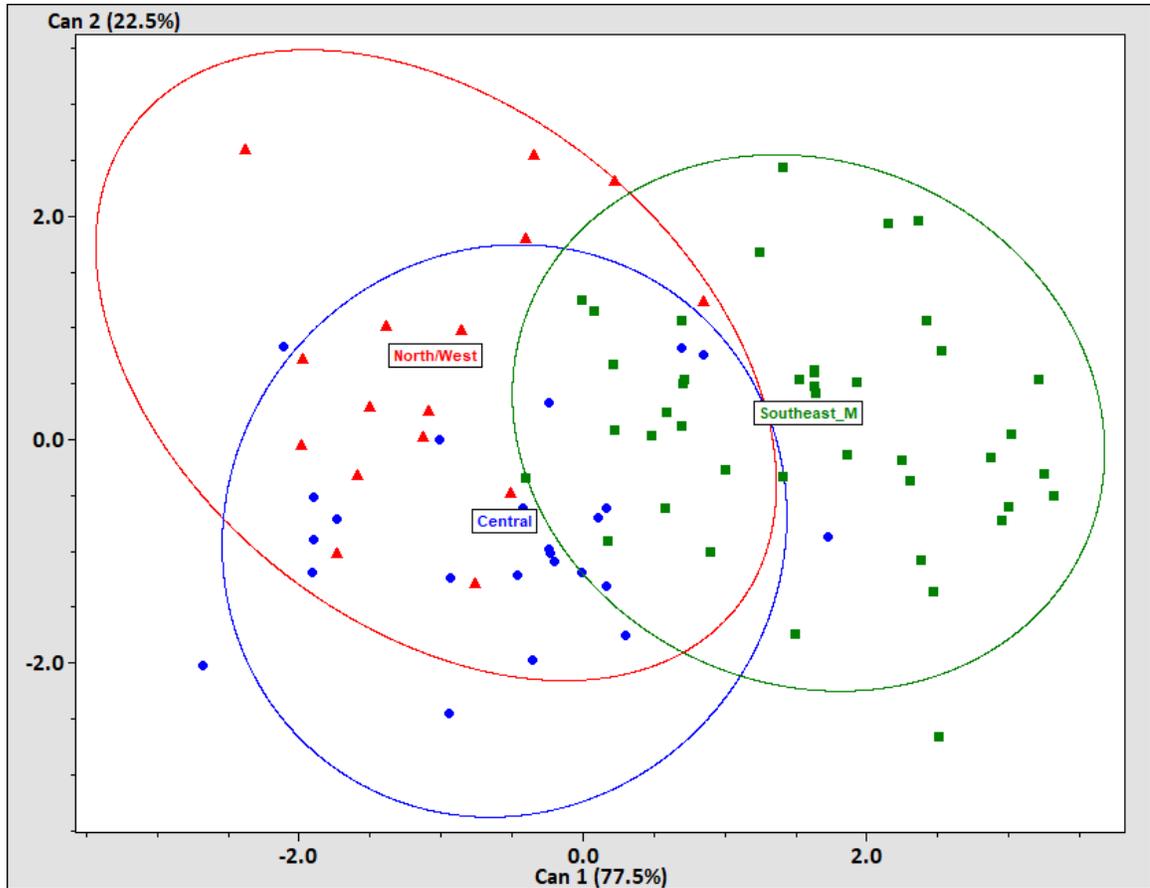
**Figure 5. Canonical Variates Plot for the Regional Mexico Comparison.** Canonical
Axis 1 demonstrates the Southeast group has a wider upper face and larger basion and
nasion angle values.

**Table 5. Mahalanobis Distance Matrix for the Regional Mexico Comparison.**

| Mahalanobis Distance Matrix | | | |
|---|---|---|---|
| | Central | NW | SE |
| Central | 0 | 2.43 | 5.53 |
| NW | 2.43 | 0 | 7.16 |
| SE | 5.53 | 7.16 | 0 |

26

Using the seven ILDs (Table 2) from the regional comparison of Mexico, the four identified Mexican male OpID individuals were compared to the regional reference groups. The posterior probability (PP) represents the probability that the unknown individual belongs to the reference group, calculated through the relative distance from each group (Jantz & Ousley 2005). OpID 0383 is from North/West Mexico and classified into the North/West group with a posterior probability of 0.501. OpID 0401-D is from Central Mexico and classified into the North/West group with a posterior probability of 0.518. OpID 0401-E is from Central Mexico and classified as into the North/West group with a posterior probability of 0.438. OpID 0441 is from an unknown region of Mexico and classified into the North/West group with a posterior probability of 0.820. These results are summarized in Table 7.

Originally Southeast females were used in the analysis in their own regional group for comparison, but with the four regional groups (Central, North/West, Southeast males, and Southeast females) the cross-validation rate was below random chance at 62.9% and when the Southeast female group was removed from the sample, the cross-validation rate increased to 75%.

To attempt to understand why classification rates were not higher, Guatemalan Mayans were included in the regional comparison with Mexico. The same methods were utilized but fifteen variables that best classified the reference groups were selected and are listed in Table 6. With the Guatemala group added to the regional groups, the cross-validation rate decreased to 66.9%. 65.1% of Southeast males, 75% of Southeast females 71.4% of Guatemalan individuals, 53.3% of North/West individuals, and 56.5% of Central Mexican individuals classified correctly. For this analysis one hundred and

seventy-eight individuals were included, with seventy-seven Guatemalan individuals all

from the FAFG sample. Twenty-three individuals were from Central Mexico, fifteen

from North/West Mexico, and sixty-three from Southeast Mexico. The Southeast sample

had forty-one males and twenty females from UADY and two males from PCOME as

shown in Figure 6. All individuals from North/West and Central Mexico are males from

PCOME. Based on the Mahalanobis Distance matrix, the Southeast group and Guatemala

are statistically different from all groups (p=<0.001). The Southeast males and females

are separated by larger values for dacryon angle (DKA) and nasion angle (NAA) on the

first axis as shown in Figure 7. The first and second axis combined explain 78% of the

variation. Southeast females were included in this analysis. Again, as seen in the regional

Mexico comparison, the Southeast group is different from the remainder of the groups

except for Guatemala.
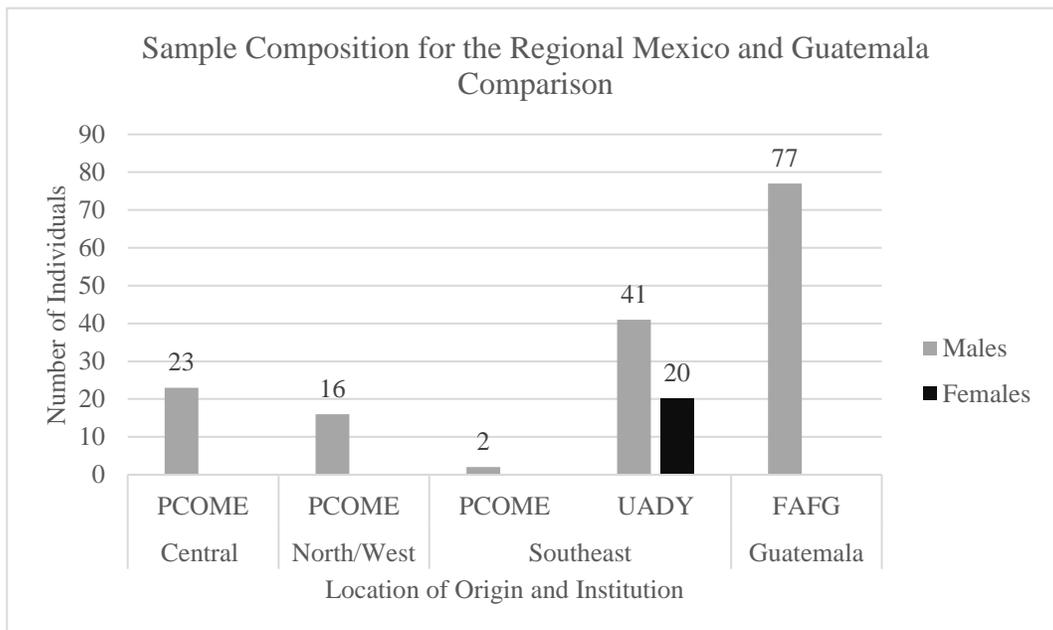


**Figure 6. Sample Composition for the Regional Mexico and Guatemala
Comparison.**
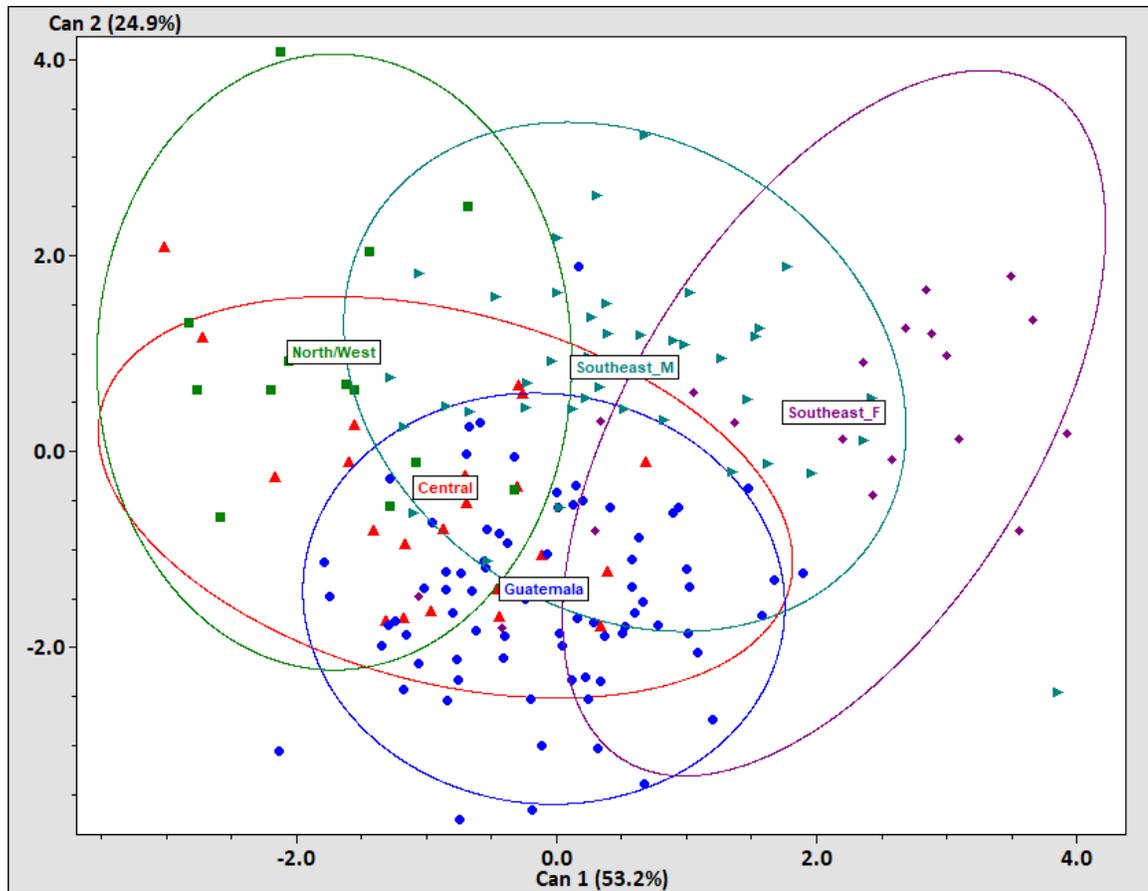
**Figure 7. Canonical Variates Plot for the Regional Mexico and Guatemala Comparison.** The first axis shows that Southeast males and females are separated by larger values for dacryon angle (DKA) and nasion angle (NAA).

**Table 6. Fourteen ILDs Selected for the Regional Mexico and Guatemala Comparison.**

| Basion Nasion Length (BNL) | Dacryon Angle (DKA) |
|---|---|
| Nasion to Bregma (NBA) | Orbital Height (OBH) |
| Biauricular Breadth (AUB) | Basion Bregma Height (BBH) |
| Glabella Occipital Length (GOL) | Biorbital Breadth (EKB) |
| Nasion Angle (NAA) | Minimum Frontal Breadth (WFB) |
| Bregma Angle (BRA) | Bijugal Breadth (JUB) |
| Interorbital Breadth (DKB) | Bizygomatic Breadth (ZYB) |

**Table 7. Results of Regional Mexico Comparison for Identified OpID Individuals.**
For each individual, birth state, regional classification and posterior probability are
displayed.

| OpID Number | Documented State | Regional Classification | Posterior |
|---|---|---|---|
| OpID 0383 | North/West | North/West | 0.501 |
| OpID 0401-D | Central | North/West | 0.518 |
| OpID 0401-E | Central | North/West | 0.438 |
| OpID 0441 | Unknown | North/West | 0.820 |

**OpID Classification**

Looking at the cross-validation rates Guatemala and Mexico demonstrated high

classification rates. With identified OpID individuals excluded, Guatemala individuals

correctly classified 90.54% of the time and Mexican individuals classified 88.61% of the

time. One hundred and fifty-five OpID individuals, both identified (n=23) and

unidentified (n=132), were compared to the Guatemalan and Mexican samples. 78%

(n=121) classified as Guatemalan and 22% (n=34) as Mexican.

When looking strictly at identified OpID individuals, 68% classified as

Guatemalan and 32% as Mexican. Overall, seven of the individuals classified correctly,

but only fourteen were from one of the two reference groups, indicating 50% classified

correctly. Nine of the identified OpID individuals are from Guatemala, five from Mexico,

and the remainder are from other countries in Central America (Nicaragua (n=1),

Honduras (n=1), and El Salvador (n=7)).

Of the five individuals from Mexico only one classified correctly and the other

four individuals incorrectly classify as Guatemalan. Of the nine individuals from

Guatemala, six classified correctly and the remaining three incorrectly classified as

Mexicans. Six of the nine individuals from Central America classified as Guatemalan and three as Mexican. Five of the seven individuals from El Salvador correctly classified as Guatemalans and the other two incorrectly classified as Mexican. The single individual from Nicaragua correctly classified as Guatemalan and the single individual from Honduras incorrectly classified as Honduran.

The posterior probabilities for classification of identified and unidentified OpID individuals are shown in Figures 8 and 9. Figure 8 demonstrates how the identified OpID individuals classified and Figure 9 demonstrates how the unidentified individuals classified. If individuals from Central America classified as Guatemalan, they were counted as correctly classified. Table 8 shows the correct country of origin and how the individual classified with the posterior probability. All posterior probabilities were rounded to the nearest tenth for the following graphics.
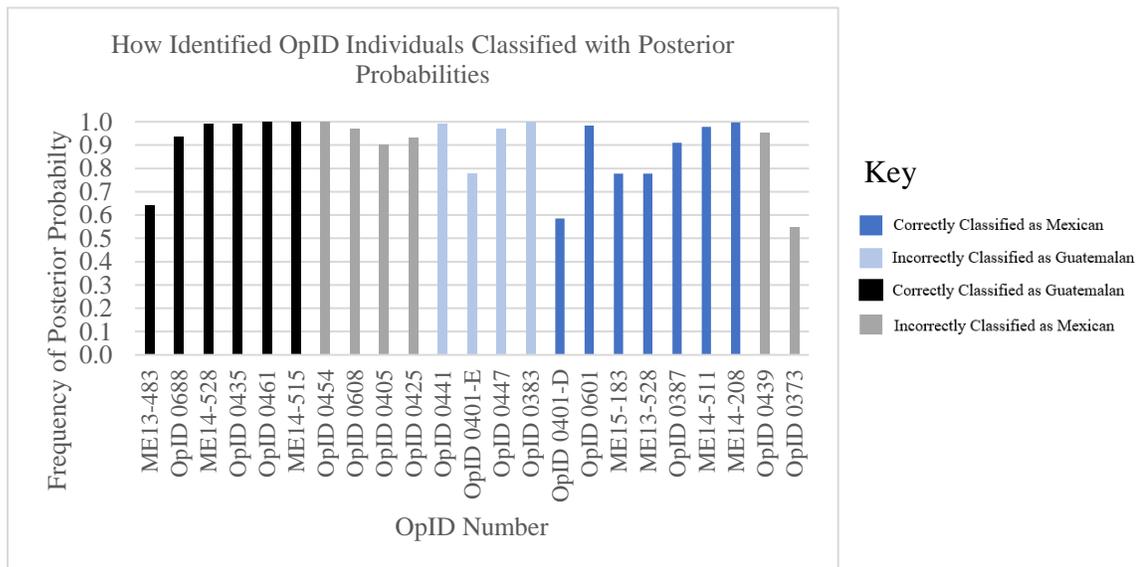


**Figure 8. Posterior Probabilities for the Classification of Identified OpID Individuals into Either Guatemala or Mexico.**

**Table 8. Identified OpID Individuals and How They Classify.**

| OpID No. | Country of Origin | Classified into | Posterior Probability |
|---|---|---|---|
| ME13-483 | Guatemala | Guatemala | 0.64 |
| OpID 0688 | Guatemala | Guatemala | 0.93 |
| ME14-528 | Guatemala | Guatemala | 0.99 |
| OpID 0435 | Guatemala | Guatemala | 0.99 |
| OpID 0461 | Guatemala | Guatemala | 1.00 |
| ME14-515 | Guatemala | Guatemala | 1.00 |
| OpID 0454 | Guatemala | Mexico | 1.00 |
| OpID 0608 | Guatemala | Mexico | 0.97 |
| OpID 0405 | Guatemala | Mexico | 0.90 |
| OpID 0425 | Honduras | Mexico | 0.93 |
| OpID 0441 | Mexico | Guatemala | 0.99 |
| OpID 0401-E | Mexico | Guatemala | 0.78 |
| OpID 0447 | Mexico | Guatemala | 0.97 |
| OpID 0383 | Mexico | Guatemala | 1.00 |
| OpID 0401-D | Mexico | Mexico | 0.59 |
| OpID 0601 | Nicaragua | Guatemala | 0.98 |
| ME15-183 | El Salvador | Guatemala | 0.78 |
| ME13-528 | El Salvador | Guatemala | 0.78 |
| OpID 0387 | El Salvador | Guatemala | 0.91 |
| ME14-511 | El Salvador | Guatemala | 0.98 |
| ME14-208 | El Salvador | Guatemala | 1.00 |
| OpID 0439 | El Salvador | Mexico | 0.95 |
| OpID 0373 | El Salvador | Mexico | 0.55 |
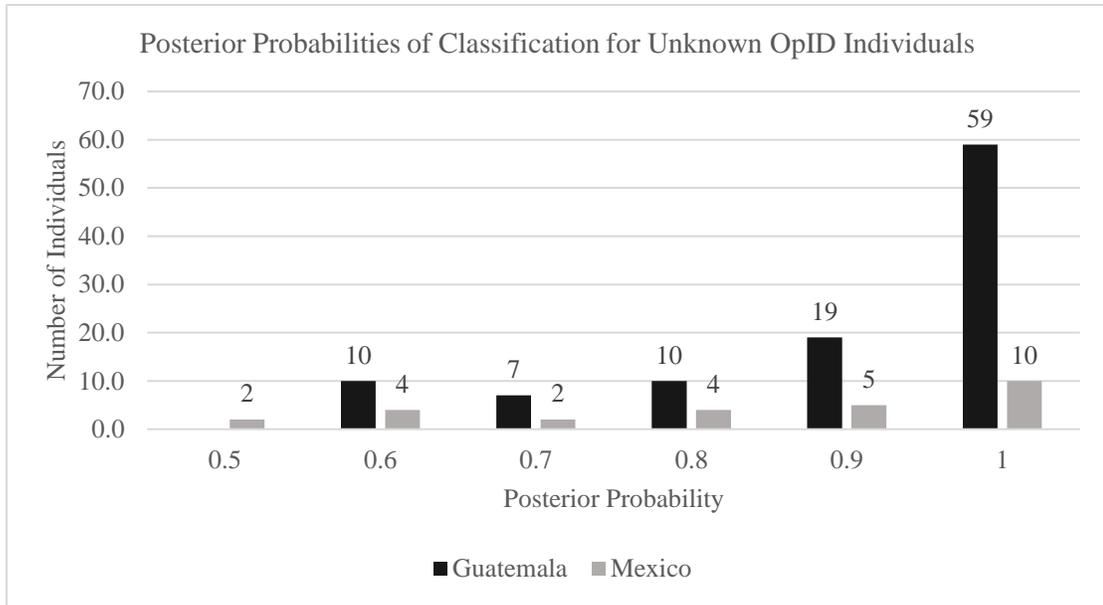
**Figure 9. Posterior Probabilities for the Classification of Unknown OpID Individuals into Either Guatemala or Mexico.**

## IV. DISCUSSION

Overall emerging patterns of craniometric variation are becoming apparent within Mexico and Guatemala is used a proxy to begin to understand the variation within Central America until more data becomes available. Comparison of OpID individuals to the known reference sample provides insight regarding the practical applications of geographic origin estimation.

### Comparison of Guatemala and Mexico

This separation between Guatemala and Mexico was expected based on population history and previous research. It also supports a more specific approach to geographic origin estimation as suggested by Spradley (2014), instead of using broad terms like Hispanic, which is less informative in a forensic setting, particularly when considering migrant remains. The reference samples within FORDISC 3.1 (Jantz & Ousley, 2005) may not be representative of the variation within Latin America to attempt a finer grained approach such as geographic origin estimation in an identification setting.

Population history suggests both Mexico and Guatemala have been influenced primarily by European and Native American gene flow with some African American contributions (Sans, 2000). But Mexico has been demonstrated to show more European ancestry and admixture than Guatemala and other Central American populations which were more influenced by Spanish and remaining indigenous populations (Rubi-Castellanos et al., 2009; Pearcy, 2006). This sample combines indigenous and non-indigenous Guatemalans which could be adding to the morphological differences seen. Even though the indigenous Guatemalans are also modern, no research has compared the

indigenous Guatemalans to migrating Guatemalans due to a previously limited sample size. We know there are mixed cultural ethnicities present in Guatemala with the push toward Ladinoization (Logan & Qirko, 1990). With Ladinoization occurring there may be more admixture occurring between indigenous and non-indigenous Guatemalans adding to the complexity of the cranial morphology within Guatemala.

The Mexican and Guatemalan individuals included in this study, are separated by their cranial vault rather than the craniofacial region which could be attributed to size. Guatemalan individuals are demonstrating larger cranial vaults than Mexican individuals, which is unexpected. A study by Jantz and Meadows Jantz (2017) found that cranial vault size was correlated with stature. Guatemalan individuals are one of the most malnourished countries and experience increased levels of nutritional stunting (WHO, 2019; The World Bank, 2010). Throughout Mexico, individuals have been shown to have a height gradient, with individuals in the North having larger stature which was correlated with a higher socioeconomic status (SES) (Castro-Porras, Rojas-Russel, Aedo-Santos, Wynne-Bannister, López-Cervantes, 2018). With these increased levels of malnutrition and stunting in Guatemala and height differences across Mexico according to SES, it is surprising that Guatemalan individuals have larger cranial vaults.

Another potential contributor could be a lack of sample size due to missing ILDs. Many individuals with recovered crania, do not have complete sets of ILDs recorded for various reasons, including damage to the existing crania or missing bones. Individuals with missing measurements are excluded from the study which severely decreases sample sizes. For this question four hundred and eighty-seven individuals were available, but

only one hundred and ninety-four were selected due to a plethora of missing measurements.

**Mexico Regional Comparison**

We are beginning to see emerging patterns of cranial variation as suggested by previous research. The Southeast group may be different from the rest of Mexico for multiple reasons. It may be because they have the most European ancestry, they are a much larger sample, or because most of this sample is composed of individuals from the Yucatan peninsula with Mayan descent and the other two regions are composed entirely of migrants from PCOME.

As shown by the cross-validated classification rates, the three regions of Mexico can be distinguished from one another 75% of the time via cranial morphology. The Southeast region is statistically different from both the North/West and Central regions based on the craniofacial region, specifically the upper face. The craniometric differences found reflect the differing degrees of European and Native American ancestry throughout Mexico (Hughes et al., 2013; Rangel-Villalobos et al., 2009; Rubi-Castellanos et al., 2009). The Southeast region is different from the other two regions potentially because they have the least amount of European ancestry and most Mayan influence in Mexico (Hughes et al., 2013; Rubi-Castellanos et al., 2009; Rangel-Villalobos et al., 2009; Eberhard et al., 2019). The North/West Mexico group is the least accurately identified which could be explained by migration within Mexico. Individuals migrating internally within Mexico have been found to be moving from one rural area to another and are moving more to the northern and southern states. Individuals migrating from Mexico to

the United States tend to be from Michoacán, Guanajuato, Zacatecas, and San Luis

Potosi, which are mostly Central states of Mexico (Aguyao-Téllez & Martínez-Navarro,

2013). Aguyao-Téllez and Martínez-Navarro (2013) found with their model of migration,

older males with less familial ties and lower education levels are the individuals

migrating to the U.S., and younger individuals that are the head of the household are

migrating more within Mexico.

When the Southeast females were included as their own regional group, the

Southeast males were misclassifying as Southeast females and I believe that could

contribute to why the cross-validation rate increased when the female group was

removed. When Guatemala was compared to the individual regions of Mexico there were

eleven Guatemalan individuals that misclassified as Central Mexico and nine that

misclassified as Southeast Mexico between the male and female group. I found it

interesting that so many Guatemalan individuals were classifying as Central Mexico, I

would have expected them to misclassify as Southeast Mexico due to the shared Mayan

ancestry. In both comparisons of the regions of Mexico, the North/West group was

misclassifying as Central and the Central group was misclassifying as the North/West

group. This could be because there is no great way to divide the North/West from the

Central region. Potentially the individuals that are misclassifying are from states that

border the dividing line which is causing the high misclassification rates. A study by

Aguyao-Téllez and Martínez-Navarro (2013) looked at internal and international

migration in Mexico and divided Mexico into five separate regions. Their line for the

North/West and Central division is dependent upon migration patterns. More exploration

into how to divide the North/West and Central regions needs to be explored potentially in

combination with linguistics, migration, and rural and urban areas. The states of Mexico show complex emerging craniometric patterns that need further exploration.

Of the studies analyzing regional ancestry in Mexico, my findings are most consistent with Hughes et al. (2013) who also found the Southeast group to be separated from the North/West and Central groups through craniometric data. The study performed by Rubi Castellanos et al. (2009) found the Central and Southeast regions to cluster and the North/West group to be separated through genetic markers rather than craniometric data. Hughes et al. (2013) used data that consisted entirely of male identified migrants from PCOME, whereas the sample used in this present research includes male and female migrants from PCOME and OpID as well as individuals from the UADY sample. All of the research combined suggests the central region shifts in classification depending on if genetic or craniometric data are being analyzed.

In combination with ancestral differences, the regions of Mexico differ in socioeconomic status and short stature. A study by Castro-Porras et al. (2018) found the southern states of Mexico to be of lower socioeconomic status and shorter in stature. The Southeastern group shows smaller cranial vaults when compared to the North/West group.

Only three of the four identified OpID individuals from Mexico have recorded states, two are from Central Mexico, one is from North/West Mexico, and one is unknown. Only one OpID individual classified into the correct region of Mexico, but the posterior probability was low. The two documented individuals from Central Mexico classified as being from North/West Mexico. As shown in the regional comparison and even the comparison including Guatemala the North/West and Central groups do not

have very accurate classification rates. This could again be due to the idea that Central

Mexico is centrally located and shares traits from the North/West group as well as fluid

in-migration in Mexico.

OpID 0383 is documented from Tamaulipas in North/West Mexico, but

Tamaulipas is right along the border of the division between North/West and Central

Mexico. OpID 0401-D is from San Luis Potosi which is also along the regional division

line. The division between North/West and Central Mexico is somewhat subjective. The

linguistic patterns show no clear-cut difference between the division of the North/West

and Central Mexico, so there may be a better way to divide the regions of Mexico to

better explain the morphological patterns being observed. Further exploration into how to

better divide the regions is needed. It is also possible that the states of Mexico are also

not good regional division lines. For the purpose of this study states of Mexico were not

divided in pieces, but that may need to be explored further in the future.

One limitation of this comparison could be the small sample size. The total

number of individuals used for the three regions is eighty-one with the Southeast group

being much larger than the North/West and Central groups combined. The Southeast

group is a combination of both Mayan descents from the late 1900s and current migrants

from PCOME, while both the North/West and Central Mexican groups are composed

entirely of migrants from the PCOME. The difference between the regions could be due

to the Mayan influence on the Southeast group or the skewed sample sizes.  All

individuals in the UADY sample with Mayan ancestry were placed in the Southeast

region group for comparison because they are assumed to be from Yucatán or the

surrounding areas (Chi Keb et al., 2013). Some individuals from this sample could have

potentially grown up in another region of Mexico, but that information is unknown which

could also be biasing the sample.

This research indicates that even though the three groups can be separated, the

large difference in cranial variation is between the Southeast region and the rest of

Mexico. There are emerging patterns of craniometric differences in the state of Mexico

and we are only beginning to understand the distribution of the variation.


**OpID Classification**

Of the one hundred and fifty-five OpID individuals compared to the Mexico and

Guatemala reference samples, the majority classified as Guatemalan, implying they are

morphologically similar to Guatemalans. But the posterior probabilities under 0.8 for

some of the individuals suggest they may not be from Guatemala, but potentially from

another Central American country rather than Mexico. It is a major assumption that when

the unknown OpID sample is compared to the Mexico and Guatemalan reference groups,

the individuals will fall within one of the two population groups. The OpID individuals

come from unknown countries of origin and it is entirely possible that more than one

individual was not born in Guatemala or Mexico. If this is holds true, the individual will

not correctly classify because they are forced into either the Mexican or Guatemalan

reference group. The reference groups also do not capture the entirety of the variation in

Guatemala or Mexico.

Most of the identified individuals from other countries in Central America

(Honduras, El Salvador, and Nicaragua) classified as Guatemalan, which would support

the isolation by distance model (Relethford, 2004a) considering Guatemala is

geographically closer to Honduras, El Salvador, and Nicaragua than Mexico. The sample size for Honduras and Nicaragua are extremely small, each with only one individual makes it difficult to estimate if other individuals from these countries would normally classify as Guatemalan.

Another issue with why the unknown and known Guatemalan individuals are not correctly classifying could be because they are non-indigenous Guatemalans or Ladinos rather than indigenous Mayans. Ladino is a term used in Guatemala and other central American countries to describe an individual with "non-Indian" genetic ancestry (Adams, 1994). If there is a significant difference between these two population groups, it could potentially explain why the OpID individuals, identified as Guatemalan, are not classifying correctly.

When the Border Patrol apprehensions are compared to this study, the majority of individuals being apprehended at the U.S. border after 2014 are from countries other than Mexico (USCBP, 2017b). In 2015, 67% of the migrants apprehended were from a country other than Mexico. In 2016, 75% were from a country other than Mexico, and in 2017, 83% were from another country other than Mexico (USCBP, 2017b). Migrants from other Central American countries are increasing in numbers over time which is what is being seen in this study. The OpID individuals when compared to the Guatemalan and Mexican reference sample, show that more than 50% are originating from a country other than Mexico. These results contrast migrant patterns in Arizona, where more migrants are originating from Mexico rather than Central America (PCOME Annual Report, 2017). The PCOME sample is composed of mostly Mexican individuals with a significant majority of males. The OpID sample (looking at the identified individuals) is composed

mostly of Central American individuals with an even distribution of males and females. Mexican individuals are migrating to support families in Mexico by sending money back, while Central American individuals are attempting to escape community violence and criminal activity (Chávez et al., 1989; Vogt, 2013). This study demonstrates that more data are needed from other Central American countries to further understand the craniometric variation seen within Central America. Unfortunately, this study has small sample sizes and the Guatemalan sample is composed of both indigenous Mayan Guatemalans and also migrant Guatemalan individuals, but due to Ladinozation these groups may overlap in identity (Logan & Qirko, 1990).

Also, there are a currently a total of twenty-five identified individuals in the OpID sample, but only twenty-three individuals were used in this research study due to available landmark measurements that were able to be collected. As more individuals are positively identified, more research can be conducted to assess how other individuals from Nicaragua or Honduras are classifying.

The findings of this research potentially present a problem with using FORDISC 3.1 (Jantz & Ousley, 2005) for classification of unknown individuals who are potentially Hispanic and migrating from Central America. The FORDISC 3.1 (Jantz & Ousley, 2005) reference sample is composed of only Guatemalan males with Mayan ancestry that are victims of genocide and a "Hispanic" group that combines individuals born in the U.S., Mexico, and Central America (Jantz & Ousley, 2005). This research demonstrates that individuals from Guatemala and Mexico can be distinguished from each other using craniometrics, implying the reference sample for comparison may be lacking. With data from the current research being analyzed and more specific groups, the country of origin

can most likely be identified for the missing person. It is also likely the complex

population history and the resulting population structure of these countries is not being

captured in the reference samples being used for this study.

 The twenty-four cranial measurements in Buikstra and Ubelaker's *Standards for*

*Data Collection from Human Skeletal Remains* (1994) were selected first in 1993 by a

committee appointed by the president of the American Academy of Forensic Sciences

Physical Anthropology Section (Spradley & Jantz, 2016). These twenty-four

measurements were later adopted by a group of researchers to encompass a necessary

standardization which were then published in Buikstra and Ubelaker (1994). Most of the

measurements used in this current research were not found in Standards (Buikstra &

Ubelaker, 1994), but instead found in Howells, (1973). Forty-five different inter-

landmark distance measurements were used, and of those only nineteen (42%) were

found in Standards (Buikstra & Ubelaker, 1994). If you combine angles, radii, fractions,

and subtenses together they make up 47% of the selected variables in the study. Overall,

more Howells (1973) measurements are being chosen over measurements in Standards

(Buikstra & Ubelaker, 1994). The measurements from Howells (1973) require advanced

instruments and more time to take the measurements, but they are demonstrating more

overall craniofacial variation (Spradley & Jantz, 2016).

## V. CONCLUSION

Considering these patterns, this research indicates geographic origin estimation can be used in lieu of broad ancestry estimation in forensic casework. The term Hispanic has been used as an all-encompassing catch all, especially when using FORDSIC 3.1 (Jantz & Ousley, 2005) to estimate ancestry. More data from other Central American countries is needed to further explore the cranial variation and compare population histories. This research suggests that finer grained approaches to country and even regional origin can be used instead of such a broad ancestry estimation as a way to potentially expedite and facilitate positive identification of migrants.

This present study uses data from four institutions including the Pima County Office of the Medical Examiner, Operation Identification at Texas State University, the School of Anthropological Sciences of the Autonomous University of Yucatán, at Mérida, and the Forensic Anthropology Foundation of Guatemala to explore geographic origin estimation of Mexico and Guatemala.

Mexico was regionally divided into the Southeast to separate the Mayan individuals from the remainder of Mexico to attempt to understand the variation present. The North/West and Central division needs further exploration because the classification rates between those two regions were very low. I believe there is more complexity to the regions that is not being captured with this regional division and the current sample between rural and urban migration, in-migration, and the cultural and linguistic patterns. Although the three regions of Mexico can be separated with patterns of cranial morphology, the Southeast region of Mexico with Mayan influence is very different from the remainder of Mexico.

When the positively identified and unidentified OpID individuals are compared to the reference sample, the majority are classifying as Guatemalan. This follows the USCBP apprehension rates of increasing "other than Mexican" and if Guatemala is used as a proxy for Central America, the migrants in Texas are more similar morphologically to Guatemala than Mexico. These visible differences support the need for more Central American data and even more data from Mexico to refine the geographic origin estimation as a way to assist in identification of unidentified remains.

This research also suggests there may be a problem with the current reference groups provided in FORDISC 3.1 (Jantz & Ousley, 2005). The Hispanic sample is comprised of individuals born in Central America, U.S., and Mexico. Guatemalans are a separate group and are composed entirely of Mayan males. The Hispanic reference sample provides a very broad range of variation which could be narrowed down by geographic region. The results of this study show Guatemala and Mexico are morphologically different and the current FORDISC 3.1 (Jantz & Ousley, 2005) reference group does not fully encompass the variation present in migrating individuals.

Future directions will be to compare indigenous and non-indigenous Guatemalans, reassess regional divisions of Mexico, compare other Central American countries and add females to the analysis when more data are obtained. Computed tomography scans may be a potential way to increase the available data for future analysis.

# APPENDIX SECTION

| Abbrev. | Measurement | Abbrev. | Measurement |
|---|---|---|---|
| ASB | Biasterionic Breadth | NFA | Nasio-Frontal Angle |
| AUB | Biauricular Breadth | NLB | Nasal Breadth |
| AVR | M1 Alveolus Radius | NLH | Nasal Height |
| BAA | Basion angle, na-pr | NOL | Nasio-Occipital Length |
| BBA | Basion Angle na-br | NPH | Nasion-Prosthion Height |
| BBH | Basion-Bregma Height | OBB | Orbital Breadth Left |
| BNL | Basion Nasion Length | OBH | Orbital Height Left |
| BPL | Basion-Prosthion Length | OCA | Occipital Angle |
| DKA | Dacryon Angle | OCC | Lambda-Opisthion Chord |
| DKB | Interorbital Breadth | OCF | Lambda-Subtense Fraction |
| DKR | Dacryon Radius | OCS | Lambda-Opisthion Subtense |
| DKS | Dacryon Subtense | PAA | Parietal Angle |
| EKB | Biorbital Breadth | PAC | Bregma-Lambda Chord |
| EKR | Ectoconchion Radius | PAF | Bregma-Subtense Fraction |
| FMB | Bifrontal Breadth | PAS | Bregma-Lambda Subtense |
| FMR | Frontomalare Radius | PRA | Prosthion Angle, na-ba |
| FOL | Foramen Magnum Length | PRR | Prosthion Radius |
| FRA | Frontal Angle | SIA | Simotic Angle |
| FRC | Nasion-Bregma Chord | SIS | Simotic Subtense |
| FRF | Nasion-Subtense Fraction | SOS | Supraorbital Projection |
| FRS | Nasion-Bregma Subtense | SSA | Zygomaxillare Angle |
| GLS | Glabella Projection | SSR | Subspinale Radius |
| GOL | Glabella Occipital Length | SSS | Zygomaxillary Subtense |
| IML | Malar Length Inferior | STB | Bistephanic Breadth |
| JUB | Bijugal Breadth | VRR | Vertex Radius |
| MAB | Palate Breadth | WCB | Minimum Cranial Breadth |
| MDB | Mastoid Width | WMH | Cheek Height |
| MDH | Mastoid Height | WNB | Simotic Chord |
| MLS | Malar Subtense | XCB | Maximum Cranial Breadth |
| NAA | Nasion Angle, ba-pr | XFB | Maximum Frontal Breadth |
| NAR | Nasion Radius | XML | Malar Length Maximum |
| NAS | Nasio-Frontal Subtense | ZMB | Bimaxillary Breadth |
| NBA | Nasion Angle, ba-br | ZMR | Zygomaxillare Radius |
| NDA | Naso-Dacryal Angle | ZOR | Zygoorbitale Radius |
| NDS | Naso-Dacryal Subtense | ZYB | Bizygomatic Breadth |

# LITERATURE CITED

Adams, R. N. (1994). Guatemalan ladinization and history. *The Americas,* 50, 527-543.

Anderson, B. E. (2008). Identifying the dead: Methods utilized by the Pima County (Arizona) Office of the Medical Examiner for undocumented border crossers: 2001-2006. *Journal of Forensic Sciences,* 53, 8-15.

Anderson, B. E., Spradley M. K. (2016). The role of the anthropologist in the identification of migrant remains in the American Southwest. *Academic Forensic Pathology,* 6, 432-438.

Aguayo-Téllez, E., Martínez-Navarro, J. (2013). Internal and international migration in Mexico: 1995–2000. *Applied Economics,* 45, 1647-1661.

Bedoya, G., Montoya, P., García, J., Soto, I., Bourgeois S., Carvajal, L., Labuda, D., Alvarez, V., Ospina, J., Hendrick P. W., Ruiz-Linares, A. (2006). Admixture dynamics in Hispanics: a shift in the nuclear genetic ancestry of a South American population isolate. *Proceedings of the National Academy of Sciences,* 103, 7234-7239.

Berk-Seligson, S., Seligson, M. A. (2016). Reported threats: the routinization of violence in Central America. *International Pragmatics Association,* 26, 583-607.

Bookstein, F. (1991). Morphometric tools for landmark data: Geometry and biology. New York (NY): Cambridge University Press 58-66.

Buikstra, J. E., Ubelaker, D. H. (1994). Standards for data collection from human skeletal remains. *Research Series, 44*.

Carson, E. A. (2006). Maximum likelihood estimation of human craniometric heritability. *American Journal of Physical Anthropology*, 131, 169-180.

Castro-Porras, L. V., Rojas-Russell, M. E., Aedo-Santos, Á., Wynne-Bannister E. G., López-Cervantes, M. (2018). Stature in adults as an indicator of socioeconomic inequalities in Mexico. *Revista Panamericana de Salud Pública,* 42, 1-29.

Chávez, L. R., Flores, E. T., López-Garza, M. (1989). Migrants and settlers: a comparison of undocumented Mexican and Central Americans in the United States. *Frontera Norte,* 1, 49-75.

Chi-Keb, J. R., Albertos-González, V. MF., Ortega-Muñoz, A., Tiesler, V. G. (2013). A new reference collection of documented human skeletons from Mérida, Yucatan, Mexico. *Journal of Comparative Human Biology*, 64, 366-376.

Eberhard, D. M., Simons, G. F., Fennig, C. D. (2019). Ethnologue; Languages of the world. Twenty-second edition. Dallas, Texas: SIL International. Online version: http://www.ethnologue.com.

Galloway, A., Birkby, W. H., Jones, A. M., Henry, T. E., Parks, B. O. (1989). Decay rates of human remains in an arid environment. *Journal of Forensic Sciences,* 34, 607-616.

Gocha, T. P., Spradley, M. K., Strand, R., (2018). Bodies in limbo: Issues in identification and repatriation of migrant remains in south Texas. In: Latham, K. E., O'Daniel, A. J. editors. *Sociopolitics of Migrant Death and Repatriation, Bioarcheology and Social Theory*. Springer International Publishing p 143-156.

Hefner, J. T., Pilloud, M. A., Buikstra, J. E., Vogelsberg, C. C. M. (2016). Brief history of biological distance analysis. In: Pilloud, M. A, Hefner, J. T., editors. *Biological Distance Analysis: Forensic and Bioarcheological Perspectives*. Elsevier Inc. p 143-156.

Hefner, J. T., Spradley, M. K. (2018). Ancestry (forensic applications). In: Trevathan, W., editors. *The international encyclopedia of biological anthropology.* John and Wiley Sons, Inc. p 1-3.

Howells, W. W. (1973). Cranial variation in man: a study by multivariate analysis of patterns of difference among recent human populations. *Peabody Museum of Archaeology and Ethnology, Harvard Univ.*

Hughes, C. E., Tise, M. L., Trammell, L. H., Anderson, B. E. (2013). Cranial morphological variation among contemporary Mexicans: Regional trends, ancestral affinities, and genetic comparisons. *American Journal of Physical Anthropology,* 151, 506-517.

Humphries, A. L., Maxwell, A. B., Ross, A. H., Ubelaker, D. H. (2015). A geometric morphometric study of regional craniofacial variation in Mexico. *International Journal of Osteoarchaelology,* 25, 795-804.

Isacson, A., Meyer, M. (2013). Border security and migration: a report from South Texas. Washington Office on Latin America, ed. Washington D.C.

Jantz, R. L., Ousley, S. D. (2005). FORDISC 3.1: Personal Computer Forensic Discriminant Functions.  Knoxville: The University of Tennessee.

Jantz, R., Meadows Jantz, L. (2017). Limb bone allometry in modern Euro-Americans. *American journal of physical anthropology,* 163, 252-263.

Kirkwood, B. (2000). The History of Mexico. Westport, Connecticut Greenwood Publishing Group.

Leo, C., O'Connor, J. E., McNulty, J. P. (2013). Combined radiographic and anthropological approaches to victim identification of partially decomposed or skeletal remains. *Radiography,* 19, 353-362.

Logan, M. H., Qirko, H. N. (1990). Ladinoization in Guatemala: A Darwinian Perspective. *Annals of the Southeastern Council on Latin American Studies,* 21, 89-98.

Massey, D. S., Durand, J., Pren, K.A. (2014). Explaining undocumented migration to the U.S. *International Migration Review,* 48, 1028-1061.

Martínez, D. E., Reineke, R.C., Rubio-Goldsmith R., Parks B.O. (2014). Structural violence and migrant deaths in Southern Arizona: Data from the Pima County Office of the Medical Examiner, 1990–2013. *Journal on Migration and Human Security,* 2, 257-286.

Mielke, H. M., Konigsberg, L. W., Relethford, J. H. (2011). Population structure and population history. In: *Human Biological Variation*. New York: Oxford University Press, p 317-343.

Moraitis, K., Spiliopoulou, C. (2010). Forensic implications of carnivore scavenging on human remains recovered from outdoor locations in Greece. *Journal of Forensic and Legal Medicine,* 17, 298-303.

Ousley, S. D. (2004). Threeskull 2.0.77, http://www.mercyhurst.edu/departments/applied_forensic_sciences/faculty_staff.html.

Pima County Office of the Medical Examiner (PCOME) Annual Report. (2017). https://webcms.pima.gov/government/medical_examiner/. Arizona, TX.

Pearcy, T. L. (2005). The History of Central America. Greenwood Publishing Group.

Rangel-Villalobos, H., Salazar-Flores, J., Dondiego, R., Anaya-Palafox, M., Nuño-Arana, I., Canseco-Ávila, L. M., Flores-Flores, G., Romero-Rentería, O., Morales-Vallejo, M. E., Muñoz-Valle, J. F., Rubi-Castellanos, R. (2009). South to North increasing gradient of paternal European ancestry throughout the Mexican territory: Evidence of Y-linked short tandem repeats. *Forensic Science International: Genetics Supplement Series,* 2, 448-450.

Relethford, J. H. (2004)a. Global patterns of isolation by distance based on genetic and morphological data. *Human Biology,* 76, 499-513.

Relethford, J. H. (2004)b. Boas and beyond: migration and craniometric variation. *American Journal of Human Biology,* 16, 379-386.

Richtsmeier, J. T., Paik, C. H., Elfert, P. C., Cole III, T. M., Dahlman, H. R. (1995). Precision, repeatability, and validation of the localization of cranial landmarks using computed tomography scans. *Cleft Palate-Craniofacial Journal,* 32, 217-227.

Rubi-Castellanos, R., Martínez-Cortés, G., Muñoz-Valle, J. F., González-Martin, A., Cerda-Flores, R. M., Anaya-Palafox, M., Rangel-Villalobos, H. (2009). Pre-Hispanic Mesoamerican demography approximates the present-day ancestry of Mestizos throughout the territory of Mexico. *American Journal of Physical Anthropology: The Official Publication of the American Association of Physical Anthropologists,* 139, 284-294.

Sans, M. (2000). Admixture studies in Latin America: from the 20th to the 21st century. *Human Biology,* 72, 155-177.

Sherwood, R. J., Duren, D. L., Demerath, E. W., Czerwinski, S. A., Siervogel, R. M., Towne, B. (2008). Quantitative genetics of modern human cranial variation. *Journal of Human Evolution,* 54, 909-914.

Spradley, M. K. (2014). Toward estimating geographic origin of migrant remains along the United States-Mexico border. *Annals of Anthropological Practice,* 38, 101-110.

Spradley, M. K., Jantz, R. L, Robinson, A., Peccerelli, F. (2008). Demographic change and forensic identification: problems in metric identification of Hispanic skeletons. *Journal of Forensic Sciences,* 53, 21-28.

Spradley, M. K. and R. L. Jantz (2016). Ancestry estimation in forensic anthropology: geometric morphometric versus standard and nonstandard interlandmark distances. Journal of Forensic Sciences, **61**, 892-897.

Spradley MK. 2013. Project IDENTIFICATION: Developing accurate identification criteria for Hispanics. (Document No. 244194). Retrieved from the National Institute of Justice: https://www.ncjrs.gov/pdffiles1/nij/grants/244194.pdf.

Spradley, M. K., Herrmann, N. P., Siegert, C. B., McDaneld, C. P. (2018) Identifying migrant remains in South Texas: policy and practice. *Forensic Sciences Research*, 4, 60-68.

Strauss, A., Hubbe, M. (2010). Craniometric similarities within and between human populations in comparison with neutral genetic data. *Human biology*, 82, 315-331.

Tise, M. L., Kimmerle, E. H., Spradley, M. K. (2014). Craniometric variation of diverse populations in Florida: Identification challenges within a border state. *Annals of Anthropological Practice,* 38, 111-123.

U.S. Customs and Border Patrol. (2017)a. United States Border Patrol Fiscal Year Southwest Border Sector Deaths Fiscal Year 1998 - 2017. U.S. Border Patrol.

U.S. Customs and Border Patrol. (2017)b. United States Border Patrol Apprehensions from Mexico and Other than Mexico Fiscal Year 2000 - 2017. U.S. Border Patrol.

U.S. Customs and Border Patrol. (2018). United States Border Patrol Fiscal Year Southwest Border Sector Deaths Fiscal Year 1998-2018. U.S. Border Patrol.

Vogt, W. A. (2013). Crossing Mexico: structural violence and the commodification of undocumented Central American migrants. *American Ethnologist*, 40, 764-780.

The World Bank. (2010). Nutrition at a Glance: Guatemala. Summary of findings. http://siteresources.worldbank.org.libproxy.txstate.edu/INTLACREGTOPNUT/Resources/Guatemala4-20-10.pdf

The World Health Organization. (WHO). (2019). Summary of findings. Nutrition Landscape Information System. http://apps.who.int/nutrition/landscape/report.aspx?iso=gtm.