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Odontometric differentiation between Southwest Hispanics, Native Americans, and European Americans

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ODONTOMETRIC DIFFERENTIATION BETWEEN SOUTHWEST HISPANICS, NATIVE AMERICANS, AND EUROPEAN AMERICANS

by

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ABSTRACT

Ancestry estimation for Hispanic Americans is increasing in importance as this minority population increases in the United States. Hispanics are historically an admixture of various geographic populations including European, Native American, and African. This combination of genes has caused many intermediate skeletal features that make identification of Hispanics a complicated process, especially when compared to Native Americans. “Hispanic” cannot efficiently encompass, as a term, the genotypic composition of multiple populations, as Hispanics from the Southwestern United States are historically a combination of Native American and European genes, whereas those from the Caribbean are historically an admixture of Native American, European, and African genes. While each of these regions can exhibit a certain combination of all three of these ancestral populations, each region has experienced a characteristic frequency of admixture. Southwest Hispanic populations are genotypically and phenotypically primarily comprised of Native American and European genes, resulting in an intermediate skeletal composition that prevents the distinct ancestry discrimination attainable by broad geographic groups.

Previous dental morphological studies (Edgar 2013) have also presented results of intermediacy and particular difficulty separating these individuals from

Native American and Asian groups; however, metric studies of the dentition of this population have yet to be investigated. Data were collected from n=569 dental casts from the James K. Economides collection which is housed at the Maxwell Museum in Albuquerque, New Mexico. Measurements included were the mesiodistal and buccolingual dimensions of the polar teeth of the morphogenetic field theory and the width and depth of the mandibular and maxillary arches. The morphogenetic field theory, as developed by Butler (1939) and adapted by Dahlberg (1945), represent the most stable teeth of the four fields of the dentition – incisors, canines, premolars, and molars. These “polar” teeth exhibit the least variation in crown size and shape.

Significant differences were identified between ancestry groups and these were subsequently used to identify allocation rates between all groups and between particular sets, or groups, of ancestries. Discriminant function equations were developed as a tool for ancestry estimation. Success was greatest when both dental crown and arcade variables were pooled together in an analysis. Results of this study indicate odontometric analyses are useful in differentiating between Native Americans and European Americans, with classification rates ranging between 75.2% and 86.3%; however, much work must be conducted before application on Hispanic populations is possible. The Southwest Hispanic population exhibited greater phenotypic similarity to the European American population and had significantly lower success in allocation than between Southwest Hispanics and Native Americans. In cases where sex was known, successful allocation decreased, although females generally exhibited greater success than males. Potential utility is observed in this study when sex is unknown, and the development of a statistical methodology utilizing the dentition is proposed.

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LIST OF ABBREVIATIONS

AA	African American (Edgar 2005, 2013)
AA	Asian American (Present Research)
ANN	Artificial Neural Network
ANOVA	Analysis of Variance
ASUDAS	Arizona State University Dental Anthropology System
BL	Buccolingual
CEJ	Cemento-enamel junction
Cerv	Cervical
Comp	Composition
CW	Canine Width
DFA	Discriminant Function Analysis
DT	Decision Tree
EA	European American
GM	Geometric Morphometrics
IW	Incisor Width
kNN	K-nearest-neighbor analysis
KPD	Kernel probability density
LC	Lower Canine
LDFA	Linear Discriminant Function Analysis
LI	Lower Incisor
LM	Lower Molar

LP	Lower Premolar
LR	Logistic Regression
Man	Mandibular
Max	Maxillary
MD	Mesiodistal
mtDNA	Mitochondrial Deoxyribose nucleic acid
MW	Molar Width
NA	Native American
NMH	New Mexico Hispanic
OMB	Office of Management and Budget
OSSA	Optimized Summed Scored Attributes method
PCOME	Pima County of the Medical Examiner
PI	Platymeric Index
PW	Premolar Width
QDFA	Quadratic Discriminant Function Analysis
RFM	Random Forest Models
SFH	South Florida Hispanics
SPSS	Statistical Package for Social Sciences
SVM	Support Vector Machines
UBC	Undocumented Border Crosser
UC	Upper Canine
UI	Upper Incisor

UM	Upper Molar
UP	Upper Premolar
V_E	Environmental Variance
V_G	Genotypic Variance
V_P	Phenotypic Variance

CHAPTER 1: Introduction

Assessing ancestry in forensic and archaeological cases primarily depends upon morphological and metric characteristics of the cranium and the postcranial skeletal elements. According to *Daubert* standards, methods of analysis of these primary characteristics must be approved through rigorous testing by researchers and constant improvement due to population variation and secular change (Daubert v. Merrell Dow Pharmaceuticals, Inc. 1993; Komar and Buikstra 2008). The importance of these standards lie in their statistical, empirical testing that can be quantified and consistently repeated with success by other investigators (Edgar 2013; Hefner and Ousley 2014). It is required that these methods have presented error rates, standardization in how the methodology should be conducted, acceptance by the scientific community, and subsequent validation by other researchers to prove accuracy and replicability (Christensen 2004).

Due to an increase in the admixture of populations as geographic boundaries become less of a deterrent and cultural restrictions become increasingly negligible in separating genotypic groups, or clines, clear indicators of a particular ancestry are less applicable to individuals. With increasing admixture and variation from such factors as nutrition and care, it is important to explore other potential avenues of analysis not already in common use for individual identification. An example of this pattern of change and development of methods is evident in the Hispanic population of the American Southwest. This population is characterized by contributions of Native American, African, and European alleles during the era of colonization and subsequently affected by varying culture and geography and temporal trends (Bertoni *et al.* 2003; Tise 2014; Vilar *et al.* 2014; Willermet and Edgar 2009). The proportion of these genetic alleles varies from region to region in North and South America, creating differing blends of populations throughout the Western Hemisphere (Sans 2000). For example, Southern Mexico was colonized later than most other areas of the country, with some locations not being colonized until the late 19th century, resulting in a higher indigenous genetic frequency in this region compared to European. In general, genetic and craniometric evidence suggest an increasing indigenous genetic frequency and decreased European frequency the further south in Central America the populations inhabit. Concurrently, African alleles also exhibit an increase in frequency from North to South (Hughes *et al.* 2013). Genetic analyses of modern Puerto Ricans have shown that Y-chromosome contributions were primarily from Europeans, with a small contribution from Africans, but never from indigenous populations. X chromosomes, however, revealed evidence of indigenous and African maternal genetics (Vilar *et al.* 2014). This sex-biased admixture has been observed in several locations throughout Central America, with concentration between European males and Native American and African females (Bryc *et al.* 2010; González-Andrade *et al.* 2007).

Many of the elements most used for ancestry estimation (the craniofacial complex and metric measurements of the long bones) are easily affected by taphonomic processes, whether through destruction of the projections and low density areas of the cranium or by producing enough to damage to landmarks to prevent accurate measurement (Lyman 2014; Willey *et al.* 1997). The use of dentition in the construction of the biological profile is a valuable alternative considering the preservation of teeth in forensic and archaeological contexts. Oftentimes, the hard tissue of teeth allows them to survive better than other skeletal elements. Also, in cases of mass disasters and commingled remains, individuals sometimes are best represented by the maxilla or mandible. For example, in the recovery of an ossuary in southern Maryland, T. Dale Stewart and Douglas Ubelaker found 100% representation of 99 individuals with the mandible (best preserved element) and 87% representation with 86 individuals with the maxilla (Ubelaker 1974). The cheek teeth often remain preserved in cases of thermal alteration of the remains due to the placement in the jaw and soft tissue protection (Dumančić *et al.* 2001; Symes *et al.* 2014).

Hispanics as a U.S. Population

The population of Hispanics is growing rapidly in the United States, reaching approximately 50.5 million people in 2010; in New Mexico, the Hispanic population comprised 46.3% of the total population in 2010, one of the only states where it is a plurality population (Ennis *et al*. 2010). According to a 2010

U.S. Census Brief, 79.94% of individuals of Hispanic status living in the American West (states including Montana, Wyoming, Colorado, New Mexico, and those west of these states) were of Mexican origin. In Arizona 87.47% of the Hispanic population is of Mexican descent (Ennis *et al. 2010*, U.S. Census Bureau 2013). Hispanics are, as of 2014, the largest minority population in the United States (Ennis *et al.* 2010).

The exact definition of the term "Hispanic" is debated between different fields and even between varying forensic anthropologists, dependent upon the region in which the forensic anthropologist is working on casework or the researcher's sample (Rhine 1990). According to Rhine (1990), "Hispanic" is a catch-all term for a population from a large geographic region with varying degrees of European, Native American, and African genetic admixture. According to the U.S. Census Bureau, Hispanic is defined as an individual whose origins are in Mexico, Puerto Rico, Cuba, Central America, South America, or any other Hispanic/Latino region (Ramirez and de la Cruz 2003). According to the Office of Management and Budget (OMB), Hispanics are individuals, or descendants of individuals, from Latin American countries or other Spanish cultures (Bertoni *et al.* 2003). The flaw with these definitions is the clustering of people from a large geographic region into a single ancestral group based upon a common language or broad, nonhomogeneous geographic distribution (Hurst 2012; Willermet and Edgar 2009). As indicated by Ross *et al.* (2004), this working definition does not efficiently distinguish biological and cultural patterns.

Despite the classification and self-identification of these individuals into a discrete sociocultural category, these categories do not reflect the actual variation and presence of genetic admixture present in the populations (Pfaff *et al*. 2001).

For the purpose of the present study, it is important to know the genetic origins of Southwestern Hispanics in order to understand metric similarities and evaluation of dental differences between Southwestern Hispanics and the ancestral populations of Native Americans and Europeans. In the context of the present study, a working definition must be established in regards to “Southwest Hispanic,” so that comparative analyses may be efficiently conducted with these data (Crews and Bindon 1991). Southwest Hispanics are defined as individuals with primary genetic ancestral lineage from pre-European contact Mexican indigenous populations and European populations largely from Spanish colonization (Willermet and Edgar 2009). It is possible that African alleles are also present in the examined population; however, genetic and phenetic studies have primarily characterized this population as a dihybrid model correlating to Native American and European genes (Bryc *et al.* 2010; Willermet and Edgar 2009). Indigenous populations contributing to the modern Hispanic population are numerous and likely impact the phenotypic expression of bone and dentition in the Hispanic population differently; however, examination of specific related populations are out of the scope of the present research but would be valuable in later analyses.

Hispanics as Undocumented Border Crossers (UBCs)

U.S.-Mexico border states highlight the importance of developing ancestry estimation techniques that successfully allocate Hispanic individuals. The Pima County Office of the Medical Examiner (PCOME), for example, receives a large number of what are termed “undocumented border-crossers,” or UBC’s, each year (Anderson 2008; Birkby 2004, Hurst 2012). The PCOME, by 2008, had processed over 750 cases concerning Hispanic individuals from Central and South America migrating over the Mexico-United States border (Birkby *et al.* 2008). This is a reflection of the shifting patterns of demographic composition, where the Hispanic population is continually changing to include greater frequencies of individuals from many different regions and backgrounds rather than a “homogenous” group of people from one location. The U.S. Border Patrol, in 2004, reported that 43% of all apprehensions of border crossers occurred along the 281 mile stretch that constitutes the Tucson sector. This small stretch of the international border makes up only 14% of the overall border (Anderson 2008).

The problem of UBC-related deaths also occurs in other border states, including California and Texas. For the years 1991, 1992, and 1993, approximately half a million migrants were apprehended by Border Patrol each year in the San Diego sector alone, which comprises 400 miles of the border (Hinkes 2008). Between 1993 and 2004, 558 migrant deaths were reported, 184 of which were determined to be unrelated to attempting entry into the United States. Most of these individuals were between 20-29 years of age; 88% were males, and almost 99% were from Mexico (Hinkes 2008). Much like cases in Arizona, illegal immigrants in Texas, tend to pass through the most sparsely populated regions of the state to avoid being caught (Birkby 2004; Glassman 2004). Migrants passing over the border oftentimes hire a *coyote* - a guide who is hired to ensure their safety and passage into the U.S. By passing through these low-density areas, migrants not only increase their chance of death by starvation or dehydration, there is also an increased chance of injury or death at the hands of the *coyote* (Fulginiti *et al.* 2004; Glassman 2004).

The most common form of death for UBCs in Arizona is attributed to heat-related illness (Parks *et al*. 2004). Most of the deaths occur between May and September, when the average temperatures range from 100-110˚F. Due to increased environmental and body temperature, mummification of the remains occurs at a faster rate in the Arizona desert (Galloway 1989; Anderson 2008) as well as the Californian Sonora Desert, where there used to be large migrant traffic (Hinkes 2008). The conditions of Arizona, with mild winters and hot, dry summers, create conditions prime for mummification of remains. At approximately nine months, exposed skeletal elements begin to show signs of bleaching and destruction of the outer cortical surface (Galloway 1989). The increase in the rate of decomposition compared to more temperate climates creates conditions necessary for identification of skeletal remains. The increased rate of decomposition also creates the problem of faster weathering of skeletal elements once exposed. While the anterior teeth may often fall out (Anderson

2008), collection of these elements or identification with the posterior dentition may be useful in identification of these remains. Many skeletal elements found in Texas had begun weathering, experienced animal scavenging, and undergone other taphonomic alterations before ever being discovered as border-crossers; these individuals may have travelled alone or with associates who may not report deaths out of fear of being sent back to their home country (Glassman 2004).

Objectives of the Present Research

The purpose of the present research is to determine if there are qualitative variables of statistical significance in the dental crowns and cervico-enamel junctions and the arcade proportions of modern American populations that may prove useful in ancestry differentiation. The utility of odontometrics as the primary modality of analysis is to reduce potential interobserver error that may be seen with subjective categorization of non-metric, or morphological, traits. The purpose of this study is to test the hypothesis that Southwest Hispanics will exhibit intermediate characteristics of both Native Americans and European Americans, but will show statistically significant differences in variables relating to the crown, cervical, and arch proportion measurements. The populations examined for this study constitute a wide span of genetic relatedness, with Native American groups predominantly Puebloan and Rio Grande tribes and European American groups likely representing multiple different European regions. The Hispanic population of New Mexico is predominantly of Mexican origin (Willermet and Edgar 2009) and exhibits primary contributions from Native American and European American alleles (Bryc *et al.* 2010). While the Native American populations examined are likely not the exact parental population of the modern Hispanic population, they present a similar geographic relation and closer genetic similarity compared to non-Southwestern Native American groups. The null hypothesis is that any differences between the sample groups are attributable solely to natural variation that is not significantly affected by ancestry and statistically significant differences will not be identified.

The first objective of the present research is to test whether statistically significant differences are present between the four analyzed populations (Hispanics, Native Americans, European Americans, and Asian Americans). It will be examined if the Hispanic population will exhibit expected effects of admixture regarding their dentition and if differences in these populations are distinct and able to be utilized in ancestry estimation. It is hypothesized that if the New Mexican Hispanic sample represents admixture of Native American and European alleles, then the population will exhibit intermediate characteristics of both Native and European Americans, but will show statistically significant differences in these variables.

The second objective is to determine whether sex has a significant impact on the utility of odontometrics for ancestry estimation and, if so, to what degree in each population does it matter. It is hypothesized that if distinct sex differences are identifiable and population-specific, then known sex will improve the efficacy of this method. It is important to present the degree of sexual dimorphism in tooth and palate dimensions that exists for each particular population, as it is unlikely that each sample has a uniform extent of dimorphism.

CHAPTER 2: Previous Research

The cranium is the most utilized portion of the skeleton in ancestry estimation, as the craniofacial region contains important genetic morphological traits and metric dimensions (DiGangi and Hefner 2013). Metric and morphological analysis of the cranium, particularly of the maxillofacial region, are commonly used by forensic anthropologists to estimate ancestry, with morphological traits being the most preferred due to their greater ability to be used on cranial fragments (Hefner 2009; Hefner and Ousley 2014; Rhine 1990).

The majority of forensic studies utilizing the dentition are associated with aging (Acharya *et al.* 2014; AlQahtani *et al.* 2010; Prince and Ubelaker 2002; Ubelaker 1989). Few studies have been conducted on using dentition for ancestry estimation in a medicolegal context, with the majority of the studies concentrating on the use of morphological traits (Edgar 2005, 2013; Hinkes 1990; Hrdlička 1920; Lasker and Lee 1957; Lease and Sciulli 2005). The large majority of dental research has focused on identifying broad population patterns and examining microevolution and population relationships and histories, as will be discussed in some detail below. Dental analyses of biological admixture are valuable avenues of research when the slow rate of change and variation in dental form caused by genetic drift is taken into consideration. Admixture increases the rate of change in trait frequency, providing the ability to draw relationships between populations. Investigation of morphological traits and metric differences in tooth size in populations allows for the ability to identify introduction of new genes and population migration and interaction (Hanihara 1967; Irish and Turner 1990).

Biological Distance

Biological distance (i.e., biodistance) is the investigation of genetic relationships between populations though comparison of phenetic trait frequencies. Biodistance analyses are valuable in the examination of population affinities, evolutionary mechanisms, and population history (Stojanowski and Schillaci 2006). Several anthropological biodistance analyses have been conducted to examine the relationship of Hispanics to the other three listed populations, as well as the relationship of Hispanics between regions through genetic and phenetic analyses (Allard *et al.* 2006; Bertoni *et al.* 2003; Bryc *et al.* 2010; Martinez-Abadias *et al.* 2006; Willermet and Edgar 2009).

In cases of biodistance analyses, an assumption must be made that the variables studied accurately reflect the genetic relationship between the sampled populations (Stojanowski and Schillaci 2006). In an admixed population, it is expected that the traits examined for biodistance analyses will present itself as an intermediate form, given the assumption that the examined traits are an accurate measure of gene interaction (Martinez-Abadias *et al.* 2006). Admixture naturally negates the exclusive frequency of traits identifiable to particular ancestral populations (Lease and Sciulli 2005). This blending of traits and ancestry boundaries produces an indistinct subpopulation that has not experienced a high degree of specialization or differentiation, and this may make allocation difficult. As shown by Moss *et al*. (1967), Harris and Rathbun (1989), and Edgar (2002) in their morphological and metric investigations of African American admixed populations, an intermediate state is approached with increasing time of the admixed population between the two parental populations. Usually, early admixed individuals exhibit a closer affinity to one parental population or another (e.g., African Americans and West Africans in Edgar [2002] or the Southwest Hispanics and Native Americans in Willermet and Edgar [2009]) but progress towards an intermediate state of expression as further genetic admixture occurs.

Due to European colonization in the Americas, admixture occurred with the indigenous populations (Willermet and Edgar 2009). Birkby *et al.* (2008) suggests the possibility that Native American ancestry predominates in Southwest Hispanic genetics. Several studies have indicated that Native American and European ancestry are likely the predominant contributors to the Southwest Hispanic population (Allard *et al.* 2006; Bertoni *et al.* 2003; Bryc *et al.* 2010; Edgar 2013). Bryc *et al.* (2010) analyzed 73,901 SNPs of the Affymetric 500K and Illumina 610-Quad panel data between Native Americans, Africans, Europeans, and Hispanics (individuals from Ecuador, Columbia, Puerto Rico, Dominican Republic, and Mexico). Whereas Hispanic populations from Dominican Republic and Puerto Rico showed the highest levels of African ancestry, individuals from Mexico and Ecuador showed the lowest levels of

African ancestry but the highest levels of Native American ancestry. Mexicans ranged from being largely Native American to largely European. As shown, the amount of genetic contributions in Hispanic individuals varies considerably, and can range anywhere from 0-90% Native American contribution (Klimentidis *et* al. 2009).

While most Hispanic populations correlate with a trihybrid model (descended from parental European, African, and Native American populations), those in the Southwest, Pennsylvania, and the Southeast most appropriately fit to a dihybrid model. Particularly in the Southwest, Native American and European genetic contributions are most prevalent (Bertoni *et al.* 2003). Allard *et al.* (2006) also examined the trihybrid model of Hispanic genetic admixture through the analysis of n=686 Hispanics, comparing the genetic composition of this sample to the four major haplogroups of Native American mitochondrial DNA, or mtDNA, (A, B, C, and D) and European and African haplogroups. Autosomal markers primarily point to European genetic components, whereas the mtDNA contribution primarily originates from Native American haplogroups. Differences in African ancestry are evident between southwestern and southeastern Hispanic groups, with the southeastern sample exhibiting a larger proportion of African genetic inheritance (Allard *et al*. 2006).

Distinct differences are exhibited in the crania of individuals labeled “Hispanic” that come from different regions, reflecting the genetic evidence of differential admixture. While the cranium is most often used for biological distance research, it is important to recognize the inherent obstacles of this region: cranial plasticity, nutritional effects, and developmental and environmental variations (Relethford 2004). Ross *et al.* (2004) used geometric morphometrics on an array of Hispanic individuals from several different locations in order to analyze the variation within the U.S.-determined “Hispanic” population. This study found a close relationship between the African sample and modern Cubans, but a lack of similarity between Africans and pre-contact Cubans. Mexicans were similar with indigenous Ecuadorians and formed a cluster with them separate from modern Cubans, Spanish, African, and pre-contact Cubans. These results suggested a greater indigenous component to Mexican ancestry compared to Cuban ancestry and argued for further distinction between Hispanic populations. Martinez-Abadias *et al*. (2006) also examined the effects of admixture on cranial morphology on a Mexican sample using geometric morphometrics (GM). According to their results, the Mexican sample fit the dihybrid model but with important temporal variations. The earlier colonial sample most closely resembled the Native American group, with the later colonial sample most closely resembling the Spanish. These results exhibit the temporal shift in phenetic expression of genetic traits, with the population reaching an increasing intermediate state and increasing genetic contribution skewing phenetic expression to the other side of the spectrum. Tise’s (2014) analysis of the craniometric data of n=751 individuals (Europeans, Hispanics, and Africans) and produced similar results to the genetic studies of Bryc *et al*. (2010) where the

Mexican sample had the highest contribution of Native American ancestry and lowest contribution of African ancestry and the Puerto Rican sample had the highest contribution of European ancestry.

Willermet and Edgar (2009), through an analysis of dental morphological features, found a closer similarity between New Mexican Hispanics and African Americans and European Americans. However, Hispanics fell within the Native American range when compared to African Americans and European Americans, and this was explained as being caused by their genetic contribution. The authors recognize the variation from previous studies and present two possible explanations: admixture between the two populations or the similarity of phenotypic characteristics between both African and European Americans. The authors favor the latter explanation due to the limited history of African Americans in New Mexico. Also, the Hispanic sample was more closely associated with early Native Americans rather than a contemporary population, suggesting that this is due to the initial occurrence of admixture taking place in the distant past.

Dental Inheritance

There is general acceptance in the field of dental anthropology that there is a significant genetic component to dental size and morphological trait expression, with the genetic contribution ranging from 56-92%, depending upon tooth and dimension (Alvesalo and Tigerstedt 1974; Blanco and Chakraborty

1976; Dempsey and Townsend 2001; Kieser 1990; Perzigian 1981; Portin and Alvesalo 1974; Scott and Turner 1997; Townsend and Brown 1978a, b). The mechanism of this genetic inheritance, however, is poorly understood. In general, the development of dental size and morphology is less under environmental influence than many other tissues of the human body, providing a stable source for population assessment with little plasticity (Scott and Turner 1997).

For an analysis of dental inheritance as it applies to the stability of phenetic frequencies in a population and the influence on the frequency in an admixed population, it is important to discuss the concept of heritability. Heritability can range from 0.0 (no genetic heritability) to 1.0 (complete genetic heritability) and is indirectly related to environmental influence on phenetic traits. The variation evident in phenetic expression can be expressed as $V_p = V_G + V_E$, where V_p is the total phenotypic variance, V_G is the genetic variance (heritability), and V_E is the environmental variance (Townsend and Brown 1978). The degree to which these two factors influence dental development is a matter of debate. While most studies show a strong proportion of heritability of tooth size, there is still a small degree of environmental influence, although seemingly less than the skeletal elements of the human body (Townsend and Brown 1978). Heritability also affects the degree to which members of a population are similar to other members of the population. Generally, members of the same population are more related to each other than to members of a different population of the same species (Hanihara and Ishida 2005; Harris 2003).

Morphogenetic Field Theory of Dental Development

The morphogenetic field theory of dental development arose as an explanation for dental development in the early 20th century. According to this theory, each type of tooth experiences a particular degree of variation in size and shape. However, one tooth from each class (incisor, canine, premolar, and molar) are the least variable and is designated the polar, or key, tooth. Within the same class, the more distal teeth are increasingly variable in morphology and size (Butler 1939; Dahlberg 1945; Townsend *et al*. 2009; Townsend and Brown 1981). The exception to this trend is the mandibular lateral incisor, which was identified as the mandibular incisor field's polar tooth by Dahlberg (1945) and Townsend *et al.* (2009). Dahlberg (1945) originally offered no supporting evidence for the change in identification of the polar tooth from Butler (1939); however, genetic studies conducted by Townsend *et al.* (2009) found a greater degree in stability of this tooth than the central incisor. Dahlberg (1945) added a fourth field to the theory, dividing the molar field into a premolar field as well. Several authors disagree with the addition of the premolar as a field, stating that the premolars are, in fact, an anterior extension of the molars (Irish and Turner 1991; Osborn 1978). The mandibular premolars are presented as supporting evidence for this idea, with the fourth premolar exhibiting a more molariform shape than the third premolar, which is the furthest from the polar tooth (the first molar) (Scott and Turner 1997). There is no consensus in the dental anthropological field whether there should be two divided fields for the posterior dentition or if there should be one molar field.

Use of Dentition in Ancestry Estimation

Dentition is a useful region of skeletal remains for ancestry estimation due to the preservation of the enamel, the degree of inheritance present, and the permanence of dental form with the development of the permanent dentition (excluding dental pathology). Limited studies, however, have been done on the use of dentition in forensic anthropology, with the exception of aging studies, with morphological analyses becoming increasingly researched within the past decade. Odontometric studies have largely been limited to sex estimation in forensic (Acharya and Mainali 2008; Cardoso 2010; İşcan and Kedici 2003; Karaman 2006; Zorba *et al*. 2011) and archaeological populations (İşcan 1989; Viciano *et* al. 2011; Viciano *et al*. 2013; Vodanovic *et* al. 2007).

Morphological

Morphological analyses are the primary modality of ancestry estimation using teeth in forensic anthropology. Dental morphology consists of variations of cusp ridges and grooves and root formations of a particular tooth (Scott and Turner 1997). Examination of these features contributes to analyses of population differences, temporal and geographic change, and biological distance analyses (Hanihara 2008; Irish and Turner 1990). The Arizona State University Dental Anthropology System (ASUDAS) is commonly used for scoring 27 standardized morphological traits (Turner *et al.* 1991). A limited number of the suite of traits analyzed by dental anthropologists to examine large-scale populations are utilized by forensic anthropologists in medicolegal contexts, primarily concentrating on shovel-shaped incisors, Carabelli's trait, cusp 7, canine mesial ridge, and occasionally multi-cusped premolars and molar complexity (Edgar 2009; Lasker and Lee 1957; Lease and Sciulli 2005; Marado and Campanacho 2013). Table 2.1 presents definitions explaining these utilized traits based on ASUDAS (Turner *et al.* 1991).

Dental morphological traits often focus on differentiation between Asian and European populations, with increasing notice on African dental traits. Lasker and Lee (1957) published a list of traits for use in medicolegal contexts, presenting an instrumental influence on ancestry estimation utilizing the dentition of an individual. They stated that shovel-shaped incisors were most common in "Mongoloids" (those of Asian ancestry) and Carabelli's trait was most common in "Whites" (those of European ancestry). In North America, shovel-shaped incisors are most commonly utilized for individuals of Native American or Hispanic ancestry (Edgar 2005). However, despite the traditional idea that Carabelli's trait tends to occur in higher frequencies in European populations and in the lowest frequencies in Asian populations, Marado and Campanacho (2013) and Edgar

(2005) found that the variation of Asian frequencies encompassed that of African populations and overlapped with various European populations.

Edgar (2002) examined the dentition of modern African Americans to determine if the genetic contribution of Western Europeans and Africans produced a dentition intermediate in morphology in African Americans. According to Edgar's results, African Americans' dentition changed dramatically from Africans and is reaching an expected intermediate between the West African and West European populations. African Americans are historically an admixed population of Europeans and Africans, and the resulting dentition is evident of this mixed genetic contribution. When determining forensic application by forming probability tables, eight traits were selected for ancestry estimation (tuberculum dentale of the upper canines, cusp variation of the lower third premolar, cusp variation of the lower fourth premolar, deflecting wrinkle of lower first molar, trigonid crest of lower first molar, mandibular cusp 5 of the lower second molar, mandibular molar cusp 6 of the lower third molar, and mandibular cusp 7 of the lower first molar) and found success in differentiating between African and European Americans. Disto-sagittal ridge and double shoveling occurred at low frequencies in Africans, African Americans, Europeans, and European Americans. The correct classification rate between these groups is up to 90% (Edgar 2002, 2005).

The combination of metric and morphological characteristics for the purpose of ancestry estimation, while becoming an increasingly popular methodology in practices of cranial ancestry estimation, has experienced some utility in dental studies. Lease and Sciulli (2005) investigated the efficacy of employing metric and morphological analyses of dental form for ancestry estimation of subadult remains. Their sample consisted of the deciduous dentition of European American and African American children, and data were collected on the mesiodistal dimensions of the mandibular canines and premolars and the presence of the cusp number of the maxillary third premolar (other morphological features were utilized only when attrition or caries prevented use of the premolar cusp number). Linear discriminant analyses provided a strong ability to correctly assign individuals to the correct ancestral group. Metric analyses identified 88% of the individuals, morphological analysis correctly identified 80.2-80.4%, and combination of these methods correctly allocated individuals 90.1-92.6%.

Odontometrics

Odontometrics is the mathematical study of tooth crown size and shape through measurements of various dimensions of the crown diameter and morphology (Harris and Rathbun 1989). Research has been widely conducted on the metric patterns between various geographic populations (Alvesalo and Tigerstedt 1974; Falk and Corruccini 1982; Hanihara and Ishida 2005; Harris and Bailit 1988; Koyoumdjisky-Kaye *et al*. 1976; Otuyemi and Noar 1996; Perzigian 1981; Townsend and Brown 1978). However, few studies have been strictly conducted on North American populations (Harris and Rathbun 1989; Moss *et al.* 1967), let alone modern United States populations, particularly in the medicolegal context.

Broad population differences in dental crown size and shape have been identified through odontometric analyses. For example, Australians, Melanesians, Sub-Saharan Africans, and Native Americans generally have the largest teeth, Asians have an intermediate size, and Western Europeans have the smallest teeth (Hanihara and Ishida 2005; Otuyemi and Noar 1996; Pilloud *et al.* 2014; Schmidt 2008; Shields *et al.* 1990). Hanihara and Ishida (2005) analyzed the mesiodistal and buccolingual dimensions of the dentition of 72 populations to understand the affinity between groups and the population differentiation that had taken place. Distinct differences in tooth crown diameter for the majority of the populations were present. Sub-Saharan and Australian dentition was very distinct from the rest of the populations examined. Results from Hanihara and Ishida's (2005) odontometric analyses were successfully able to differentiate between geographic populations as well as traditional genetic and craniometric techniques of population differentiation.

Pilloud *et al*. (2014) recorded both buccolingual and mesiodistal measurements of all teeth on both sides of the dental arcade in n=5631 individuals from several different regions of the world (broadly labeled as Africa, Asia, or Europe). A final sample of n=508 was used for the final analysis due to missing data for certain variables from the inability to take particular random measurements (all statistical treatments to correct this resulted in poor model performance). In this case, only individuals with complete dentition were used for these analyses. Discriminant function analyses were used to estimate classification accuracy, utilizing first the polar teeth of the morphogenetic field theory and then all available teeth measured. Discriminant function equations were produced separating males and females and utilizing a two-step analysis. Equations were first produced to distinguish African/Asian groups from European groups, and then a second set to distinguish between African and Asian. While broad geographic trends are noticeable from statistical analyses, the small sample sizes of European and African groups suggest that overfitting may occur. Knowing the sex of the individual produces significantly higher classification rates.

Koyoumdjisky-Kaye *et al.* (1976) investigated the differences between Kurdish and Yemenite Jewish populations to examine developmental conditions of children living in Israel. This study explored the mesiodistal and buccolingual dimensions and arch width and depth of n=197 children. The investigators found statistical significance with arch width and mesiodistal length of the maxillary central incisors and canines and the mandibular lateral incisors and canines between both populations. Otuyemi and Noar (1996) examined n=30 Nigerian children and n=30 Northern European individuals, finding that the mesiodistal crown diameters were generally larger in the Nigerian sample, whereas the only significant differences in the buccolingual dimensions were for the mandibular central incisors and the maxillary canines.

Variation in size of the occlusal surface of molars has also been investigated in regards to differentiation between broad populations. The occlusal polygon is shaped by producing linear measurements between the tips of the four cusps of the maxillary molar (Morris 1986). In the initial study of this metric analysis of morphological shape, Morris (1986) found a significant difference separating Papago from Bantu, Bushmen, Asiatic Indians, and Europeans in two of the four angles.

Few studies have been conducted on local populations in the United States, and those that have been done have primarily focused on African Americans and European Americans. Moss *et al*. (1967) analyzed the odontometrics of American Black and White populations. They found that the American Black population was an intermediate form of South African and European dentitions, indicating a hybrid state for American Blacks due to admixture of African and European populations. There were only occasional statistically significant differences between American Blacks and Whites, although those of African descent tended toward overall larger teeth. Harris and Rathbun (1989) explored the crown diameters of a 19th century South Carolina American Black population. Harris and Rathbun (1989) found a similar significant difference between American Black and White populations in terms of mesiodistal crown diameters and an increased amount in the posterior dentition of American Blacks compared to Asians and Europeans. As evident in these two studies of African American samples, admixed populations exhibit an increasing trend toward an intermediate state between the two parental populations (similar to the morphological intermediacy of dentition in the African American population as concluded by Edgar [2002]).

Several researchers express concern over the efficacy of odontometric analyses for population differentiation, particularly on the small-scale necessary for forensic purposes (Falk and Corrucini 1982; Hanihara and Ishida 2005; Harris 2003). Hanihara and Ishida (2005) recognized the conflict of the use of odontometrics in modern populations on a smaller evolutionary level; however, they do suggest its efficacy on a larger geographic scale. Less than 20% of the diversity in odontometrics occurs between populations, while the remaining percentage is variation within a geographic population (Hanihara and Ishida 2005). Falk and Corruccini (1982) also express concerns for the utility of odontometrics in ancestry estimation. Using a sample of 100 skulls, the authors compared craniometrics to odontometrics (including cervical measurements) in an attempt to separate five distinct populations: Whites, Blacks, Eskimos, Mongolians, and Amerindians. Craniometrics were found to be a better discriminator between the populations than odontometrics and cervical measurements of teeth were as efficient in assessing population affinity as traditional crown measurements. Harris (2003) found that ancestry and sex accounted for little variation in tooth crown dimensions, with 4.9% and 1.2%

effect, respectively. Harris (2003) argues that there is little utility for the use of odontometrics in identification protocols. Much like the results of Hanihara and Ishida (2005), the majority of variance is within a population rather than between populations (Harris 2003).

Geometric Morphometrics

The development of geometric morphometrics (GM) and its increasingly popular use in forensic anthropological analyses has produced an emerging body of research on ancestry estimation using this technology. For example, Kenyhercz *et al.* (2013) analyzed the utility of occlusal polygons of maxillary and mandibular first and second molars for ancestry estimation of n=109 American Whites and n=81 American Blacks. Classification rates ranged from 62.7% to 87.9%, depending upon the variables selected for stepwise discriminant function analysis. The maxillary second molar and mandibular first molar showed the least significant difference in size; however, they provided the most successful classification rates. The greater variability in size and shape of the Black sample’s molars may be due to the fact that they either had a longer temporal span to develop such large variation, or the history of admixture with the American White population may have introduced variation. The maxillary second molar was the most discriminatory tooth investigated.

Ancestry Estimation Research Regarding the Hispanic Population

Investigation of Hispanic populations has focused primarily on the morphological and metric aspects of the skeleton (Birkby *et al.* 2008; Hurst 2012; Jantz 2004; Rhine 1990; Slice and Ross 2004; Spradley *et al.* 2008), although a limited number of studies have been conducted toward morphological structures of the Hispanic dentition (Birkby *et al.* 2008; Edgar 2013). This research has concentrated primarily in the Southwest and Southeast United States, where the largest concentrations of Hispanic individuals live and are respectively characterized by varying genetic composition.

Cranial morphological traits are most frequently used in ancestry estimation of Hispanic individuals. Birkby *et al.* (2008) analyzed the efficiency of a group of traits used by the PCOME to identify Hispanic ancestry. The PCOME uses shoveled anterior teeth, anterior malar projection, a short posterior occipital shelf, a nasal sill that is relatively dull, an oval window visualization between zero and partial, enamel extensions on the molars, nasal overgrowth, a wide frontal process on the zygomatic bone, platymeria of the femur, and a sharp medial crest on the femur to identify Hispanics. Many of these traits are expressed in an intermediate form between Europeans and Native Americans. Some of the cases investigated by the PCOME have shown traits suggesting African ancestry, which is possible due to some of the Mexican population having a genetic contribution from African descendants. In these cases, it is difficult to determine if the expressed traits are from such contributions or if they are within the normal spectrum of morphological variability.

A follow-up study of Birkby *et al*.'s (2008) undertaken by Hurst (2012) examined the utility of the traits used by the PCOME to identify Hispanics. Six of the characteristics used were present in high frequencies in Hispanic populations (shoveling of anterior teeth, anterior malar projection, enamel extensions, dull nasal sill, wide frontal process of the zygomatic, and little to no oval window), while seven were useful in discrimination function analyses (the previous six traits and the occipital shelf). Of the traits presented by Birkby *et al*. (2008), nasal overgrowth, the short occipital shelf, and the frontal process of the zygomatic proved to be the least useful. The presented suite of traits to use for identification of Southwest Hispanics were: shoveled incisors, a moderate anterior malar projection, a blunt or guttered nasal sill, a partially visible oval window, enamel extensions on the molars, intermediate nasal spine, a medium nasal aperture width, and alveolar prognathism. There was much variation of these features in Southwest Hispanics, and many that had been claimed to be of a high frequency were found to not be in a significant portion of the population (for example, no nasal overgrowth and a short occipital shelf) (Hurst 2012).

Hefner (2014) analyzed the efficacy of multiple different statistical treatments of morphological traits in ancestry estimation of American Whites (n=193), Blacks (n=225), and Hispanics (n=125). In this study, artificial neural networks (ANNs), optimized summed scored attributes method (OSSA), support vector machines (SVM), random forest models (RFM), linear discriminant function analysis (LDFA), quadratic discriminant function analysis (QDFA), logistic regression (LR), decision tree (DT), K-nearest-neighbor analysis (kNN), and Kernel probability density (KPD) were used to analyze six morphological traits of the cranium: anterior nasal spine, inferior nasal aperture, interorbital breadth, nasal aperture width, nasal bone structure, and post-bregmatic depression. Of these statistical methods, ANNs, OSSA, SVM, and RFM had the highest classification rates, with at least 85% success. ANN had the highest rate at 87.8%. Every method except for KPD showed the highest success in classification for Blacks and the lowest success with Hispanic individuals; KPD was the most successful at identifying Hispanics.

Spradley *et al.* (2008) investigated multiple aspects of the biological profile for the Southwest Hispanic population using several craniometric variables and the platymeric index (PI). A stepwise discriminant function analysis selected 28 variables for use in differentiation. Using these variables Guatemalan Mayans, American Whites, and Hispanics were grouped together and separated from American Blacks. Hispanics were intermediate on the axis between Guatemalan Mayans and American Whites. The analysis only provided a classification of 45% of Hispanics into the correct ancestry group. When only Hispanics and American Whites were compared to each other, 81% of Hispanics were classified correctly. The PI for Hispanics did not show any tendency towards platymeria. While platymeria is often used in differentiation of American Whites and Native

Americans (Birkby *et al.* 2008; Wescott 2005), the utility of this morphological trait showed no significance between these two groups. In fact, Hispanics show less platymeria than Whites, rather than intermediate as would be expected.

An increasing trend in statistical treatments of combined metric and morphological investigations for ancestry estimation has developed in forensic anthropology. Jantz (2004) conducted a preliminary study on the utility of cranial morphological and metric traits in differentiating Mexican Americans from European and African Americans. Mexican American crania appeared to have smaller dimensions, shorter vaults, and narrower faces and orbits. Morphological traits position Mexican Americans between European, African, and Native Americans. Thompson and Boyd (2012) compared the use of metric versus morphological cranial traits in ancestry differentiation between n=14 Hispanics and n=36 American Whites and Blacks. Morphological traits presented a higher classification rate than metric comparisons in the Hispanic sample – 71-93% versus 29% (considering posterior probabilities increased the classification rate to 43%), respectively. Combination of both metric and morphological analyses produced an overall success rate of Hispanic individuals to 88%.

Geometric morphometric analysis of the palate for ancestry estimation has recently been investigated for medicolegal contexts. Maier *et al.* (2014) also investigated the use of palates for the purpose of ancestry estimation. Variables observed included palate shape curves and depth using crania from the PCOME, William M. Bass Donated Skeletal Collection, and the National Museum of

Natural History. It was concluded that palate shape was a useful indicator of ancestry, particularly when conducted through computer analyses. Admixture was concluded as a possible influencing variable for change in palate shape as Hispanic individuals tended to show the relative parabolic shape of Europeans. The overall accuracy for ancestry estimation was 58%, greater than chance, but not quite reaching the accepted standards of forensic practice. Kenyhercz *et al.* (2014) investigated n=287 crania using geometric morphometrics for the ancestry differentiation value of the maxillary palate. Using Generalized Procrustes analysis, the researchers found correct classification between 65.5-89.3% of the time, depending on the type of analysis and if Procrustes coordinates or their scores were used. Higher classification rates were found in this study than Maier *et al*. (2014), likely due to the addition of random forest modeling. Whites were classified correctly at 92.9%, Hispanics at 90.1%, and Blacks at 84.1% of cases. Blacks were usually misclassified as Hispanics, whereas Whites were usually misclassified as Hispanic. Hispanics had an intermediate morphology of the palate, with a slight jutting out of the maxilla and were misidentified as either of the two other groups.

One of the first studies specifically examining the morphology of Hispanic dentition (particularly from two different regions of the United States) for forensic purposes was conducted by Edgar (2013). A sample consisting of African Americans (AA), European Americans (EA), New Mexico Hispanics (NMH), and Southern Florida Hispanics (SFH) was examined to differentiate between these groups and also act as validation of traditionally used methods of identification. Formulae were developed for forensic case work that were useful in differentiation between AA/EA and NMH/SFH (66.7%-89.3%), and between AA and EA (71.4%-100.0%) but did not meet the same success in differentiating between NMH and SFH (46.2%-72.7%). This lack of success may be due to similar ancestral backgrounds for both populations. The success in differentiating AA/EA from NMH/SFH is largely due to the characteristics shared by Asians, Native Americans, and Hispanics that are not present in the AA/EA group. Both Hispanic populations originate from a common ancestry, and so identification based upon dental variation is difficult.

CHAPTER 3: Materials and Methods

Measurements were made on dental casts that are a part of the James K. Economides Orthodontic Collection held at the Maxwell Museum, University of New Mexico in Albuquerque, New Mexico (Edgar 2009; Komar and Grivas 2008). This collection was developed from a donation of orthodontic records from a retired orthodontist, Dr. James K. Economides, in Albuquerque, New Mexico, U.S.A. These casts were collected from 1972 to 1999 and were donated to the Museum in 2005. The collection consists of de-identified treatment histories, radiographs, cephalometrics, dental casts, and images and includes individuals of both sexes and multiple ancestries (2014). Access to dental care may affect utility of these variables on those with untreated crowding, malocclusion, and attrition; however, individual tooth dimensions may still prove useful for identification.

The benefit of this collection is the large sample of modern individuals representing a broad range of ancestries. Ancestry was determined in this collection by eight observers in the Laboratory of Human Osteology through examination of patient records for name, address, skin color, facial features, and hair type (Edgar *et al.* 2011). Patient name was the primary indicator for Asian and Hispanic Americans, while skin color was the predominant indicator for European Americans (Edgar *et al.* 2011). The majority of the Native Americans in the sample are Navajo and Zuni. Also represented are Puebloan Tribes from the Rio Grande region (Laguna, Acoma, Sandia, Isleta, and Okhay Owinge) and Jicarilla and Mescalero Apache, estimated by address information of the patients and data from insurance providers (Heather Edgar, pers. comm.).

A total of n=569 individuals were randomly selected for the analysis: n=161 Native Americans, n=202 New Mexico Hispanics, n=165 European Americans, n=43 Asian Americans. The parameters of the demographic sample are presented in Table 3.1. All Asian Americans available for analysis were examined (Edgar 2009). Asian Americans were selected as a comparative group representing close phenetic and genetic relationships.

Measurements were taken on the maxillary central incisors, the mandibular lateral incisors, canines, third premolars, and the first molars of both arcades of each individual using Mitutoyo digital calipers calibrated to 0.01 mm. Being the least variable teeth of the dentition in terms of morphological features (according to the morphogenetic field theory) may decrease the possibility of variable crown features that may interfere with standard measurements or that could produce increased variability that would interfere with results.

The following dimensions, as defined by Hillson *et al.* (2005), Morrees (1962), and Vodanovic *et al.* (2007) were collected:

Maximum mesiodistal crown diameter: the distance between two parallel planes; the most mesial and distal points of the crown.

Maximum buccolingual crown diameter: the distance between two parallel planes; perpendicular to the mesiodistal diameter the most lingual and buccal points of the crown.

Maximum buccolingual crown diameter (non-perpendicular): the most lingual and buccal points of the crown perpendicular to the occlusal surface.

Mesiodistal cervical diameter: maximum mesiodistal dimension parallel to the occlusal and perpendicular to the buccolingual dimension measured along the cervical part of the crown.

Buccolingual cervical diameter: maximum measurement from the buccal to the lingual surface along the cement-enamel junction; perpendicular to the mesiodistal diameter.

In addition, the dental arch width and depth and the proportions of each class of tooth with the overall size of the dentition (i.e., the relationship of the molars, premolars, canines, and incisors with the rest of the teeth) were examined. Arch width and depth were used as defined by Koyoumdjisky-Kaye *et al*. (1976) and Lindsten *et al*. (2002):

Arch width: measurements between analogues on each side of the dental arch.

Arch depth: the perpendicular distance from the most labial transverse lane of the central incisors to the most mesial transverse plane of the first molars.

The left side of the dental arcade was measured for the analysis with the right side used if the antimere on the left was missing or had too much attrition, calculus, or any pathological change, to produce an accurate measurement. Ectopic teeth were not measured for the present analysis, particularly as they would affect arch width between antimeres. All data regarding sex and ancestry were withheld during data collection to avoid bias.

Statistical Analysis

Data were computed in SPSS version 22 for multiple statistical treatments. Summary statistics were computed for all variables for both ancestry and sex, with mean measurements and standard deviations calculated. Also calculated were 95% confidence intervals for the measurements obtained.

One-way ANOVA analyses were computed for all measurements between all ancestries and then between individual pairs of ancestries (i.e., European Americans and Native Americans, Southwest Hispanics and Asian Americans, etc.). Sexual dimorphism for each variable was also investigated with all ancestries pooled together and between ancestries. ANOVAs were conducted in order to determine statistically significant variables for identification of ancestry and sex that may be used in discriminant function analyses. Results below $p=0.05$ indicated statistical significance.

Discriminant function analysis (DFA) was used to determine efficacy in allocating individuals to the correct ancestral group. Results presented are both the original and cross-validated classifications. Cross-validation DFA involves leaving out one individual and subsequently classifying that same individual against the rest of the sample as a method of cross-checking to provide a reliable function. Using a stepwise procedure produces the identification of variables with the highest ability to discriminate between populations and can then be subsequently utilized in further DFA testing. Wilk's Lambda enables the identification of those variables most discriminatory in the populations examined. Results presented include both independent and stepwise classification rates for comparison.

Discriminant function analysis was conducted on multiple combinations of variables and groups. Asian Americans were included in the analysis for comparison; however, due to the limited sample size of this population, analyses were also conducted excluding this population. Discriminant function analyses were run on all populations and between pairs of populations (i.e., European Americans and Native Americans, Southwest Hispanics and Asian Americans, etc.) to determine its efficacy as a tool of validation of other ancestry estimation methods. Discrimination function analysis was also utilized in estimating sex within populations to determine the impact of sex-specific identification to the overall analysis and to determine the degree of sexual dimorphism within each population. This is primarily to determine if there are particular population-specific requirements for this mode of analysis.

Due to missing data, a large portion of the sample was removed from the analysis in a stepwise DFA, reducing the overall sample size. Removal of non-statistically significant variables and variables with fewer than 80% of available data were excluded from the final analysis in order to utilize as much of the sample as possible and provide robust data.

Interobserver error was tested by three individuals, dividing analyses between crown, cervical, and arcade proportion measurements using the same type of caliper. Intraobserver error was tested by the same individual on the same 10% of the sample on all variables. Due to missing teeth and the inability to take particular measurements, there is an inequality in sample size for each Student’s t-test depending on the variable examined. Student’s t-tests were used to determine the significance of inter- and intraobserver error tests. Results with a p-value below p=0.05 indicated statistical significance and, therefore, a high rate of error.

CHAPTER 4: Results

Summary statistics including mean sizes, standard error, and 95% confidence intervals are presented in Tables 4.1-4.3. Table 4.1 presents the summary statistics of each ancestry with males and females pooled together, whereas Tables 4.2 and 4.3 present sex-specific information on males and females, respectively. The means were utilized to determine broad population differences and trends between the four studied populations. Due to missing data, the initial sample set of n=569 was reduced in SPSS. Various methods to account for these missing data have been attempted; however, all techniques reduced allocation rates, and so some individuals with missing data were removed from the analyses.

Due to the small sample size of Asian Americans compared to the other three populations, trends between the four populations are not easily identifiable. Consistently, with the exclusion of the Asian American population, European Americans had smaller measurements on average from Native Americans and Southwest Hispanics, with Hispanics being intermediate, and Native Americans having the largest.

Native Americans consistently displayed the largest means for all variables except for the buccolingual dimensions of the maxillary canine (Hispanics are equal in size), mandibular incisor (Hispanics have a greater mean), mandibular canine (Hispanic are larger), mandibular premolar (Hispanics are larger), the maxillary incisor composition (Hispanics are larger), the maxillary and mandibular arch depth (both European Americans and Hispanics are larger), and the mandibular molar arch width (Hispanics are larger).

Several variables were removed from DFA analysis due to inability to take measurements on dental casts or inefficiency in a medicolegal context. Cervical measurements were removed due to the lack of access to the cemento-enamel junction at the base of the dental crown and the high degree of interobserver error that occurred as a result of this problem. Also removed, though being statistically significant for each population, were the dental class composition variables. These variables were found to be impractical for forensic purposes, as the anterior dentition often shows severe winging, midline diastema, crowding, or ectopic eruption, and the posterior dentition often shows removal of teeth (i.e. premolar in dental cases of the molars due to dental care). Two types of measurements for the buccolingual dimension of maxillary molars were tested during this study, as biological anthropologists often differ in how they take these measurements (Hillson *et al.* 2005). Based on Wilks' lambda and error test results, Hillson and colleagues' (2005) definition of the buccolingual dimension indicating that the measurement must occur on the bulges of the crown and are not necessarily parallel to the occlusal surface is not used in DFA equations that involve dental crown size.

Ancestry Estimation

Multiple combinations of ancestry groups were analyzed using Univariate ANOVA to compare measurement between samples for statistical significance at the $p \leq 0.05$ level with ancestry as the independent variable and each measurement being the dependent variable. Results for these analyses, including the F-values and p-values, are depicted in Tables 4.4-4.8. In general, mesiodistal and buccolingual dimensions of the mandibular molar and maxillary premolars were consistently significant in all comparisons. The maxillary canine and mandibular incisor were not significant in only one analysis in the buccolingual dimension between Hispanics and Native Americans ($p = 0.932$ and $p=0.702$, respectively). Maxillary incisors did not show any significance between any ancestries. Of the 26 remaining variables examined out of the original 52 (the exclusion of cervical and dental field composition variables), 18 variables were significant between all four populations; 20 variables were significant between Hispanics, Native Americans, and European Americans; 14 were significant between Hispanics and Native Americans; 21 were significant between Hispanics and European Americans; and 19 were significant between Native Americans and European Americans.

Post-hoc Tukey-HSD analyses revealed Hispanics being more significantly different from European Americans with respect to most variables than Native Americans (Table 4.9). This significant difference differs from the rates produced from DFA analysis as discussed later; however, this may be a reflection of small sample size or the statistically significant variables between the two populations having less discrimination potential between European Americans and Hispanics compared to those variables significant between Native Americans and Hispanics.

Analyses were further conducted by both separating types of variables and combining them to determine the differential success rates of dental crown size and arcade proportions in the allocation of individuals into an ancestry group and the effect of pooling these two sets together. Classification rates were estimated using all variables dental crown size, all variables of arcade dimensions, combined total variables, statistically significant variables of dental crown size, statistically significant variables of arcade dimensions, and pooled statistically significant variables, as presented in Tables 4.10-4.20. These are divided between independent and stepwise analyses and include the overall cross-validated classification rate and the percentage of correctly identified individuals in every ancestry group. Table 4.12 exhibits classification rates produced when all crown and arcade proportion measurements are included, and Table 4.15 presents rates for only statistically significant variables. Tables 4.10 and 4.11 present classification rates developed for all respective variables (dental crown versus dental arcade); whereas Tables 4.13 and 4.14 present classification rates developed for only those variables of each type that were found to be statistically significant.

Initial analyses were performed on all available sample groups (Southwest Hispanics, Native Americans, European Americans, and Asian Americans) to determine efficacy of allocation of all four sample populations. Classification rates were consistently low, no matter the combination of variables and type of analysis. With stepwise analyses statistically significant arch dimension variables were the lowest at 42.1%, followed by all dental crown variables (45.5%), statistically significant dental crown dimensions (47.6%),all dimensions (50.3%),all statistically significant dimensions (50.9%), and all arch dimensions (51.7%). Independent analyses were lowest with statistically significant arch dimensions (47.5%), followed by all dental crown dimensions (52.3%), statistically significant dental crown dimensions (52.5%), all arch dimensions (53.2%), all statistically significant dimensions (56.9%), and all dimensions (59.5%). The breakdown of correct classification rates for each ancestry group is also visible in the tables. The highest classification rate for stepwise analyses (51.7%) is broken down into Southwest Hispanics at 53.1%, Native Americans at 64.3%, European Americans at 49.1%, and Asian Americans at 0.0%. The highest classification rate for independent analyses (59.5%) is broken down into Southwest Hispanics at 48.6%, Native Americans at 76.7%, European Americans at 63.3%, and Asian Americans at 0.0%.

Due to the small sample size of Asian Americans, this group was subsequently removed from the analysis to compare the populations of more equal size. This caused an increase in correct classification rate for both independent and stepwise analyses. Stepwise analyses were lowest with statistically significant dental crown dimensions (47.0%), followed by statistically significant arch dimensions (49.9%), all statistically significant dimensions (54.1%), all dental crown dimensions (54.2%), all dimensions (55.8%), and all arch dimensions (55.9%). Independent analyses were lowest with statistically significant arch dimensions at 50.3%, followed by statistically significant dental crown dimensions (55.7%), all arch dimensions (56.6%), all dental crown dimensions (57.6%), all dimensions (63.9%), and all statistically significant dimensions (66.2%). Analyzing the sets of variables with the most successful classification rates, the correct classification of each group is also visible. The highest classification rate for stepwise analyses (55.9%) is broken down to Southwest Hispanics at 55.9%, Native Americans at 63.9%, and European Americans at 46.9%. The highest classification rate for independent analyses (66.2%) is broken down into Southwest Hispanics at 50.0%, Native Americans at 78.6%, and European Americans at 67.6%.

Classification rates were also produced between pairs of ancestry groups in circumstances where anthropologists attempt to differentiate between two populations as a validation of an estimation approached by other techniques. Native Americans and European Americans represent the two most unrelated populations studied, and results of DFA analyses reflect the divide in genotypes between these populations. Stepwise analyses were lowest at 75.2% when only statistically significant dental crown variables were analyzed and highest at

83.3% when all dimensions were pooled. Independent analyses were least successful when only significant dental crown variables were utilized (75.4%) and were most successful when all dimensions were pooled (86.3%).

Hispanics and Native Americans were analyzed in a similar manner as those analyses including three or more populations. The lowest classification rates between these two populations were 61.2% in stepwise analyses when statistically significant arch dimensions were isolated and 61.1% in independent analyses when the same type of variables was used. The most successful classification rates were 74.4% in stepwise analyses when all dental crown dimensions were used and 78.2% in independent analyses when all dimensions were examined. Arch dimensions were the least successful discriminating variables between these two populations, suggesting that palate morphology is not as efficient an indicator as crown size.

The classification rates produced between Hispanics and European Americans exhibited the lowest success, particularly when dental crown dimensions were isolated. The lowest classification rates were 57.2% in stepwise analyses utilizing all dental crown variables and 59.5% in independent analyses utilizing the same type of variable. Classification rates were most efficient in stepwise analyses when all statistically significant dimensions were used (65.9%) and when all dimensions were pooled in independent analyses (70.8%). While dental crown variables appeared to be the least efficient discriminating variables between these two populations, dental arcade variables were not significantly more successful (62.6% for independent analyses and 62.4% for stepwise analyses when all arch dimensions were used). Hispanics and European Americans appear to exhibit greater phenotypic similarity to each other in both arcade and crown dimensions.

For most discriminant functions involving Native Americans, this group presented the highest rates of successful classification. The exception to this was the Hispanic population, which was successfully allocated at a considerably higher amount when dental arcade variables were isolated. As discussed below when examining important sex differences in allocation accuracies, this greater classification rate for the Hispanic population is not representative of a diagnostic trait of ancestry, but is a result of the general tendency of Hispanic, Native, and European American males to exhibit arch dimensions similar to the Hispanic mean. As the Hispanic population is characterized as this intermediate metric state, this population exhibits a successful; classification rate, but the other populations are more likely to be misclassified as Hispanic.

Figure 4.1 presents the separation of Hispanic, Native, and European American samples around their respective centroids when both dental crown and arcade variables are pooled into the analysis. While there is a general tendency of individuals to cluster around the centroid of their particular ancestry, certain exceptions and trends are evident. Native American cases have a greater degree of clustering around their respective centroid in comparison to the other two populations where smaller Hispanic individuals and larger European

American individuals present a great deal of overlap. This exhibits the lower rate of success in differentiation of Hispanic and European Americans and their tendency to misclassify as the other in the majority of incorrect classifications. Native Americans appear to exhibit the least variation in dental crown and arcade size dimensions, whereas European Americas display the most variation.

Discriminant function equations were developed to classify between ancestry groups, as presented in Table 4.22. These equations are an example of what could be utilized during a medicolegal investigation and should be used to estimate the ancestry of a sex-unknown individual. Equation 1a is used to differentiate between Native Americans, European Americans, and Hispanics. The following three equations are used to separate between ancestry pairs. An individual is able to be run through several of these equations to determine what the ancestry group of best fit is. For example, if an individual classifies as Native American in the original equation and in the equation differentiating Native Americans from European Americans, a validation equation differentiating between Hispanics and Native Americans may be conducted to determine ancestry. Based on classification rates presented above, this is still rudimentary and is not ready for forensic purposes; however, this provides an example of how these equations may be used.

Sex-Specific Estimation

Summary statistics are presented for males and females of each sample in Tables 4.2 and 4.3, including means, standard errors, and 95% confidence intervals. Males consistently exhibited larger means than females, indicative of sexual dimorphism that has been noted in the dentition. The means for all variables for the male sample were larger than the means for all female ancestry groups.

ANOVA were performed to determine statistically significant variables for each sample group and the degree to which these variables are sexually dimorphic, as can be seen in Tables 4.24-4.27 with associated F-values and p-values. The variables differ in degree of sexual dimorphism depending upon the observed population, with canines consistently being the most dimorphic teeth in the dentition, particularly the maxillary canines. The mandibular incisors consistently displayed little dimorphism except in the mesiodistal dimension for European Americans ($p<0.001$) and Native Americans ($p<0.003$). Of the 51 investigated variables, Hispanics displayed dimorphism in all but 10 variables (Table 4.24), Native Americans exhibited dimorphism in all but 12 variables (Table 4.25), and European Americans exhibited dimorphism in all but 10 variables (Table 4.26). The ANOVA results between Asian American males and females are also presented in Table 4.27, but they are not discussed at length due to the small sample size and resulting erratic means. The metric dimensions of the palate are the most sexually dimorphic in the European American sample, with all values p=0.49 or less with the exception of the maxillary premolar width at p=0.215. The Hispanic sample presents dimorphism in the maxillary canine (p=0.014), premolar (p=0.020), and molar (p=0.006), and the mandibular molar (p=0.001) widths. The Native American sample has the least amount of dimorphism in the palate, with the only significant variables being the molar widths, p=0.006 and p=0.001, respectively, and the maxillary arch depth (p=0.001). The composition for all tooth fields were also significant in every population, likely a reflection of the sex differences in the size of the teeth, resulting in proportional differences in their appearance in the dental arcades.

Due to differences present in male and female means for each variable and differential degrees of sexual dimorphism in each variable in all populations, classification rates were estimated for both independent and stepwise discriminant function equations for the same combination of populations as previously reported. As sex-specific ancestry estimation methods should be conducted when available, it is important to determine the effect of sex on the efficacy of odontometric analyses. DFA presented largely poor results, possibly as a result of small sample sizes. Analyses conducted on variables of statistical significance tended to be more successful at classifying males than using all variables in an analysis, whereas the opposite seems to be true of females. Females tended to have higher classification rates than males. For example, for independent analyses between Native Americans and European Americans, males were correctly classified 48.1% of the cases (56.3% - NA, 36.4% - EA) and females were correctly classified 83.0% of cases (89.3% - NA, 73.7% - EA).

The breakdown of male and female classification rates for each set reveals notable trends, as presented in Tables 4.16-4.20. Hispanics are the most correctly identified ancestry for males in all instances except when statistically significant variables alone are pooled in an independent analysis with more than two comparative ancestry populations (Table 4.15). Native American males are the second-most correctly identified ancestry for males in comparisons of more than two populations, while Europeans appear to have a higher allocation rate when compared in pairs.

Particularly low classification results were obtained with examination of the dental arcade variables. The overall classification rate for differentiating between Hispanics, Native Americans, and European Americans was 39.5%. Hispanics were correctly classified in 60.7% of cases, Native Americans in 7.7% of cases, and European Americans in 27.0% of cases. To better examine this high degree of misclassification, these three groups were plotted around their group centroids (Figures 4.6 and 4.7). Present is a large cluster of individuals around the Hispanic centroid, with the majority of Native Americans clustering around the Hispanic centroid, and European Americans only moderately distanced from the Hispanic centroid. When paying attention to the exact classification rates, it was observed that 88.5% of Native Americans and 67.6% of European Americans were misclassified as Hispanic. This strongly indicates a tendency towards intermediacy in European and Native Americans – an intermediacy reflected in the admixed Hispanic population.

Females do not present the same large degree of misclassification in dental arcade measurements as males, indicating a greater degree of separation. Figure 4.6 and 4.7 shows Hispanics, Native Americans, and European Americans plotted by their canonical discriminant functions around their group centroids. In this case, Hispanics present a large degree of variability, with an almost equal number of cases clustering around the European American centroid as the Native American centroid and tighter clustering of the latter two groups around their respective centroids. European Americans were misclassified 38.1% of the cases as Hispanic, indicating variability in palate shape, while Native Americans were correctly classified in 84.3% of cases, indicating little variability. Hispanics, however, were correctly classified in only 40.0% of cases, showing more misclassifications than correct classifications. Hispanics were almost equally misclassified as European American as they were Native American, with rates of 28.0% to 32.0%, respectively.

These dramatic differences between males and females in arcade dimensions do not appear to be as strong in dental crown dimensions. While similar trends in classification rates occur (Hispanic males are classified correctly more often than Native American males and Native American females are classified correctly more often than Hispanic males), the occurrences of misclassification are much lower. For example, the classification rate males is

68.8%, with Hispanics correctly classified in 78.6% of cases and Native Americans correctly classified in 55.0% of cases. The classification rate of females is 70.4%, with Hispanics correctly classified in 52.6% of cases and Native Americans classified correctly in 80.0% of cases. Dental crown dimensions appear to show more distinct trends based on ancestry and less sex-related impact as palate metrics.

Figures 4.2 and 4.3 present cluster patterns of females and males of Southwest Hispanics, Native Americans, and European Americans, respectively. These figures present increased separation of cases based on ancestry, although clustering around the centroid is stronger in the case of females over males. This greater degree of clustering correlates with the general higher classification rate of females compared to males, as discussed below. Despite the decrease in mixture of cases, classification rates appear to be lower when separating sex as a variable, urging further research to clarify the reason for this. Classification rates remained the highest when differentiating between Native Americans and European Americans and lowest when differentiating between all four sample populations.

In order to investigate the success rate of differentiating an individual into the correct ancestry group and sex, females were subsequently coded into different numbers for DFA, essentially acting as three separate ancestries. Results of these can be found in Table 4. Figure 4.8 presents the cluster of individuals around their respective centroids. As noted in the figure, females consistently exhibited smaller measurements and are associated with males of the same ancestry. Overlap between each group does occur, particularly between Hispanics and European Americans; however, definite clustering is observable. Hispanic and European American males show the greatest degree of overlap, with their respective group centroids the closest to each other.

Also, in order to investigate the impact of sex on the efficacy of this method, DFA in order to correctly classify sex were conducted, with results presented in Table 4.29. Particularly significant is the 62.6% classification rate with inclusion of only dental crown dimensions when differentiating between males and females with pooled Native American, Hispanic, and European American samples. Females were correctly allocated in 70.1% of cases and males correctly classified in 53.2% of cases. With only dental arcade variables, sex was correctly identified in 68.9% of cases (56.5% - males; 78.4% females). Inclusion of all variables produced a classification rate of 70.4% (males 60.9% and females at 77.4%).

DFA were conducted on specific populations, as well, to gain an idea on individual population sex estimation rates. Hispanics were correctly classified by sex in 80.0 % of cases when all dimensions were observed (90.0% for males, 66.7% for females), 57.4% when all crown dimensions were observed (64.3% for males, 47.4% for females), and 55.0% when all arch dimensions were observed (70.5% for males and 36.0% for females). Native Americans were correctly identified in 65.1% of cases when all dimensions were observed (46.7% for males, 75.0% for females), 69.1% for all crown dimensions (60.0% for males, 74.3% for females), and 75.0% when all arch dimensions are observed (38.5% for males, and 88.6% for females). European Americans were correctly identified in 73.3% of cases when all dimensions were observed (72.7% for males, 73.7% for females), 62.2% for all crown dimensions (42.9% for males, 73.9% for females), and 53.2% for all arch dimensions (51.4% for males, 54.8% for females).

Observer Error

Intraobserver Error

To test the replicability of each measurement, both inter-and intraobserver error Student t-tests were conducted on approximately 10% of the sample. Due to inability to take particular measurements (e.g. missing teeth, attrition, pathological changes, etc.), actual sample sizes varied between each measurement. Results of these tests are presented in Table 4.34. The majority of statistically significant measures consisted of the buccolingual dimensions (mandibular incisor at p=0.009, premolar at p=.000, and molar at p=.010), a similar trend found in interobserver error tests. Measures of this type depend upon Type II landmarks in which the maximum point of curvature are used as defining points of measurement. As a result, these measurements were the most difficult to take, unlike the mesiodistal dimensions, where oftentimes the maximum points are also the points of contact with occluding teeth and so provide a secondary visual cue for landmark identification. Fluctuating sample sizes also affect the p-value for the conducted error tests. However, most variables were not statistically significant and show general replicability.

Interobserver Error

Results of these tests are presented in Tables 4.30-4.33. Five dental crown measurements were statistically significant: maxillary incisor mesiodistal (p=0.012), maxillary molar buccolingual (p=0.002) and mesiodistal (p=0.011), mandibular incisor buccolingual (p=0.000), and mandibular canine buccolingual (p=0.035) dimensions. Three out of the five measurements were buccolingual dimensions, possibly due to the difficulty in efficiently observing the maximum point on the bulges of the crowns. Hillson *et al.*'s (2005) interpretation of the buccolingual dimension of the molar was found to experience a high rate of error in both inter- and intraobserver error tests and the Wilks' lambda for equations was low, eliminating the variable for all analyses. Dental crown variables had moderate error but exhibited the highest amount of agreement and the most efficient variables to take. Error largely occurred due to a few cases of great distance between the present researcher's measurements and the tester's measurements rather than a common trend among all measurements. The rotation of the maxillary molar and fluctuating shape and size likely resulted in difficulty in taking the mesiodistal dimension, as often the dental cast would need to be rotated and careful projection of a perpendicular line to the mesial portion of the dental arcade would be necessary to compensate for the less clear orientation of this tooth. The casting of soft tissue in the sample may have also increased difficulty in taking measurements of the anterior dentition, as gum cover is often variable in this region and so obscures the maximum lingual point and cingulum. Past studies have suggested particular difficulty with buccolingual measurements of the anterior dentition (Acharya and Mainali 2007; Acharya and Mainali 2008; İşcan and Kedici 2003; Karaman 2006).

In general, the highest amount of error occurred in the arch and cervical measurements both of which are not typical measurements initially learned by students and may require further training and experience. Difficulties also occur with greater distance and indistinct landmarks (i.e., arch width at the molar where the distance is large compared to the other variables and landmarks are the center of the most mesiolingual cusp). This particular problem may be exacerbated with increased attrition. Statistically significant measures of the dental arcade exhibit a pattern of wider distance measurements (posterior dentition distance compared to closer anterior dentition) and an indistinct cranial landmark, alveolon. Cervical measurements are also particularly difficult to take on dental casts, as highlighted by these error tests and were not used in these analyses.

CHAPTER 5: Discussion

Broad population differences in odontometric and dental arcade size were identified, with European Americans tending toward the smallest teeth, Native Americans with the largest, and Southwest Hispanics with an intermediate size. Hispanics, however, often showed larger buccolingual dimensions of the mandibular dentition than Native Americans. Asian Americans present more randomness in dental size, lacking any distinct pattern or trend, but this may be a result of the considerably smaller sample size in comparison to the other three populations. European Americans consistently presented the narrowest mandibular and maxillary palates, with Native Americans tending towards the widest. These results are comparable to traditional analyses of dental palate morphology (Rhine 1990). Southwest Hispanics exhibited the largest mean arch depth in the maxillary palate, whereas European Americans had the largest mean depth for the mandibular palate. These mean differences corroborate with the observations made by several researchers where Hispanic skeletal features tend to reflect an intermediate morphology and metric state between Native Americans and Europeans, supporting the conclusion that the dentition is a similar proxy and reflects the genotypic history of the Southwest Hispanic population similarly to the skeleton.

Males consistently exhibited larger metrics than females as generally expected due to robusticity, with males and females individually following the same ancestry trends as previously discussed. The observation proposed by Spradley *et al.* (2008) concerning the gracile nature of Hispanic male skeletons does not appear to be true of their dentition, with Hispanic male means consistently higher than the female means of all ancestry groups, particularly of European females. This is not to say that overlap and variation does not exist; however, in general, Hispanic male dentition and arcade proportions are generally larger than respective female measurements in all sample populations.

Based on these results, tooth size exhibited particular patterns regarding ancestry and sex, individually impacting expression of dental size and accuracy rates. These results clearly showed a sex impact on how size and palate morphology was differentiated between populations; however, ancestry differentiation was reduced when congruent ancestry and sex estimation was attempted rather than attempting both estimations separately.

Ancestry Estimation

Concerning the first hypothesis of the present research, comparisons of the four examined populations exhibit intermediacy of Southwest Hispanics in mean size between Native Americans and European Americans and statistical significance in many dimensions. The admixture histories of the examined Hispanic sample population are identifiable in the size of the dentition and the dental arcade similarly to dental morphology and skeletal metrics and morphology (Birkby *et al.* 2008; Edgar 2013; Hurst 2012; Spradley *et al.* 2008)

Discriminant function analyses conducted to determine the degree of separation between these groups reveal clustering of these populations around their respective centroids, correct allocation at a rate higher than chance, and a greater difference between Native Americans and Hispanics rather than Hispanics and European Americans.

ANOVA results presented important differences between populations, with variable significance between measurements at the $p \leq 0.05$ level (Tables 4.4-4.8). Canines, the mandibular incisors, and the posterior dentition of both arcades consistently appeared as significant indicators of ancestry in all sets of populations. The maxillary incisor in any dimension did not present statistical significance in differentiation between populations. In fact, it exhibited the least amount of significance of any dimension or tooth in each analysis that it was included. The most significant measurements tended to be those of the mesiodistal dimension. These measurements have also exhibited high utility in sex estimation investigations compared to buccolingual dimensions (Acharya and Mainali 2007, 2008; Townsend and Brown 1979), and the results presented here also suggest their higher ancestry indication ability compared to buccolingual dimensions. However, much like Acharya and Mainali (2008), mesiodistal dimensions alone should not be depended upon.

Examining the degree of misclassifications between Hispanics, Native Americans, and European Americans reveals a particular trend expected when studying an admixed population. When including all variables of the dental crown and arcade, correct classifications are 54.3% for Hispanics, 76.7% for Native Americans, and 56.7% for European Americans. Hispanics are misclassified as Native American in 22.9% of cases and as European American in 22.9% of cases. This shows an even misidentification split between the two parental populations due to similar phenotypic qualities of both to the Hispanic population. Hispanic males are misclassified as European American males in 30.0% of cases and as Native American at almost the same rate (20.0% of cases). Hispanic females are most often misclassified as Native American females (40.0% of cases) but, again, are almost as often misclassified as European American (33.3% of cases). When breaking down classifications by sex, it is apparent that the similarity between sexes of different populations helps to explain the high degree of misclassification in the initial analysis.

In the same example, Native Americans are most often misclassified as Hispanic (20.9% of cases), and European Americans are also most often misclassified as Hispanic (40.0%). The two parental populations on either end of the size spectrum, when misclassified, are most likely to be classified into the intermediate-sized population. This is to be expected, as European Americans and Native Americans represent the two ends of the spectrum. Larger-than-average Native Americans will still be classified as Native American and smaller-than-average European Americans will still be classified as European American. The opposite of these instances will cause these individuals to be classified as Hispanic. Both Native American and European American males are most often misclassified as Hispanic, in 20.0% and 45.5% of cases, respectively. The same is not true of females. Native American females are most often misclassified as Hispanic (26.7% of cases); however, 26.3% of European American females are misclassified as Native American compared to 15.8% of cases misclassified as Hispanic. The general pattern, however, is that misclassifications of Hispanics will be relatively even between European and Native Americans, and misclassifications of Native Americans and European Americans will generally be as Hispanic.

Dental crown dimensions were more successful in allocation of ancestry groups only in differentiation between Southwest Hispanics, Native Americans, and European Americans (57.6% versus 56.6%). Arcade dimensions, particularly arch width, are more distinct between these groups rather than dental crown size, although these differences in allocation rates were minimal, with only one rate 0.9% more successful than the respective rate produced by dental crown variables (Southwest Hispanics and European Americans at 59.5% versus 62.6%). Arch depth, however, never presented statistical significance in any ancestry comparisons and were lowest between Southwest Hispanics and European Americans (maxillary p=0.605; mandibular p=0.808). These results suggest that while the curvature of the palates appears to be significantly different between populations, the length of the palate is a poor indicator. Maxillary incisor width (p=0.133), maxillary molar width (p=0.888), and mandibular molar width (p=0.248) presented little significance in differentiating between Hispanic and Native Americans, suggesting that the morphology of the palate is not as useful an indicator between these two populations as it is between Hispanics and European Americans. Southwest Hispanics were more successfully differentiated from Native Americans than European Americans by dental arcade shape, suggesting palate morphology more similar to European. This finding is similar to results obtained by Maier *et al*. (2014), who used geometric morphometrics on African American, Southwest Hispanics, and European American palates to estimate ancestry. Maier and colleagues (2014) found their Hispanic sample to have a parabolic shape similar to Europeans.

In general, independent discriminant function analyses and the inclusion of all variables performed more efficiently than conducting stepwise analyses and focusing on statistically significant variables. However, these differences are minor and suggest that in a given situation where limited variables are available for use, stepwise analyses may be conducted with caution. Also, as can be seen in Tables 4.10-4.12, inclusion of all measured variables rather than only statistically significant variables resulted in a generally higher classification rate, except when analyzing all ancestry groups. This difference, however, is minor. Most significant is the fact that when all variables are included in the analysis, the success rate increases from 66.7%-72.5% to 75.6%-78.2% between Southwest Hispanics and Native Americans, encouraging measurement of all available variables rather than selecting only a few. Stepwise discriminant functions do exhibit utility, though not reaching as much success as independent variable analyses. However, these results suggest that when few variables are available for measurement, identification may be possible between Native and European Americans and between Native Americans and Southwest Hispanics.

Allocation of all four sample populations was limited in its success, with the lowest classification rate being 52.3% when only dental crown variables are examined. In the majority of tests, Asian Americans were always misclassified, suggesting the sample size was either too small in comparison, or the population exhibit measurements too similar to other populations investigated. There was only a slight increase when Asian Americans were removed from the analysis. Hispanics consistently increased in successful allocation in these cases, suggesting the possibility that Asian Americans were frequently misclassified as Hispanic.

Equations developed by DFA allocate individuals into ancestral groups most successfully between Native Americans and European Americans. This is not surprising, as these two groups are less genotypically similar to each other than they are to Southwest Hispanics or Asian Americans. The classification rates found between these two populations are comparable to those of Pilloud *et al.* (2014). As Native Americans were placed in the Asian category in their study, the classification rate in the present study between European and Native Americans is comparable, despite use of only polar teeth compared to all of the teeth on the left side. Pilloud *et al.* (2014) had a success rate of 87.4%

compared to 83.7% in the present research when only dental crown variables are examined.

As indicated by Birkby *et al*. (2008), Bryc *et al.* (2010), and Hurst (2012), Southwest Hispanic genotypes are primarily a European impact on Native American genotypes, meaning that Native American genes predominate. Differentiation between Hispanics and European Americans were consistently less successful than allocation between Hispanics and Native Americans, despite previous studies indicating that this population likely exhibits greater contributions of Native American genotypes. These results suggest that while a significant portion of the Hispanic population exhibit intermediate measurements between Native and European Americans, a large number are phenotypically similar to the European American population. This pattern may not be representative of the Hispanic population as a whole. Different regions and populations have experienced different admixture histories and may self-report their ancestry differently, and so this pattern should not be applied universally to all Hispanic individuals. This is surprising as fewer variables were significant between Native Americans and Hispanics than between European Americans and Hispanics.

Several studies have found a similar greater phenotypic similarity to Europeans in Hispanic populations. Hughes *et al.* (2013) investigated the patterns of admixture in Mexico using craniometrics and found that the proportion of European alleles increases from south to north and Native American ancestry increases from north to south. This similarity to modern European Americans in dental size has also been found with dental morphological trait frequencies of the Hispanic population. As discussed by Willermet and Edgar (2009), New Mexican Hispanics presented dental morphological characteristics at frequencies and degrees more similar to early Native Americans compared to modern Native Americans, suggesting that admixture largely occurred in the past and greatly reduced as time progressed. Essentially, the introduction of new Native American genes quickly diminished after initial contact, resulting in a disparity between modern Native American populations and Hispanics. The sample of Albuquerque, New Mexico Hispanics investigated in the study exhibited a greater percentage of European genes than Native American. The metrics of the present analysis agree with this determination. Such differences may not be applicable to other Hispanic populations and should be investigated accordingly. Lower classification rates than between Native and European Americans were to be expected due to their intermediate size between the parental populations and as Hispanics often phenotypically tend towards one ancestral group or another (Birkby *et al.* 2008).

Results presented in this analysis suggest a possibility in inclusion for biological profile analyses, although more research must be done in this area before full utilization can be achieved. When examining stepwise analyses and the strong classification rates produced by the examination of just three variables, this provides strong motivation to promote odontometric analyses in forensic investigations and archaeological analyses.

Sex-Specific Estimation

Regarding the second hypothesis of the present research, while important population-specific sex differences were identified, known sex produced an adverse effect on successful allocation. Multiple ANOVA and summary statistics conducted on each population between males and females displayed differential variables of statistical significance for sexual dimorphism (Tables 4.24 - 4.27). Southwest Hispanics and European Americans displayed the greatest degree of dimorphism in dental crown dimensions. Hispanic males have been reported to be often misclassified as female due to the gracile nature of their skeletal elements (Spradley *et al.* 2008); however, dimorphic characteristics within the population appear to be high compared to the other populations. The gracile nature of the Hispanic skeleton may not be reflected in the size of the dentition, as the average size for males and females for each dimension were larger than those of European Americans. Asian Americans displayed the lowest degree of sexual dimorphism; however, this population also represents a small sample size, so these results must be approached with caution.

Maxillary canines appear to be the most sexually dimorphic in all populations, with both buccolingual and mesiodistal measurements statistically significant in Southwest Hispanics and Native Americans, and only the mesiodistal measurement significant in European Americans. These results corroborate with those of other odontometric studies where canines are the most dimorphic teeth in the dentition (Hillson 1996; Saunders *et al.* 2007; Viciano *et al.*

2011). Mandibular incisors, however, appear to be the least sexually dimorphic, presenting statistical significance only in the mesiodistal dimension in European and Native Americans and no significance in any dimension in Southwest Hispanics and Asian Americans. Hispanic males and Native American females were the most correctly identified groups.

As sex appeared to increase classification results slightly in some initial statistical analyses, males and females were separated for individual investigation; however, identification of ancestry on a known-sex individual produced a lower classification rate. This adverse effect of known-sex may be partially due to small sample sizes, particular significant variables that were not included in the analysis, noise, or a combination of these factors and/or others. The Native American sample, for example, had a large disparity in males and females, and due to the problem of missing data, this disparity was further exaggerated and may have negatively affected classification.

An example of differential variable selection comes from the maxillary incisor, which is significant between males and females in the Hispanic sample, with the buccolingual dimension $p=0.01$ and the mesiodistal dimension at $p=0.18$. However, as these dimensions were not presented as good indicators of ancestry differences, they were not included in the sex-specific DFA analyses. While significant overlap between populations was also thought to be a possibility for this decrease in successful allocation, Figures 4.2 and 4.3 present the clustering of individuals around respective centroids based upon ancestry when sex is known, indicating that there should be increased success with sex-known individuals. Further research and larger sample sizes should be conducted to investigate the unexpected decrease in success when sex is known. In general, however, females were classified correctly more often than males, a trend also found by Pilloud *et al.* (2014). This is likely due to lower variance in measurements.

Dental arch dimensions present a separate pattern from the general decrease in efficiency when sex is known. Tables 4.14 and 4.17 exhibit an increase in classification of females compared to sex-unknown classifications in ancestry pair analyses. The Hispanic-Native American rate increases from 69.5% to 81.3%, and the Native American-European American rate increases from 81.1% to 82.1% in females. Females also exhibited a different pattern with stepwise analyses when all variables are utilized with the same ancestry pairs, as can be seen in Tables 4.12 and 4.18. The Hispanic-Native American rate increases from 70.0% to 77.5%, and the Hispanic-European American rate increases from 62.7% to 69.7%. Females again exhibited an increase in successful classification with stepwise analyses in the Native American-European American (78.3 to 83.1%) and Hispanic-European American (57.2% to 60.8%) rates. Males exhibited an increase in successful allocation when all ancestries were included in an independent analysis (52.7% to 53.6%) and Hispanics-Native Americans-European Americans (57.6% to 58.1%); however, these increases are by less than one percent and not as significant of an increase in the case of female classification rates.

Sex differences were found in the expression of dental arcade size, with males exhibiting greater variation within an ancestry group and females exhibiting greater variation between ancestry groups. Males exhibited greater variation based on sex rather than ancestry and a tendency towards the intermediate size of the Hispanic population. An example of this is the classification rates of Hispanics, Native Americans, and European Americans when examining only dental arcade dimensions. Hispanics are correctly classified in 60.7% of cases with misclassifications of 14.8% as Native American and 24.6% as European American. Native Americans, however, are correctly classified in only 7.7% of cases, with a large misclassification rate as Hispanic in 88.5% of cases and European American in 3.8% of cases. European Americans also reveal a higher tendency to misclassified as Hispanic in 67.6% of cases rather than be correctly classified as European American (27.0%). Native Americans and European Americans appear to have a tendency towards this intermediate size that overlaps significantly with Hispanics, causing an overclassification of Hispanic individuals. Females do not exhibit this pattern and appear to be concentrate around their respective ancestry centroids more distinctively.

This pattern in dental arcade variables is not as significant regarding isolated dental crown variables. These variables appear to have distinct ancestry and sex trends, with little difference between males and females (although females do appear to also have less variation in dental size). As shown in Figures 4.5 and 4.6, aside from the occasional case of outliers, individuals are markedly separated based on ancestry as compared to dental arcade variables (Figures 4.7 and 4.8). Hispanic and European American males exhibit a distinct overlap in cases, unsurprising considering their phenetic similarity and resulting low classification rate (Figures 4.4, 4.6, and 4.8).

The reason for these different patterns between dental crown dimensions and metrics of the dental arcade may be a reflection of what structures comprise these variables. The crown of the tooth is composed of enamel that is arranged in interlocked prisms and dentine that is composed of odontoblasts arranged in tubules (Hillson 1996). Bone, however, has three basic types of cells (osteocytes, osteoblasts, and osteoclasts) are arranged in Haversian systems in compact bone and is comprised of a dense cortical bone and a light trabecular bone (White and Folkens 2005). These differences result in two different structures and developmental processes that may affect ancestry or sex-related genetic influences. These two different components of the body have different developmental structures and patterns, genetic influences, and experience different levels of environmental influence. Therefore, the sexually dimorphic expression of the dental arcade variables (measure of skeletal structure) presents different trends than those of the dental crown variables (measures of tooth structure).

Due to the large amount of variation in dental size within a population compared to the narrow amount of growth and size teeth are able to develop, it is likely that significant overlap appears between populations. Sex estimation studies utilizing odontometrics have largely investigated one or two broad geographic populations. The presence of three related populations in this study presents lower sex discrimination potential than other previous studies (Pilloud *et al.* 2014), as these populations exhibit similar degrees of dimorphism and metric expression. Further investigation into the potential for sex estimation for each separate population would be valuable. As sex-specific patterns are noticeable in each ancestry assessment analysis and each population presents its own degree of dimorphism in dental crown and arcade dimensions it is likely that sex assessment utilizing the dentition would benefit from population-specific methods.

Results reveal a great deal of overlap between ancestries when sex is accounted for, causing an overestimation of Hispanic ancestry. However, while sex is most often incorrectly determined when attempting to classify an individual’s ancestry and sex, the individual’s ancestry is correctly identified between 66.7% and 86.7%, depending upon the ancestry and sex of the individual. This suggests that while males and females of each ancestry cluster around their particular centroids, when misclassified, males are likely to be misclassified as females of the same ancestry and vice versa.

Analysis of these populations as a sex-independent technique has potential a tool of ancestry estimation. Odontometrics, arcade dimensions, and both types of measurements pooled together perform relatively well for assessment between particular set of populations, ranging from 75.4% to 86.3% when analyzing European and Native Americans, showing significant promise when distinguishing between broad geographic populations. With a classification rate of 78.3% when all variables are included in the analysis, differentiation between Southwest Hispanics and Native Americans suggests differentiation between admixed populations may be possible with measurements of the dental crown and arcade. The range of success in correct allocation of Southwest Hispanics from European Americans (59.5% - 72.3%) fits partially within the range of success found by Edgar (2013), 66.7% - 89.3%, when using dental morphological traits to distinguish African or European Americans from Hispanics.

When an individual underwent congruent ancestry-sex estimations (individuals were forced into an ancestry-sex pair rather than simply ancestry or sex), the majority of individuals were correctly classified into ancestry but not into sex. As shown in Table 4.28, correct ancestry classification occurred as follows: Native American males – 86.7%; Native American females – 67.9%; Hispanic males – 70.0%; and Hispanic females – 66.7%. This shows a tendency for individuals to be correctly classified into ancestry when sex is unknown. This is likely due to the greater amount of variation accounted for when examining broad ancestry variation rather than the smaller groups and variation limits constructed by six individual groups. Oftentimes, the individual was classified as the next smallest or largest group. For example, if a Hispanic male was smaller than the average male mean, rather than be classified as a Hispanic female, the individual may be classed as a European male. Estimation of ancestry with sex unknown allowed for a greater degree of correct ancestry allocation. Therefore, the results indicate that sex should not be accounted for when estimating ancestry, but may be estimated separately.

Overall, metric distinctions were visible between ancestral groups when sex was not known. These distinctions were most prominent between ancestries of comparatively little genetic similarity (European vs. Native American) and least evident between European Americans and Hispanics. When sex was simultaneously estimated with ancestry, correct classification rates were severely reduced due to particular sex differences in types of variables. For example, dental arcade measurements for males tended towards an intermediate measurement characteristic of the Hispanic male centroid, compared to a greater degree of distinction between females of the same ancestral populations. Males display less variation between populations but greater variation within a population, while females display a greater degree of variation between populations and a greater degree of uniformity within a population. The reason for this is unknown and requires further investigation of dental metrics and morphology in conjunction with dental genetic and development research.

The results presented in the previous chapter are similar to the findings in other studies (Edgar 2013; Kenyhercz *et al.* 2014; Maier *et al.* 2014; Pilloud *et al.* 2014; Spradley *et al.* 2008); however, the lack of a comparative African American sample in the present analysis deviates from the majority of studies that have examined Hispanic populations. However, certain similarities are observable, and classification rates are similar to those studies previously published. For instance, overall correct classification of all populations was not as successful as those finding of Pilloud *et al.* (2014), who found success in 71.3% of cases when sex was not known. The authors utilized an African sample population and examined more teeth in the dentition.

The classification rates obtained using isolated dental arcade variables are comparable to those found by Maier *et al*. (2014), who found successful allocation in 58.0% of cases. The primary difference between these studies, however, is that Maier and colleagues (2014) utilized geometric morphometrics and had a Black sample opposed to a Native American sample. Kenyhercz *et al*. (2014) found correct classification in approximately 87.0% of all cases, with Hispanics correctly classified in 90.1% of cases using random forest modeling. Alternative statistical treatments, differing sample populations, and the use of geometric morphometrics could contribute to the classification rate differences between the present study and Maier *et al.* (2014) and Kenyhercz *et al.* (2014).

The majority of studies find difficulty in correct allocation when including the Hispanic population due to the varying genetic admixture histories of the populations (Bertoni *et al.* 2003; Bryc *et al.* 2010; Edgar 2013; Hefner and Ousley 2014; Klimentidis 2009; Spradley *et al.* 2008). This is due in part to the general admixed nature of the population, but also to the large degree in variation of the levels of admixture depending on region and even on the individual case. It is unwise to lump Hispanics into either an European or Native American category for medicolegal purposes due to its nature as an "ethnic" label and the genetic composition of the population. Therefore, if a technique is to be successful in identifying ancestry, it must be able to successfully estimate those of Hispanic ancestry as a separate entity. Current practices of estimating three broad geographical populations forces forensic anthropologists to dismiss the Hispanic population as a category or lump Hispanics into either an Asian or European category.

Successful differentiation between European Americans, Native Americans, and Hispanics was more successful than allocation rates found by Spradley *et al.* (2008) when all sample populations were compared to each other. Utilizing DFA, successful allocation occurred in only 45% of Hispanic cases, as compared to the lowest classification rate in the present study, 46.8% (statistically significant arch dimensions). However, successful allocation between European Americans and Hispanics only, has a lower success rate than that found by Spradley *et al.* (2008), with a maximum successful classification of 64.9% and 78.3%, respectively, versus 81.0% and 87.0%.

Hefner *et al.* (2014) found the lowest classification rate with the Hispanic population when using DFA to allocate American Whites, Blacks, and Hispanics. Hefner *et al.* (2014), however, found greater success in classification using morphoscopic traits of the cranium with an overall classification rate with 75.0% in independent analyses and 78.0% in stepwise analyses, with Hispanics correctly classified in 72.0% and 73.9% of all cases, respectively. Results are also not as high as those found by Edgar (2013), who investigated dental morphological traits between African, European, and Hispanic Americans and found successful allocation in 66.7% to 89.3% of cases.

The results presented here should not be applied to populations outside of the United States, particularly as those populations selected for analysis were chosen to represent closely related groups on a regional scale. The results for the selected Hispanic population should also not be utilized on Caribbean Hispanic populations, as well, as genetic studies have shown that population to be comprised of a higher African allele contribution. The results of this study show the importance of developing standards for the Hispanic population which displays varying admixture histories. Due to this variation in genetic contributions, it is important to not group this significant demographic population into either European or Asian-derived populations. The results of the present research suggest that the dentition of the Hispanic population presents similar trends to skeletal morphological and metric characteristics identified in past studies, where some individuals fall in an intermediate state, but other individuals are more closely related to one parental population or another (Birkby *et al.* 2008; Edgar 2013; Hefner and Ousley 2014; Spradley 2008). It would be valuable to identify whether this is due simply to varying degrees of genetic admixture or from the presence of dominance in certain traits for consideration in the development of applicable ancestry estimation methods.

CHAPTER 6: Conclusions

Both odontometric and arcade dimension analyses as conducted in the present study indicate that there is potential for the use of this procedure in forensic investigations. Due to the growing Hispanic population and the forensic casework conducted in U.S.-Mexico border states on UBCs (Birkby 2004; Fulginiti 2008; Glassman 2004; Hinkes 2008; Parks *et al.* 2004; Ramirez and de la Cruz 2003), there is increasing necessity to develop effective methods of ancestry estimation for a historically admixed population that is constituted of varying degrees of genetic contributions. It is therefore increasingly important to be able to distinguish between Hispanics, Native Americans, and European Americans. However, there are significant differences in the admixture histories of Hispanics throughout Central America and the Caribbean concerning patterns of Native American, African, and European admixture that must be accounted for. The present research exhibits metric differences in the dentition of Hispanics, Native Americans, and European Americans that may be utilized in a medicolegal context.

The first hypothesis was supported by the present research, with significant differences found between populations and Hispanics exhibiting intermediacy in size of dental crown and arcade variables. Odontometric data show similar trends as bone, teeth, and genetic studies concerning not only the general admixed history of the population, but the specific model of the New

Mexican Hispanic population (Bertoni *et al.* 2003; Bryc *et al.* 2010; Willermet and Edgar 2009). The second hypothesis, however, must be rejected due to the adverse effect of known sex on the efficacy of ancestry allocation. Population-specific differences were identified and significant sexual dimorphism was exhibited in European and Hispanic American variables; however, the separation of individuals into an ancestry-sex classification further decreased the amount of variation accepted into a group classification.

ANOVAs presented significant differences between all populations examined, with the majority of measured variables presenting statistical significance. Due to the difficulty and high error of cervical measurements, further research is necessary to determine utility of these measurements in the estimation of ancestry. Analysis of these variables is imperative in conditions of pathological conditions of dental remains or cases of severe attrition where dental crown measurements are negatively affected.

The classification rates of all sets of populations present potential as a valuable methodological analysis in construction of the biological profile. These classification rates were developed from measurements relating to eight out of a total of thirty-two (25%) potential teeth. Subsequent research on complete dentitions would be valuable in analysis of odontometric efficacy in ancestry estimation. Also, due to missing data, sample sizes were skewed between population sets and may often have created overestimated or underestimated classification rates. Further research on complete sets of dentition and the utility of statistics to compensate for missing data would be useful. Classification rates for broad geographic groups represented as a part of the United States population have indicated utility in a medicolegal context. The problem enters with identification of an admixed population.

Future research should also include Hispanic individuals from other geographic regions, both within and outside of the United States, as well as related populations to these groups. For example, Southeast Hispanics and African Americans should be investigated to determinate rates of allocation with these two related populations, as well as available resources on indigenous Caribbean populations related to Southeast Hispanics. It would also be valuable to further examine sex differences between males and females. As observed in the present study, females exhibited less variation in dental size and arcade differences than males when analyzing variation due to ancestry.

Several factors for improvement were determined during the course of the present research to benefit future courses of research. These include: cervical measurements on dental casts, standardization of measurement of morphological structures, statistical sample sizes, and dental asymmetry. Measurements along the cemento-enamel junction (CEJ) line may exhibit utility in the estimation of ancestry in anthropological investigations; however, research into this type of dental measurement was found to be particularly difficult on dental casts and were subsequently removed from the final analyses. This is largely because of the presence of soft tissue (gums) exhibited on the casts occluding the exact line of the CEJ. Aside from the inability to determine where the exact location of this line existed, it was nearly impossible to take the measurements in the mesiodistal dimension due to the occlusion of teeth, the presence of cast material, and the inability to move teeth to expose the CEJ. These investigations should take place on a skeletal sample in which the soft tissue is missing and the cervical lines are clearly distinguished.

Important to address is the need to create standardization on the measurement of teeth with particular morphological features. Such issues are not addressed in the literature, preventing the ability to compensate for such variations. For example, Carabelli's trait can be present in the form of a slight divet in the tooth, a miniscule enlargement on one of the cusps, or even as a complete accessory cusp on the tooth. Tuberculum dentale, an accessory cusp on canines, presents a similar problem. Individuals with such morphological traits are therefore likely to be measured larger than the actual crown size. Removal of the particular measurement of this trait is subject to a high degree of error and subjectivity as to where it begins and ends and is not the best solution to this matter.

Future research based on the present study should involve the rest of the teeth and investigation of dental asymmetry (and if this affected those teeth measured on the right rather than the left). Utilizing more teeth would be particularly beneficial when investigating the possibility of an individual of mixed ancestry where increased variables may be necessary to increase assurance of allocation (Pilloud *et al.* 2014). There are three primary forms of dental asymmetry: directional, antisymmetry, or fluctuating asymmetry (Barrett *et al.* 2012). Directional asymmetry and antisymmetry are the occurrence of greater development on one side of the dentition over the other, with antisymmetry being more variable. Fluctuating asymmetry, however, consists of random deviations from perfect symmetry due to stresses during growth and development (Barrett *et al.* 2012). These variations in dental development may cause significant differences in sizes of both sides of the dentition and may affect calculations when the right side of the dentition is used rather than the left (Barrett *et al.* 2012; Guatelli-Steinberg *et al.* 2006).

While the present research focused on the application of odontometrics in the process of ancestry estimation, the results provide the basis for several avenues of research and results for several applications. Results present different patterns related to ancestry and sex between tooth size and morphology of the palate, with similar variation based on sex and ancestry for dental crown size and greater variation based on ancestry than sex for dental arcade dimensions. These differences are likely due to the development and organizational structure of these two regions and the low level of plasticity in the dentition compared to bone. Also, dental traits evolve at a slow pace, possibly affecting the phenotypic expression of admixture in a process that has occurred in an evolutionary short span of time, compared to the faster changing skeletal structure (Hillson 1996). Comparisons between dental and skeletal studies of admixture patterns would be valuable in understanding the medicolegal, demographic, and clinical implications. While morphological and odontometric traits of the teeth have been established as appropriate proxies for analyses of biological relationships between populations, the present research promotes investigating the degree of evolutionary change that the dentition undergoes in comparison to bone and how these differential patterns may affect population variation studies.

Dental crown and arcade measurement data may be incorporated into a statistical program that is user-friendly for forensic anthropological investigations to minimize the calculation of large discriminant function equations (Pilloud *et al.* 2014). Particularly beneficial of this type of analysis is the ability to compensate for missing data. As FORDISC 3.1 (Jantz and Ousley 2005) will perform estimations of ancestry and sex based on the available measurements, this will overlook issues of missing teeth, attrition, or pathological damage and is argued for preparation by the present author.

Based on the present results, discriminant function analyses are not able to estimate ancestry and sex accurately at the same time. Success substantially increases when an individual is simply classified into an ancestry group and then classified into a sex. Estimation of sex using any combination of variables currently does not approach sufficient standards for practical application; however, estimation of ancestry when sex is not known does approach potential for inclusion between particular pairs of populations. What is suggested in the construction of a statistical program for the calculation of sex and ancestry utilizing odontometrics is the processing of two separate DFA steps, one for sex estimation, and the other for ancestry. This problem lies in the overlap between sexes within a particular ancestry and the variation that causes overlap between the lower limits of one ancestry and the upper limits of the other.

Incorporating odontometrics into construction of the biological profile requires more research on Southwest and Hispanic Caribbean populations. However, the classification rate (86.3%) obtained with the inclusion of all measured dimensions between Native Americans (93.0%) and European Americans (76.7%) presents distinct potential for use. Odontometrics between these broad populations is comparable to other traditional ancestry estimation techniques; however, when identifying the Southwest Hispanic populations, other studies have revealed more potential (Edgar 2013; Hefner *et al.* 2014). Due to the ability to utilize a taphonomically well-preserved and low-plastic region of the human body, it is recommended that further research goes into the analysis of odontometrics.

It is also suggested that any use of this methodology be restricted to a sex-unknown case, as applying a sex-specific technique causes an individual often to be misclassified into the wrong sex, although not necessarily the wrong ancestry. This is due to the large degree of overlap within an ancestry group, depending on the type of variables included. An increase in sample size and in teeth measured may help to separate groups further; however, this is currently not the case. Estimation of sex and ancestry utilizing the metric qualities of the dentition is suggested to occur separately rather than at the same time.

Genetic and phenetic studies have exhibited the great degree in variation of Hispanic populations, with self-reported Hispanics having varying levels of genetic contributions from the parental populations – Native Americans and Europeans (Bryc *et al.* 2010; Klimentidis 2009). This large variety in the American Southwest presents a great deal of difficulty in accurately estimating the ancestry of an admixed population that may often present morphological or metric characteristics that most closely resemble one parental population or another rather than a middle intermediate state. The term “Hispanic” is largely used to describe an ethnic population rather than to explain a geographic-related group of people. Due to the genetic nature of the population, it is difficult to provide an easily designated group for classification. The results of the present study suggests that possibility for differentiation may be possible between Hispanics and their parental populations, but the varying degree of admixture and natural variation may prevent this significant population from achieving the same rate of successful allocation as those populations based on more widespread geographic differences.

APPENDIX A: Tables

Table 2.1. Dental morphological traits commonly utilized. Definitions by Turner *et al.* (1991).

Trait	Definition
Shovel-shaped incisors	Presence of lingual marginal ridges; scored on a 0-7 scale
Carabelli's trait	Maxillary molars; pit, groove, depression, or accessory cusp present on the lingual surface of the mesiolingual cusp (protocone); scored on a 0-7 scale
Cusp 7	Mandibular molars; occurs on the lingual groove between cusps 2 and 4; most common on the first molar; scored on a 0-4 scale
Canine mesial ridge	Present on the maxillary canine; mesiolingual marginal ridge is similar in size to the distolingual marginal ridge; mesial ridge may be more pronounced than distal ridge; scored on a 0-3 scale
Multi-cusped premolars	Maxillary premolars; small accessory cusps on the mesial and/or distal ends of the sagittal grooves; scored on a 0-1 scale

Table 3.1. Population composition of research sample.

Ancestry	Sex	n
Hispanic	Males	102
	Females	100
Native American	Males	51
	Females	110
European American	Males	82
	Females	81
Asian American	Males	19
	Females	24
Total	Males	254
	Females	315
		569

Table 4.1. Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (males and females combined).

	Southwest Hispanics			**Native Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
UI-Cerv BL	7.21	.05	7.12 – 7.31	7.29	.04	7.21 – 7.38
UI-CervMD	8.54	.05	8.44 – 8.64	8.73	.06	8.62 – 8.84
UI-CrownBL	6.99	.04	6.90 – 7.08	7.05	.04	6.96 – 7.13
UI-CrownMD	8.67	.05	8.58 – 8.76	8.73	.05	8.63 – 8.82
UC-CervBL	8.35	.06	8.24 – 8.46	8.35	.05	8.25 – 8.46
UC-CervMD	7.88	.04	7.81 – 7.96	8.17	.05	8.08 – 8.26
UC-CrownBL	7.98	.05	7.88 – 8.09	7.98	.05	7.88 – 8.08
UC-CrownMD	7.78	.04	7.70 – 7.86	8.02	.04	7.94 – 8.10
UP-CervBL	9.37	.05	9.28 – 9.46	9.55	.07	9.43 – 9.68
UP-CervMD	6.42	.04	6.34 – 6.50	6.55	.04	6.47 – 6.63
UP-CrownBL	9.16	.05	9.07 – 9.26	9.38	.06	9.27 – 9.49
UP-CrownMD	6.92	.04	6.84 – 7.00	7.22	.04	7.14 – 7.30
UM-CervBL	11.45	.05	11.36 – 11.53	11.63	.05	11.54 – 11.73
UM-CervMD	9.93	.05	9.83 – 10.03	10.20	.05	10.10 – 10.31
UM-CrownBL	11.21	.05	11.12 – 11.30	11.44	.04	11.36 – 11.53
UM-CrownBL(Alt)	11.33	.05	11.24 – 11.42	11.51	.04	11.43 – 11.60
UM-CrownMD	11.03	.05	10.93 – 11.14	11.09	.06	10.98 – 11.20
LI-Cerv BL	6.27	.04	6.20 – 6.35	6.31	.04	6.23 – 6.39
LI-CervMD	5.43	.05	5.35 – 5.51	5.60	.04	5.51 – 5.67
LI-CrownBL	6.09	.04	6.01 – 6.16	6.07	.04	5.99 – 6.15
LI-CrownMD	5.97	.03	5.90 – 6.03	6.21	.04	6.14 – 6.29
LC-CervBL	7.46	.06	7.35 – 7.57	7.32	.06	7.21 – 7.42
LC-CervMD	6.68	.04	6.60 – 6.76	7.00	.04	6.92 – 7.08
LC-CrownBL	7.13	.06	7.02 – 7.25	6.98	.06	6.87 – 7.09
LC-CrownMD	6.75	.04	6.67 – 6.83	6.98	.04	6.90 – 7.06
LP-CervBL	7.89	.04	7.81 – 7.97	7.78	.05	7.69 – 7.88

Table 4.1 (Continued). Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (males and females combined).

	Southwest Hispanics			**Native Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
LP-CervMD	6.68	.05	6.59 – 6.77	6.70	.05	6.59 – 6.80
LP-CrownBL	7.62	.04	7.54 – 7.70	7.57	.04	7.49 – 7.64
LP-CrownMD	6.93	.04	6.85 – 7.00	7.01	.04	6.93 – 7.09
LM-CervBL	10.61	.05	10.52 – 10.70	10.83	.05	10.74 – 10.93
LM-CervMD	11.16	.05	11.06 – 11.26	11.41	.05	11.30 – 11.51
LM-CrownBL	10.43	.04	10.35 – 10.52	10.74	.04	10.65 – 10.82
LM-CrownMD	11.28	.06	11.16 – 11.39	11.67	.06	11.55 – 11.78
MaxIncisorComp	31.00	.24	30.54 – 31.47	30.97	.31	30.35 – 31.59
MaxCanineComp	15.46	.24	15.28 – 15.64	15.93	.31	15.75 – 16.11
MaxPreComp	27.31	.09	27.07 – 27.55	28.13	.09	27.79 – 28.47
MaxMolarComp	42.04	.12	41.63 – 42.46	42.13	.17	41.66 – 42.60
ManIncisorComp	21.83	.15	21.54 – 22.12	22.15	.16	21.84 – 22.46
ManCanineComp	13.47	.09	13.29 – 13.64	13.63	.07	13.49 – 13.77
ManPreComp	28.45	.14	28.19 – 28.72	28.49	.18	28.14 – 28.83
ManMolarComp	44.45	.28	43.89 – 45.00	45.13	.26	44.62 – 45.64
Max Arch Depth	27.18	.20	26.78 – 27.58	26.86	.23	26.41 – 27.31
MaxIncisorWidth	8.78	.08	8.63 – 8.94	8.97	.09	8.78 – 9.5
MaxCanineWidth	34.65	.21	34.24 – 35.07	35.79	.22	35.36 – 36.22
MaxPreWidth	30.37	.23	29.92 – 30.82	31.14	.21	30.71 – 31.56
MaxMolarWidth	40.83	.24	40.35 – 41.31	40.89	.20	40.49 – 41.29
Man Arch Depth	22.20	.18	21.84 – 22.56	21.95	.17	21.61 – 22.29
ManIncisorWidth	15.91	.15	15.63 – 16.20	16.55	.19	16.18 – 16.91
ManCanineWidth	26.44	.19	16.07 – 16.81	27.51	.19	27.15 – 27.88
ManPreWidth	28.65	.20	28.27 – 29.04	29.49	.17	29.15 – 29.82
ManMolarWidth	35.74	.25	35.24 – 36.23	35.36	.21	34.95 – 35.76

Table 4.1 (Continued). Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (males and females combined).

	European Americans			**Asian Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
UI-Cerv BL	7.21	.05	7.11 – 7.30	7.08	.12	6.84 – 7.31
UI-CervMD	8.50	.05	8.40 – 8.60	8.44	.08	8.27 – 8.61
UI-CrownBL	6.94	.05	6.84 – 7.04	6.83	.12	6.60 – 7.07
UI-CrownMD	8.64	.05	8.55 – 8.73	8.54	.08	8.38 – 8.69
UC-CervBL	8.18	.06	8.06 – 8.29	8.10	.10	7.90 – 8.30
UC-CervMD	7.63	.05	7.53 – 7.73	7.95	.10	7.75 – 8.14
UC-CrownBL	7.73	.06	7.62 – 7.85	7.69	.09	7.50 – 7.88
UC-CrownMD	7.54	.04	7.45 – 7.62	7.79	.08	7.63 – 7.96
UP-CervBL	9.22	.05	9.12 – 9.32	9.43	.11	9.21 – 9.66
UP-CervMD	6.20	.04	611 – 6.28	6.37	.07	6.23 – 6.51
UP-CrownBL	8.96	.05	8.87 – 9.05	9.40	.08	9.23 – 9.56
UP-CrownMD	6.69	.04	6.60 – 6.78	7.20	.08	7.04 – 7.37
UM-CervBL	11.31	.06	11.85 – 11.44	11.35	.11	11.12 – 11.58
UM-CervMD	9.96	.07	9.82 – 10.10	9.92	.11	9.69 – 10.14
UM-CrownBL	11.01	.06	10.90 – 11.12	11.14	.10	10.94 – 11.34
UM-CrownBL(Alt)	11.11	.06	10.99 – 11.22	11.24	.10	11.04 – 11.45
UM-CrownMD	11.00	.07	10.86 – 11.13	11.14	.14	10.86 – 11.42
LI-Cerv BL	6.16	.05	6.06 – 6.26	6.18	.09	6.0 – 6.36
LI-CervMD	5.15	.05	5.06 – 5.23	5.27	.08	5.10 – 5.44
LI-CrownBL	5.88	.05	5.79 – 5.97	6.01	.08	5.85 – 6.18
LI-CrownMD	5.78	.03	5.72 – 5.85	5.80	.06	5.68 – 5.93
LC-CervBL	7.28	.06	7.16 – 7.40	7.32	.10	7.11 – 7.52
LC-CervMD	6.49	.05	6.40 – 6.59	6.65	.08	6.49 – 6.81
LC-CrownBL	6.88	.06	6.76 – 7.00	6.98	.10	6.77 – 7.19
LC-CrownMD	6.57	.04	6.49 – 6.65	6.68	.07	6.54 – 6.83
LP-CervBL	7.85	.05	7.75 – 7.95	7.86	.11	7.64 – 8.09

Table 4.1 (Continued). Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (males and females combined).

	European Americans			**Asian Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
LP-CervMD	6.49	.07	6.36 – 6.62	6.42	.11	6.19 – 6.65
LP-CrownBL	7.500	.05	7.40 – 7.59	7.68	.10	7.48 – 7.88
LP-CrownMD	6.78	.04	6.70 – 6.87	6.96	.07	6.82 – 7.11
LM-CervBL	10.50	.06	10.39 – 10.61	10.49	.14	10.22 – 10.77
LM-CervMD	10.79	.06	10.66 – 10.91	11.02	.13	10.76 – 11.29
LM-CrownBL	10.25	.05	10.15 – 10.35	10.67	.19	10.29 – 11.05
LM-CrownMD	10.83	.07	10.69 – 10.97	11.45	.12	11.21 – 11.70
MaxIncisorComp	30.06	.21	29.65 – 30.48	31.29	.32	30.63 – 31.94
MaxCanineComp	14.80	.21	14.62 – 14.98	15.51	.32	15.21 – 15.82
MaxPreComp	26.74	.09	26.41 – 27.07	28.08	.15	27.34 – 28.81
MaxMolarComp	41.19	.17	40.64 – 41.73	41.89	.36	41.04 – 42.73
ManIncisorComp	21.37	.14	21.10 – 21.65	22.24	.29	21.66 – 22.82
ManCanineComp	12.97	.08	12.81 – 13.12	13.32	.16	13.01 – 13.64
ManPreComp	28.02	.17	27.68 – 28.36	28.79	.28	28.22 – 29.36
ManMolarComp	42.74	.27	42.21 – 43.28	44.56	.55	43.38 – 45.74
Max Arch Depth	27.02	.28	26.46 – 27.58	26.26	.59	25.06 – 27.45
MaxIncisorWidth	8.50	.08	8.35 – 8.64	8.76	.11	8.54 – 8.99
MaxCanineWidth	32.95	.23	32.51 – 33.40	35.14	.35	34.44 – 35.84
MaxPreWidth	29.39	.26	28.88 – 29.90	32.13	.48	31.15 – 33.11
MaxMolarWidth	39.35	.29	38.77 – 39.92	42.02	.49	41.01 – 43.02
Man Arch Depth	22.30	.25	21.81 – 22.79	22.07	.43	21.20 – 22.93
ManIncisorWidth	15.19	.14	14.93 – 15.46	16.05	.36	15.32 – 16.78
ManCanineWidth	25.12	.18	24.77 – 25.47	26.70	.34	26.01 – 27.39
ManPreWidth	26.95	.24	26.49 – 27.42	28.96	.42	28.11 – 29.82
ManMolarWidth	34.42	.29	33.85 – 34.99	36.69	.55	35.58 – 37.81

Table 4.2. Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (males only).

	Southwest Hispanics			**Native Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
UI-Cerv BL	7.31	.07	7.18 – 7.45	7.56	.08	7.39 – 7.72
UI-CervMD	8.72	.07	8.59 – 8.85	9.07	.10	8.86 – 9.28
UI-CrownBL	7.05	.06	6.92 – 7.18	7.28	.08	7.11 – 7.45
UI-CrownMD	8.77	.06	8.65 – 8.89	8.96	.09	8.78 – 9.15
UC-CervBL	8.58	.08	8.43 – 8.73	8.59	.10	8.39 – 8.80
UC-CervMD	8.05	.05	7.94 – 8.15	8.39	.09	8.21 – 8.57
UC-CrownBL	8.19	.07	8.04 – 8.33	8.19	.10	8.00 – 8.39
UC-CrownMD	7.93	.05	7.83 – 8.03	8.21	.08	8.05 – 8.37
UP-CervBL	9.50	.06	9.38 – 9.63	9.85	.11	9.63 – 10.08
UP-CervMD	6.48	.06	6.36 – 6.59	6.66	.08	6.50 – 6.82
UP-CrownBL	9.30	.06	9.17 – 9.42	9.60	.11	9.37 – 9.83
UP-CrownMD	7.02	.06	6.90 – 7.14	7.34	.08	7.17 – 7.50
UM-CervBL	11.64	.06	11.52 – 11.75	11.90	.09	11.71 – 12.08
UM-CervMD	10.03	.07	9.89 – 10.18	10.43	.10	10.24 – 10.62
UM-CrownBL	11.39	.06	11.28 – 11.51	11.71	.09	11.53 – 11.88
UM-CrownBL (Alt)	11.53	.06	11.41 – 11.64	11.78	.08	11.62 – 11.93
UM-CrownMD	11.21	.07	11.06 – 11.35	11.29	.10	11.09 – 11.49
LI-Cerv BL	6.32	.05	6.22 – 6.42	6.36	.08	6.19 – 6.52
LI-CervMD	5.49	.06	5.38 – 5.60	5.81	.08	5.65 – 5.96
LI-CrownBL	6.14	.06	6.03 – 6.25	6.05	.08	5.89 – 6.21
LI-CrownMD	6.02	.05	5.92 – 6.11	6.39	.07	6.24 – 6.53
LC-CervBL	7.74	.08	7.58 – 7.90	7.53	.12	7.30 – 7.76
LC-CervMD	6.96	.06	6.85 – 7.07	7.34	.07	7.21 – 7.48
LC-CrownBL	7.41	.09	7.23 – 7.59	7.12	.13	6.86 – 7.37
LC-CrownMD	7.02	.06	6.91 – 7.13	7.24	.07	7.10 – 7.38
LP-CervBL	8.06	.06	7.94 – 8.17	8.03	.08	7.87 – 8.20
LP-CervMD	6.78	.07	6.64 – 6.91	6.78	.09	6.60 – 6.96

Table 4.2 (Continued). Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (males only).

	Southwest Hispanics			**Native Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
LP-CrownBL	7.75	.05	7.64 – 7.85	7.78	.08	7.63 – 7.94
LP-CrownMD	7.05	.05	6.94 – 7.15	7.10	.08	6.94 – 7.27
LM-CervBL	10.73	.06	10.61 – 10.85	11.02	.08	10.85 – 11.18
LM-CervMD	11.39	.07	11.26 – 11.53	11.77	.10	11.57 – 11.97
LM-CrownBL	10.54	.06	10.42 – 10.66	10.92	.07	10.77 – 11.06
LM-CrownMD	11.51	.07	11.37 – 11.65	11.94	.09	11.75 – 12.12
MaxIncisorComp	31.47	.31	30.85 – 32.09	32.01	.63	30.69 – 33.33
MaxCanineComp	15.73	.13	15.46 – 15.99	16.39	.18	16.03 – 16.75
MaxPremolarComp	27.60	.17	27.26 – 27.94	28.77	.31	28.14 – 29.40
MaxMolarComp	42.60	.29	42.02 – 43.18	43.05	.38	42.27 – 43.83
ManIncisorComp	22.15	.21	21.73 – 22.58	22.79	.39	22.00 – 23.59
ManCanineComp	13.78	.12	13.55 – 14.01	14.00	.16	13.69 – 14.32
ManPremolarComp	28.87	.20	28.46 – 29.27	28.97	.38	28.21 – 29.74
ManMolarComp	45.41	.37	44.67 – 46.16	46.11	.37	45.35 – 46.87
Max Arch Depth	27.37	.31	26.75 – 27.98	27.94	.49	26.95 – 28.92
Max Incisor Width	8.89	.12	8.65 – 9.12	9.13	.14	8.85 – 9.41
Max Canine Width	35.17	.33	34.52 – 35.83	36.01	.42	35.16 – 36.86
Max Premolar Width	30.90	.34	30.23 – 31.57	31.71	.38	30.95 – 32.48
Max Molar Width	41.47	.34	40.79 – 12.15	41.71	.38	40.95 – 42.47
Man Arch Depth	22.38	.26	21.86 – 22.89	21.82	.40	21.03 – 22.62
Man Incisor Width	15.90	.22	15.46 – 16.33	17.00	.34	16.31 – 17.69
Man Canine Width	26.72	.29	26.14 – 27.29	27.78	.38	27.00 – 28.55
Man Premolar Width	29.00	.30	28.42 – 29.59	29.72	.31	29.10 – 30.34
Man Molar Width	36.49	.36	35.78 – 37.20	36.39	.43	35.53 – 37.24

Table 4.2 (Continued). Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (males only).

	European Americans			**Asian Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
UI-Cerv BL	7.33	.08	7.18 – 7.48	7.15	.24	6.64 – 7.66
UI-CervMD	8.64	.08	8.49 – 8.79	8.58	.11	8.35 – 8.81
UI-CrownBL	7.05	.07	6.90 – 7.19	6.86	.23	6.38 – 7.35
UI-CrownMD	8.76	.07	8.62 – 8.90	8.63	.12	8.38 – 8.88
UC-CervBL	8.30	.10	8.09 – 8.50	8.19	.18	7.84 – 8.55
UC-CervMD	7.85	.07	7.71 – 7.99	8.24	.11	8.01 – 8.48
UC-CrownBL	7.83	.11	7.62 – 8.04	7.79	.15	7.48 – 8.11
UC-CrownMD	7.78	.07	7.65 – 7.91	8.03	.12	7.78 – 8.29
UP-CervBL	9.36	.07	9.23 – 9.49	9.69	.10	9.48 – 9.90
UP-CervMD	6.27	.07	6.13 – 6.40	6.49	.09	6.30 – 6.67
UP-CrownBL	9.06	.06	8.94 – 9.19	9.50	.11	9.27 – 9.73
UP-CrownMD	6.77	.06	6.65 – 6.89	7.36	.10	7.15 – 7.57
UM-CervBL	11.55	.08	11.39 – 11.71	11.74	.11	11.51 – 11.97
UM-CervMD	10.18	.11	9.96 – 10.40	10.19	.15	9.89 – 10.50
UM-CrownBL	11.24	.08	11.08 – 11.40	11.46	.14	11.17 – 11.74
UM-CrownBL (Alt)	11.36	.08	11.21 – 11.52	11.54	.13	11.28 – 11.80
UM-CrownMD	11.23	.10	11.04 – 11.42	11.28	.13	11.00 – 11.57
LI-Cerv BL	6.09	.07	5.94 – 6.24	6.29	.15	5.98 – 6.60
LI-CervMD	5.21	.06	5.09 – 5.34	5.29	.10	5.09 – 5.50
LI-CrownBL	5.82	.07	5.67 – 5.97	6.12	.14	5.82 – 6.42
LI-CrownMD	5.90	.04	5.82 – 5.99	5.84	.10	5.63 – 6.06
LC-CervBL	7.33	.10	7.13 – 7.52	7.38	.21	6.93 – 7.82
LC-CervMD	6.73	.07	6.59 – 6.86	6.90	.14	6.60 – 7.20
LC-CrownBL	6.89	.10	6.68 – 7.10	6.99	.20	6.57 – 7.42
LC-CrownMD	6.77	.05	6.66 – 6.87	6.78	.14	6.47 – 7.08
LP-CervBL	7.98	.07	7.85 – 8.11	8.25	.17	7.89 – 8.60
LP-CervMD	6.66	.10	6.47 – 6.85	6.74	.13	6.47 – 7.00

Table 4.2. Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (males only).

	European Americans			**Asian Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
LP-CrownBL	7.63	.06	7.51 – 7.76	7.99	.16	7.64 – 8.33
LP-CrownMD	6.89	.06	6.76 – 7.01	7.18	.10	6.96 – 7.39
LM-CervBL	10.71	.07	10.57 – 10.85	10.86	.13	10.59 – 11.13
LM-CervMD	11.01	.09	10.82 – 11.19	11.40	.18	11.02 – 11.78
LM-CrownBL	10.40	.07	10.26 – 10.53	10.80	.14	10.51 – 11.10
LM-CrownMD	11.09	.09	10.91 – 11.27	11.75	.14	11.46 – 12.05
MaxIncisorComp	30.69	.32	30.04 – 31.34	31.65	.44	30.71 – 32.59
MaxCanineComp	15.03	.15	14.73 – 15.34	16.01	.19	15.61 – 16.41
MaxPreComp	27.36	.24	26.88 – 27.84	29.04	.38	28.22 – 29.85
MaxMolarComp	41.85	.32	41.21 – 42.49	42.73	.47	41.66 – 43.80
ManIncisorComp	21.74	.22	21.30 – 22.18	22.04	.47	20.03 – 23.05
ManCanineComp	13.31	.11	13.08 – 13.53	13.82	.27	13.25 – 14.40
ManPreComp	28.51	.25	28.01 – 29.01	29.66	.24	29.16 – 30.17
ManMolarComp	43.43	.37	42.66 – 44.19	45.59	.64	43.94 – 47.24
Max Arch Depth	27.89	.36	27.17 – 28.61	27.89	.79	26.23 – 29.55
Max Incisor Width	8.80	.11	8.58 – 9.02	8.92	.16	8.58 – 9.25
Max Canine Width	33.48	.38	32.73 – 34.23	36.04	.39	35.23 – 36.85
Max Premolar Width	29.71	.40	28.92 – 30.51	33.83	.63	32.49 – 35.16
Max Molar Width	40.18	.44	39.31 – 41.06	43.37	.72	41.87 – 44.88
Man Arch Depth	22.85	.33	22.20 – 23.51	22.74	.56	21.55 – 23.93
Man Incisor Width	15.53	.21	15.11 – 15.94	16.22	.60	14.95 – 17.49
Man Canine Width	25.78	.27	25.25 – 26.30	27.19	.43	26.28 – 28.10
Man Premolar Width	27.45	.35	26.76 – 28.15	30.06	.56	28.88 – 31.25
Man Molar Width	35.34	.38	34.58 – 36.09	38.01	.68	36.57 – 39.45

Table 4.3 (Continued). Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (females only).

	Southwest Hispanics			**Native Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
UI-Cerv BL	7.12	.06	7.00 – 7.24	7.18	.05	7.08 – 7.28
UI-CervMD	8.37	.08	8.22 – 8.52	8.57	.06	8.46 – 8.70
UI-CrownBL	6.93	.06	6.81 – 7.06	6.95	.05	6.85 – 7.04
UI-CrownMD	8.56	.07	8.43 – 8.69	8.60	.05	8.49 – 8.70
UC-CervBL	8.13	.07	7.99 – 8.27	8.24	.06	8.13 – 8.36
UC-CervMD	7.71	.05	7.61 – 7.81	8.07	.05	7.97 – 8.17
UC-CrownBL	7.79	.07	7.65 – 7.93	7.88	.06	7.77 – 7.99
UC-CrownMD	7.64	.06	7.53 – 7.76	7.93	.04	7.85 – 8.02
UP-CervBL	9.23	.06	9.11 – 9.35	9.42	.08	9.27 – 9.57
UP-CervMD	6.36	.06	6.25 – 6.47	6.49	.04	6.41 – 6.58
UP-CrownBL	9.02	.06	8.90 – 9.15	9.27	.06	9.16 – 9.39
UP-CrownMD	6.81	.05	6.71 – 6.91	7.16	.04	7.07 – 7.25
UM-CervBL	11.24	.06	11.12 – 11.36	11.51	.05	11.41 – 11.62
UM-CervMD	9.82	.07	9.67 – 9.95	10.10	.06	9.98 – 10.22
UM-CrownBL	11.02	.06	10.89 – 11.15	11.32	.05	11.23 – 11.41
UM-CrownBL (Alt)	11.12	.06	11.00 – 11.24	11.39	.05	11.29 – 11.48
UM-CrownMD	10.84	.07	10.70 – 10.98	10.99	.07	10.85 – 11.12
LI-Cerv BL	6.23	.05	6.12 – 6.33	6.29	.04	6.20 – 6.38
LI-CervMD	5.36	.06	5.24 – 5.48	5.51	.05	5.40 – 5.61
LI-CrownBL	6.04	.05	5.94 – 6.14	6.07	.05	5.99 – 6.16
LI-CrownMD	5.91	.05	5.82 – 6.00	6.14	.05	6.04 – 6.23
LC-CervBL	7.22	.07	7.08 – 7.35	7.22	.06	7.11 – 7.34
LC-CervMD	6.43	.05	6.33 – 6.53	6.84	.04	6.76 – 6.93
LC-CrownBL	6.90	.07	6.77 – 7.04	6.92	.06	6.81 – 7.04
LC-CrownMD	6.50	.05	6.41 – 6.59	6.87	.04	6.78 – 6.96
LP-CervBL	7.72	.06	7.61 – 7.83	7.68	.05	7.57 – 7.78
LP-CervMD	6.59	.06	6.46 – 6.71	6.66	.06	6.54 – 6.79

Table 4.3 (Continued). Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (females only).

	Southwest Hispanic			**Native Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
LP-CrownBL	7.49	.05	7.39 – 7.60	7.47	.04	7.39 – 7.56
LP-CrownMD	6.81	.05	6.71 – 6.91	6.98	.05	6.89 – 7.07
LM-CervBL	10.47	.07	10.34 – 10.60	10.75	.05	10.65 – 10.86
LM-CervMD	10.89	.07	10.75 – 11.02	11.25	.06	11.14 – 11.36
LM-CrownBL	10.31	.06	10.19 – 10.43	10.65	.05	10.55 – 10.75
LM-CrownMD	10.96	.08	10.81 – 11.16	11.53	.07	11.39 – 11.67
MaxIncisorComp	30.55	.34	29.86 – 31.24	30.35	.27	29.79 – 30.90
MaxCanineComp	15.19	.12	14.95 – 15.43	15.73	.10	15.53 – 15.92
MaxPremolarComp	27.02	.16	26.69 – 27.34	27.86	.20	27.46 – 28.27
MaxMolarComp	41.39	.28	40.83 – 41.95	41.81	.28	41.25 – 42.37
ManIncisorComp	21.55	.20	21.15 – 21.96	21.90	.15	21.60 – 22.20
ManCanineComp	13.12	.12	12.88 – 13.36	13.47	.07	13.33 – 13.62
ManPremolarComp	28.05	.17	27.71 – 28.39	28.28	.19	27.90 – 28.65
ManMolarComp	43.36	.36	42.65 – 44.08	44.76	.31	44.13 – 45.39
Max Arch Depth	26.99	.26	26.47 – 27.51	26.38	.23	25.92 – 26.85
Max Incisor Width	8.68	.10	8.49 – 8.87	8.89	.12	8.66 – 9.13
Max Canine Width	34.14	.26	33.64 – 34.65	35.68	.25	35.18 – 36.19
Max Premolar Width	29.84	.30	29.24 – 30.44	30.87	.26	30.36 – 31.38
Max Molar Width	40.13	.33	39.47 – 40.80	40.52	.23	40.06 – 40.98
Man Arch Depth	22.00	.25	21.50 – 22.50	22.01	.18	21.65 – 22.36
Man Incisor Width	15.93	.19	15.55 – 16.32	16.34	.22	15.91 – 16.77
Man Canine Width	26.15	.23	25.69 – 26.62	27.40	.21	26.99 – 27.81
Man Premolar Width	28.27	.24	27.78 – 28.75	29.39	.20	28.98 – 29.79
Man Molar Width	34.81	.32	34.18 – 35.45	34.90	.22	34.47 – 35.32

Table 4.3 (Continued). Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (females only).

	European Americans			**Asian Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
UI-Cerv BL	7.09	.07	6.96 – 7.22	7.02	.09	6.82 – 7.21
UI-CervMD	8.35	.07	8.22 – 8.48	8.32	.12	8.07 – 8.57
UI-CrownBL	6.82	.07	6.69 – 6.96	6.81	.10	6.61 – 7.01
UI-CrownMD	8.53	.05	8.40 – 8.65	8.46	.10	8.26 – 8.67
UC-CervBL	8.08	.07	7.95 – 8.22	8.02	.12	7.78 – 8.27
UC-CervMD	7.45	.06	7.32 – 7.57	7.70	.13	7.43 – 7.97
UC-CrownBL	7.66	.07	7.52 – 7.79	7.62	.12	7.37 – 7.87
UC-CrownMD	7.34	.05	7.25 – 7.44	7.60	.09	7.41 – 7.79
UP-CervBL	9.07	.08	8.91 – 9.22	9.21	.17	8.85 – 9.57
UP-CervMD	6.12	.06	6.01 – 6.23	6.27	.10	6.05 – 6.48
UP-CrownBL	8.84	.07	8.71 – 8.98	9.31	.11	9.07 – 9.55
UP-CrownMD	6.60	.06	6.48 – 6.73	7.06	.12	6.81 – 7.32
UM-CervBL	11.05	.09	10.87 – 11.23	11.01	.16	10.68 – 11.34
UM-CervMD	9.73	.09	9.55 – 9.91	9.68	.15	9.36 – 9.99
UM-CrownBL	10.75	.07	10.63 – 10.88	10.86	.12	10.62 – 11.11
UM-CrownBL (Alt)	10.83	.07	10.69 – 10.97	10.99	.14	10.70 – 11.27
UM-CrownMD	10.74	.09	10.57 – 10.91	10.96	.26	10.38 – 11.53
LI-Cerv BL	6.21	.07	6.07 – 6.35	6.08	.11	5.86 – 6.31
LI-CervMD	5.08	.06	4.95 – 5.21	5.26	.13	4.97 – 5.53
LI-CrownBL	5.92	.06	5.81 – 6.03	5.92	.09	5.74 – 6.11
LI-CrownMD	5.66	.04	5.57 – 5.75	5.77	.08	5.60 – 5.94
LC-CervBL	7.22	.07	7.08 – 7.36	7.27	.09	7.10 – 7.45
LC-CervMD	6.28	.06	6.16 – 6.39	6.47	.07	6.32 – 6.62
LC-CrownBL	6.86	.07	6.72 – 7.00	6.97	.10	6.76 – 7.18
LC-CrownMD	6.39	.05	6.29 – 6.49	6.62	.07	6.48 – 6.75
LP-CervBL	7.33	.08	7.59 – 7.88	7.55	.12	7.31 – 7.79
LP-CervMD	6.31	.08	6.14 – 6.48	6.16	.16	5.83 – 6.49

Table 4.3 (Continued). Summary statistics for Southwest Hispanics, Native Americans, European Americans, and Asian Americans (females only).

	European Americans			**Asian Americans**		
	Mean	SE	95% Confidence Interval	Mean	SE	95% Confidence Interval
LP-CrownBL	7.36	.07	7.23 – 7.49	7.44	.09	7.24 – 7.63
LP-CrownMD	6.68	.06	6.57 – 6.80	6.78	.08	6.62 – 6.95
LM-CervBL	10.28	.08	10.12 – 10.45	10.15	.20	9.72 – 10.58
LM-CervMD	10.57	.08	10.41 – 10.73	10.67	.15	10.35 – 10.98
LM-CrownBL	10.09	.07	9.96 – 10.23	10.54	.34	9.81 – 11.27
LM-CrownMD	10.54	.10	10.35 – 10.74	11.15	.16	10.81 – 11.49
MaxIncisorComp	29.65	.26	29.12 – 30.18	30.95	.47	29.96 – 31.93
MaxCanineComp	14.59	.11	14.38 – 14.80	15.07	.18	14.69 – 14.45
MaxPremolarComp	26.09	.20	25.70 – 26.49	27.30	.50	26.22 – 28.37
MaxMolarComp	40.55	.42	39.70 – 41.40	41.35	.56	40.13 – 42.56
ManIncisorComp	21.05	.17	20.71 – 21.39	22.40	.36	21.65 – 23.15
ManCanineComp	12.66	.10	12.45 – 12.86	12.95	.14	12.66 – 13.25
ManPremolarComp	27.40	.22	26.97 – 27.83	28.02	.41	27.16 – 28.89
ManMolarComp	42.12	.36	41.40 – 42.84	43.94	.75	42.23 – 45.64
Max Arch Depth	26.08	.42	25.23 – 26.92	24.78	.75	23.22 – 26.35
Max Incisor Width	8.22	.09	8.04 – 8.40	8.64	.16	8.31 – 8.96
Max Canine Width	32.59	.27	32.06 – 33.12	34.33	.51	33.27 – 35.39
Max Premolar Width	29.07	.33	28.41 – 29.73	30.69	.55	29.55 – 31.83
Max Molar Width	38.51	.37	37.78 – 39.24	40.73	.56	39.57 – 41.89
Man Arch Depth	21.71	.36	20.99 – 22.43	21.39	.61	20.10 – 22.68
Man Incisor Width	14.92	.17	14.59 – 15.25	15.91	.44	14.99 – 16.83
Man Canine Width	24.53	.22	24.09 – 24.96	26.28	.51	25.22 – 27.33
Man Premolar Width	26.50	.31	25.88 – 27.11	27.92	.53	26.80 – 29.04
Man Molar Width	33.38	.40	32.57 – 34.18	35.21	.73	33.65 – 36.77

Table 4.4. ANOVA results including F-values and p-values between Southwest Hispanics, European Americans, Native Americans, and Asian Americans. *indicates statistical significance ($p \leq 0.05$).

Variable	F	Sig
Maxillary Incisor Cervical BL	2.136	.097
Maxillary Incisor Cervical MD*	4.946	.002
Maxillary Incisor Crown BL	2.280	.080
Maxillary Incisor Crown MD	1.825	.143
Maxillary Canine Cervical BL*	3.137	.027
Maxillary Canine Cervical MD*	9.609	.000
Maxillary Canine Crown BL*	.4394	.005
Maxillary Canine Crown MD*	6.290	.000
Maxillary Premolar Cervical BL*	6.514	.000
Maxillary Premolar Cervical MD*	5.157	.002
Maxillary Premolar Crown BL*	7.663	.000
Maxillary Premolar Crown MD*	11.614	.000
Maxillary Molar Cervical BL*	3.316	.021
Maxillary Molar Cervical MD	2.619	.052
Maxillary Molar Crown BL*	5.348	.001
Maxillary Molar Crown BL Non-perpendicular*	4.647	.004
Maxillary Molar Crown MD	.165	.920
Mandibular Incisor Cervical BL*	2.961	.033
Mandibular Incisor Cervical MD*	12.380	.000
Mandibular Incisor Crown BL*	4.497	.004
Mandibular Incisor Crown MD*	13.178	.000
Mandibular Canine Cervical BL*	3.619	.014
Mandibular Canine Cervical MD*	13.662	.000
Mandibular Canine Crown BL*	5.027	.002
Mandibular Canine Crown MD*	9.644	.000
Mandibular Premolar Cervical BL	1.048	.372
Mandibular Premolar Cervical MD	.425	.735
Mandibular Premolar Crown BL	2.202	.089
Mandibular Premolar Crown MD	2.446	.065
Mandibular Molar Cervical BL*	3.285	.022
Mandibular Molar Cervical MD*	11.377	.000
Mandibular Molar Crown BL*	9.072	.000
Mandibular Molar Crown MD*	15.906	.000

Table 4.4 (continued). ANOVA results including F-values and p-values between Southwest Hispanics, European Americans, Native Americans, and Asian Americans. * indicates statistical significance ($p \leq 0.05$).

Maxillary Incisor Composition	2.002	.117
Maxillary Canine Composition*	11.651	.000
Maxillary Premolar Composition*	8.088	.000
Maxillary Molar Composition	2.020	.114
Mandibular Incisor Composition	2.283	.081
Mandibular Canine Composition*	4.630	.004
Mandibular Premolar Composition	1.632	.184
Mandibular Molar Composition*	7.843	.000
Maxillary Arch Depth	.549	.649
Maxillary Incisor Width	.995	.396
Maxillary Canine Width*	8.293	.000
Maxillary Premolar Width*	9.607	.000
Maxillary Molar Width*	5.474	.001
Mandibular Arch Depth	1.528	.208
Mandibular Incisor Width*	4.729	.003
Mandibular Canine Width*	6.053	.001
Mandibular Premolar Width*	8.849	.000
Mandibular Molar Width*	4.009	.008

Table 4.5. ANOVA results including F-values and p-values between Southwest Hispanics, European Americans, and Native Americans. * indicates statistical significance ($p \leq 0.05$).

Variable	F	Sig
Maxillary Incisor Cervical BL	.997	.370
Maxillary Incisor Cervical MD*	5.224	.006
Maxillary Incisor Crown BL	1.555	.212
Maxillary Incisor Crown MD	.769	.464
Maxillary Canine Cervical BL*	3.064	.048
Maxillary Canine Cervical MD*	35.036	.000
Maxillary Canine Crown BL*	6.604	.001
Maxillary Canine Crown MD*	31.511	.000
Maxillary Premolar Cervical BL*	9.354	.000
Maxillary Premolar Cervical MD*	17.341	.000
Maxillary Premolar Crown BL*	16.309	.000
Maxillary Premolar Crown MD*	35.868	.000
Maxillary Molar Cervical BL*	9.499	.000
Maxillary Molar Cervical MD*	6.247	.002
Maxillary Molar Crown BL*	18.899	.000
Maxillary Molar Crown BL Non-perpendicular*	16.044	.000
Maxillary Molar Crown MD	.559	.572
Mandibular Incisor Cervical BL*	3.484	.031
Mandibular Incisor Cervical MD*	25.687	.000
Mandibular Incisor Crown BL*	8293	.000
Mandibular Incisor Crown MD*	34.625	.000
Mandibular Canine Cervical BL*	3.058	.048
Mandibular Canine Cervical MD*	33.268	.000
Mandibular Canine Crown BL*	4.992	.007
Mandibular Canine Crown MD*	24.024	.000
Mandibular Premolar Cervical BL	1.396	.249
Mandibular Premolar Cervical MD*	4.394	.013
Mandibular Premolar Crown BL	2.324	.099
Mandibular Premolar Crown MD*	7.665	.001
Mandibular Molar Cervical BL*	11.608	.000
Mandibular Molar Cervical MD*	29.228	.000
Mandibular Molar Crown BL*	27.604	.000
Mandibular Molar Crown MD*	43.974	.000

Table 4.5 (continued). ANOVA results including F-values and p-values between Southwest Hispanics, European Americans, and Native Americans. * indicates statistical significance ($p \leq 0.05$).

Maxillary Incisor Composition*	4.944	.008
Maxillary Canine Composition*	36.315	.000
Maxillary Premolar Composition*	19.595	.000
Maxillary Molar Composition*	4.542	.011
Mandibular Incisor Composition*	6.338	.002
Mandibular Canine Composition*	17.391	.000
Mandibular Premolar Composition	2.776	.064
Mandibular Molar Composition*	18.612	.000
Maxillary Arch Depth	.477	.621
Maxillary Incisor Width*	7.303	.001
Maxillary Canine Width*	37.197	.000
Maxillary Premolar Width*	12.605	.000
Maxillary Molar Width*	11.521	.000
Mandibular Arch Depth	.685	.504
Mandibular Incisor Width*	16.492	.000
Mandibular Canine Width*	38.240	.000
Mandibular Premolar Width*	36.715	.000
Mandibular Molar Width*	7.246	.001

Table 4.6. ANOVA results including F-values and p-values between Southwest Hispanics and European Americans. * indicates statistical significance ($p \leq 0.05$).

Variable	F	Sig
Maxillary Incisor Cervical BL	.017	.898
Maxillary Incisor Cervical MD	.402	.527
Maxillary Incisor Crown BL	.842	.359
Maxillary Incisor Crown MD	.224	.636
Maxillary Canine Cervical BL*	4.632	.032
Maxillary Canine Cervical MD*	16.838	.000
Maxillary Canine Crown BL*	10.132	.002
Maxillary Canine Crown MD*	17.396	.000
Maxillary Premolar Cervical BL*	5.064	.025
Maxillary Premolar Cervical MD	14.549	.000
Maxillary Premolar Crown BL*	9.525	.002
Maxillary Premolar Crown MD*	14.082	.000
Maxillary Molar Cervical BL	3.553	.060
Maxillary Molar Cervical MD	.099	.753
Maxillary Molar Crown BL*	8.475	.004
Maxillary Molar Crown BL Non-perpendicular*	9.482	.002
Maxillary Molar Crown MD	.181	.671
Mandibular Incisor Cervical BL	3.729	.054
Mandibular Incisor Cervical MD*	20.875	.000
Mandibular Incisor Crown BL*	13.510	.000
Mandibular Incisor Crown MD*	15.244	.000
Mandibular Canine Cervical BL*	5.144	.024
Mandibular Canine Cervical MD*	8.985	.003
Mandibular Canine Crown BL*	9.173	.003
Mandibular Canine Crown MD*	9.887	.002
Mandibular Premolar Cervical BL	.286	.593
Mandibular Premolar Cervical MD*	6.297	.013
Mandibular Premolar Crown BL*	4.437	.036
Mandibular Premolar Crown MD*	6.335	.012
Mandibular Molar Cervical BL	2.333	.128
Mandibular Molar Cervical MD*	21.032	.000
Mandibular Molar Crown BL*	7.647	.006
Mandibular Molar Crown MD*	25.245	.000

Table 4.6. ANOVA results including F-values and p-values between Southwest Hispanics and European Americans. * indicates statistical significance ($p \leq 0.05$).

Maxillary Incisor Composition*	8.333	.004
Maxillary Canine Composition*	27.173	.000
Maxillary Premolar Composition*	8.397	.004
Maxillary Molar Composition*	6.425	.012
Mandibular Incisor Composition*	4.894	.028
Mandibular Canine Composition*	17.436	.000
Mandibular Premolar Composition*	4.623	.032
Mandibular Molar Composition*	18.337	.000
Maxillary Arch Depth	.268	.605
Maxillary Incisor Width*	6.447	.012
Maxillary Canine Width*	28.166	.000
Maxillary Premolar Width*	8.000	.005
Maxillary Molar Width*	14.905	.000
Mandibular Arch Depth	.059	.808
Mandibular Incisor Width*	11.682	.001
Mandibular Canine Width*	24.752	.000
Mandibular Premolar Width*	30.304	.000
Mandibular Molar Width*	12.010	.001

Table 4.7. ANOVA results including F-values and p-values between Southwest Hispanics and Native Americans. * indicates statistical significance ($p \leq 0.05$).

Variable	F	Sig
Maxillary Incisor Cervical BL	1.474	.226
Maxillary Incisor Cervical MD*	6.157	.014
Maxillary Incisor Crown BL	.858	.355
Maxillary Incisor Crown MD	.664	.416
Maxillary Canine Cervical BL	.001	.980
Maxillary Canine Cervical MD*	24.250	.000
Maxillary Canine Crown BL	.007	.932
Maxillary Canine Crown MD*	17.423	.000
Maxillary Premolar Cervical BL*	6.124	.014
Maxillary Premolar Cervical MD*	5.078	.025
Maxillary Premolar Crown BL*	9.009	.003
Maxillary Premolar Crown MD*	26.155	.000
Maxillary Molar Cervical BL*	8.169	.005
Maxillary Molar Cervical MD*	13.745	.000
Maxillary Molar Crown BL*	12.727	.000
Maxillary Molar Crown BL Non-perpendicular*	8.238	.004
Maxillary Molar Crown MD	.491	.484
Mandibular Incisor Cervical BL	.451	.502
Mandibular Incisor Cervical MD*	8.071	.005
Mandibular Incisor Crown BL	.147	.702
Mandibular Incisor Crown MD*	22.731	.000
Mandibular Canine Cervical BL	3.231	.073
Mandibular Canine Cervical MD*	28.995	.000
Mandibular Canine Crown BL	3.584	.059
Mandibular Canine Crown MD*	15.558	.000
Mandibular Premolar Cervical BL	2.783	.096
Mandibular Premolar Cervical MD	.066	.798
Mandibular Premolar Crown BL	.877	.350
Mandibular Premolar Crown MD	2.612	.107
Mandibular Molar Cervical BL*	12.254	.001
Mandibular Molar Cervical MD*	11.318	.001
Mandibular Molar Crown BL*	24.536	.000
Mandibular Molar Crown MD*	22.527	.000

Table 4.7. ANOVA results including F-values and p-values between Southwest Hispanics and Native Americans. * indicates statistical significance ($p \leq 0.05$).

Maxillary Incisor Composition	.006	.940
Maxillary Canine Composition*	12.635	.000
Maxillary Premolar Composition*	16.078	.000
Maxillary Molar Composition	.075	.784
Mandibular Incisor Composition	2.137	.145
Mandibular Canine Composition	2.027	.155
Mandibular Premolar Composition	.020	.888
Mandibular Molar Composition	3.231	.074
Maxillary Arch Depth	1.108	.293
Maxillary Incisor Width	2.268	.133
Maxillary Canine Width*	13.696	.000
Maxillary Premolar Width*	5.739	.017
Maxillary Molar Width	.039	.844
Mandibular Arch Depth	.981	.323
Mandibular Incisor Width*	7.419	.007
Mandibular Canine Width*	16.219	.000
Mandibular Premolar Width*	9.881	.002
Mandibular Molar Width	1.341	.248

Table 4.8. ANOVA results including F-values and p-values between European Americans and Native Americans. * indicates statistical significance ($p \leq 0.05$).

Variable	F	Sig
Maxillary Incisor Cervical BL	1.729	.190
Maxillary Incisor Cervical MD*	9.569	.002
Maxillary Incisor Crown BL	3.330	.069
Maxillary Incisor Crown MD	1.585	.209
Maxillary Canine Cervical BL*	2.125	.024
Maxillary Canine Cervical MD*	67.027	.000
Maxillary Canine Crown BL*	10.398	.001
Maxillary Canine Crown MD*	68.415	.000
Maxillary Premolar Cervical BL*	16.728	.000
Maxillary Premolar Cervical MD*	37.097	.000
Maxillary Premolar Crown BL*	33.304	.000
Maxillary Premolar Crown MD*	79.539	.000
Maxillary Molar Cervical BL*	16.868	.000
Maxillary Molar Cervical MD*	7.238	.008
Maxillary Molar Crown BL*	38.065	.000
Maxillary Molar Crown BL Non-perpendicular*	31.889	.000
Maxillary Molar Crown MD	1.036	.310
Mandibular Incisor Cervical BL*	5.781	.017
Mandibular Incisor Cervical MD*	50.780	.000
Mandibular Incisor Crown BL*	10.639	.001
Mandibular Incisor Crown MD*	70.463	.000
Mandibular Canine Cervical BL	.308	.580
Mandibular Canine Cervical MD*	66.622	.000
Mandibular Canine Crown BL	1.648	.200
Mandibular Canine Crown MD*	52.473	.000
Mandibular Premolar Cervical BL	.988	.321
Mandibular Premolar Cervical MD*	6.777	.010
Mandibular Premolar Crown BL	1.573	.211
Mandibular Premolar Crown MD*	15.254	.000
Mandibular Molar Cervical BL*	21.177	.000
Mandibular Molar Cervical MD*	56.172	.000
Mandibular Molar Crown BL*	55.487	.000
Mandibular Molar Crown MD*	84.811	.000

Table 4.8. ANOVA results including F-values and p-values between European Americans and Native Americans. * indicates statistical significance ($p \leq 0.05$).

Maxillary Incisor Composition*	5.645	.019
Maxillary Canine Composition*	80.129	.000
Maxillary Premolar Composition*	33.574	.000
Maxillary Molar Composition*	6.906	.009
Mandibular Incisor Composition*	13.655	.000
Mandibular Canine Composition*	38.872	.000
Mandibular Premolar Composition*	4.049	.045
Mandibular Molar Composition*	40.516	.000
Maxillary Arch Depth	.155	.694
Maxillary Incisor Width*	14.843	.000
Maxillary Canine Width*	79.550	.000
Maxillary Premolar Width*	27.363	.000
Maxillary Molar Width*	18.431	.000
Mandibular Arch Depth	1.163	.282
Mandibular Incisor Width*	33.838	.000
Mandibular Canine Width*	86.722	.000
Mandibular Premolar Width*	76.048	.000
Mandibular Molar Width*	7.178	.008

Table 4.9. Results of Post-Hoc Tukey HSD Test between all variables. Southwest Hispanic, Native Americans, and European Americans.

Variable	(I) Ancestry	(J) Ancestry	Mean Difference (I-J)	Significance
UI-Crown BL	Southwest Hispanic	Native American	-.05844	.630
		European American	.06095	.607
	Native American	Southwest Hispanic	.05844	.630
		European American	.11939	.183
	European American	Southwest Hispanic	.06095	.607
		Native American	-.11939	.183
UI-CrownMD	Southwest Hispanic	Native American	-.05529	.692
		European American	.03119	.880
	Native American	Southwest Hispanic	.05529	.692
		European American	.08648	.436
	European American	Southwest Hispanic	-.03119	.880
		Native American	.08648	.436
UC-CrownBL	Southwest Hispanic	Native American	.00637	.996
		European American	.25577	.003
	Native American	Southwest Hispanic	-.00637	.996
		European American	.24940	.006
	European American	Southwest Hispanic	-.25577	.003
		Native American	-.24940	.006
UC-CrownMD	Southwest Hispanic	Native American	-.23770	.000
		European American	.24904	.000
	Native American	Southwest Hispanic	.23770	.000
		European American	.48674	.000
	European American	Southwest Hispanic	-.24904	.000
		Native American	-.48674	.000
UP-Crown BL	Southwest Hispanic	Native American	-.21387	.005
		European American	.20858	.009
	Native American	Southwest Hispanic	.21387	.005
		European American	.42245	.000

Table 4.9 (continued). Results of Post-Hoc Tukey HSD Test between all variables. Southwest Hispanic, Native Americans, and European Americans.

Variable	(I) Ancestry	(J) Ancestry	Mean Difference (I-J)	Significance
	European American	Southwest Hispanic	-.20858	.009
		Native American	-.42245	.000
UP-CrownMD	Southwest Hispanic	Native American	-.29773	.000
		European American	.23020	.000
	Native American	Southwest Hispanic	.29773	.000
		European American	.52793	.000
	European American	Southwest Hispanic	-.23020	.000
		Native American	-.52793	.000
UM-CrownBL	Southwest Hispanic	Native American	-.23004	.002
		European American	.20791	.007
	Native American	Southwest Hispanic	.23004	..002
		European American	.43795	.000
	European American	Southwest Hispanic	-.20791	.007
		Native American	-.43795	.000
UM-CrownMD	Southwest Hispanic	Native American	-.05440	.784
		European American	.03595	.901
	Native American	Southwest Hispanic	.05440	.784
		European American	.09035	.547
	European American	Southwest Hispanic	-.03595	.901
		Native American	-.09035	.547
LI-CrownBL	Southwest Hispanic	Native American	.02114	.927
		European American	.21774	.000
	Native American	Southwest Hispanic	-.02114	.927
		European American	.19660	.003
	European American	Southwest Hispanic	-.21774	.000
		Native American	-.19660	.003
LI-CrownMD	Southwest Hispanic	Native American	-.24762	.000
		European American	.18657	.001
	Native American	Southwest Hispanic	.24762	.000

Table 4.9 (continued). Results of Post-Hoc Tukey HSD Test between all variables. Southwest Hispanic, Native Americans, and European Americans.

Variable	(I) Ancestry	(J) Ancestry	Mean Difference (I-J)	Significance
		European American	.43420	.000
	European American	Southwest Hispanic	-.18657	.001
		Native American	-.43420	.000
LC-CrownBL	Southwest Hispanic	Native American	.15363	.137
		European American	.25945	.006
	Native American	Southwest Hispanic	-.15363	.137
		European American	.105801	.434
	European American	Southwest Hispanic	-.25945	.006
		Native American	-.10581	.434
LC-CrownMD	Southwest Hispanic	Native American	-.22499	.000
		European American	.18382	.004
	Native American	Southwest Hispanic	.22499	.000
		European American	.40880	.000
	European American	Southwest Hispanic	-.18382	.004
		Native American	-.40880	.000
LP-CrownBL	Southwest Hispanic	Native American	.05242	.621
		European American	.12857	.080
	Native American	Southwest Hispanic	-.05242	.621
		European American	.07615	.436
	European American	Southwest Hispanic	-.12857	.080
		Native American	-.07615	.436
LP-CrownMD	Southwest Hispanic	Native American	-.08858	.234
		European American	.14319	.034
	Native American	Southwest Hispanic	.08858	.234
		European American	.23177	.034
	European American	Southwest Hispanic	-.14319	.234
		Native American	-.23177	.000
LM-CrownBL	Southwest Hispanic	Native American	-.30535	.034
		European American	.18131	.000

Table 4.9 (continued). Results of Post-Hoc Tukey HSD Test between all variables. Southwest Hispanic, Native Americans, and European Americans.

Variable	(I) Ancestry	(J) Ancestry	Mean Difference (I-J)	Significance
	Native American	Southwest Hispanic	.30535	.000
		European American	.48667	.012
	European American	Southwest Hispanic	-.18131	.000
		Native American	-.48667	.000
LM-CrownMD	Southwest Hispanic	Native American	-.38862	.012
		European American	.44742	.000
	Native American	Southwest Hispanic	.38862	.000
		European American	.83604	.000
	European American	Southwest Hispanic	-.44742	.000
		Native American	-.83604	.000
Max Arch Depth	Southwest Hispanic	Native American	.32043	.596
		European American	.17699	.855
	Native American	Southwest Hispanic	-.32043	.596
		European American	-.14344	.910
	European American	Southwest Hispanic	-.17699	.855
		Native American	.14344	.910
Max Incisor Width	Southwest Hispanic	Native American	-.18048	.254
		European American	.28148	.041
	Native American	Southwest Hispanic	.18408	.254
		European American	.46196	.000
	European American	Southwest Hispanic	-.28148	.041
		Native American	-.46196	.000
Max Canine Width	Southwest Hispanic	Native American	-1.13810	.001
		European American	1.66081	.000
	Native American	Southwest Hispanic	1.13810	.001
		European American	2.79891	.000
	European American	Southwest Hispanic	-1.66081	.000
		Native American	-2.79891	.000

Table 4.9 (continued). Results of Post-Hoc Tukey HSD Test between all variables. Southwest Hispanic, Native Americans, and European Americans.

Variable	(I) Ancestry	(J) Ancestry	Mean Difference (I-J)	Significance
Max Premolar Width	Southwest Hispanic	Native American	-.76542	.048
		European American	.98270	.009
	Native American	Southwest Hispanic	.76542	.048
		European American	1.74812	.000
	European American	Southwest Hispanic	-.98270	.009
		Native American	-1.74812	.000
Max Molar Width	Southwest Hispanic	Native American	-.06364	.982
		European American	1.46559	.000
	Native American	Southwest Hispanic	.06364	.982
		European American	1.52923	.000
	European American	Southwest Hispanic	-1.46559	.000
		Native American	-1.52923	.000
Man Arch Depth	Southwest Hispanic	Native American	.25019	.641
		European American	-.07299	.964
	Native American	Southwest Hispanic	-.25019	.641
		European American	-.32318	.511
	European American	Southwest Hispanic	.07299	.964
		Native American	.32318	.511
Man Incisor Width	Southwest Hispanic	Native American	-.63343	.011
		European American	.70096	.004
	Native American	Southwest Hispanic	.63343	.011
		European American	1.33439	.000
	European American	Southwest Hispanic	-.70096	.004
		Native American	-1.33439	.000
Man Canine Width	Southwest Hispanic	Native American	-1.07387	.000
		European American	1.31263	.000
	Native American	Southwest Hispanic	1.07387	.000
		European American	2.38649	.000

Table 4.9 (continued). Results of Post-Hoc Tukey HSD Test between all variables. Southwest Hispanic, Native Americans, and European Americans.

Variable	(I) Ancestry	(J) Ancestry	Mean Difference (I-J)	Significance
	European American	Southwest Hispanic	-1.31263	.000
		Native American	--2.38649	.000
Man Premolar Width	Southwest Hispanic	Native American	-.83341	.008
		European American	1.67050	.000
	Native American	Southwest Hispanic	.83341	.008
		European American	2.50391	.000
	European American	Southwest Hispanic	-1.67050	.000
		Native American	-2.50391	.000
Man Molar Width	Southwest Hispanic	Native American	.37974	.517
		European American	1.31706	.001
	Native American	Southwest Hispanic	-.37974	.517
		European American	.93732	.026
	European American	Southwest Hispanic	-1.31706	.001
		Native American	-.93732	.026

Table 4.10. Independent and stepwise discriminant function analyses (all dental crown dimensions).

Independent	Stepwise	Ancestries Included
52.3% SH: 46.8% NA: 70.9% EA: 43.2% AA: 10..0%	45.5% SH: 37.0% NA: 53.8% EA: 55.8% AA: 0.0%	All
57.6% SH: 51.1% NA: 70.9% EA: 45.9%	54.2% SH: 33.0% NA: 74.7% EA: 59.3%	SH, NA, EA
72.5% SH: 70.2% NA: 74.5%	74.4% SH: 74.5% NA: 74.4%	SH, NA
83.7% NA: 87.3% EA: 78.4%	78.3% NA: 83.3% EA 72.4%	NA, EA
59.5% SH: 68.1% EA: 48.6%	57.2% SH: 65.1% EA: 46.9%	SH, EA

Table 4.11. Independent and stepwise discriminant function analyses (all arch dimensions).

Independent	Stepwise	Ancestries Included
53.2% SH: 55.0% NA: 68.8% EA: 48.1% AA: 0.0%	51.7% SH: 53.1% NA: 64.3% EA: 49.1% AA: 0.0%	All
56.6% SH: 52.3% NA: 69.8% EA: 46.8%	55.9% SH: 55.9% NA: 63.9% EA: 46.9%	SH, NA, EA
72.9% SH: 73.3% NA: 72.5%	69.5% SH: 75.0% NA: 63.5%	SH, NA
84.0% NA: 83.3% EA: 84.8%	82.1% NA: 82.5% EA: 81.5%	NA, EA
62.6% SH: 74.8% EA: 45.6%	62.4% SH: 79.9% EA: 38.9%	SH, EA

Table 4.12. Independent and stepwise discriminant function analyses (all dimensions).

Independent	**Stepwise**	**Ancestries Included**
59.5% SH: 48.6% NA: 76.7% EA: 63.3% AA: 0.0%	50.3% SH: 45.7% NA: 56.8% EA: 63.3% AA: 0.0%	All
63.9% SH: 54.3% NA: 76.7% EA: 56.7%	55.8% SH:44.8% NA: 72.7% EA:52.5%	SH, NA, EA
78.2% SH: 77.1% NA: 79.1%	70.0% SH: 68.9% NA: 71.3%	SH, NA
86.3% NA: 93.0% EA: 76.7%	83.3% NA: 95.6% EA: 71.4%	NA, EA
70.8% SH: 74.3% EA: 66.7%	62.7% SH: 68.9% EA: 54.7%	SH, EA

Table 4.13. Independent and stepwise discriminant function analyses (statistically significant dental crown dimensions).

Independent	**Stepwise**	**Ancestries Included**
52.5% SH: 46.9% NA: 73.2% EA: 42.0% AA: 17.6%	47.6% SH: 47.6% NA: 61.7% EA: 44.3% AA: 0.0%	All
55.7% SH: 48.4% NA: 70.4% EA: 44.0%	47.0% SH: 30.8% NA: 68.1% EA: 44.3%	SH, NA, EA
66.7% SH: 60.3% NA: 74.1%	65.8% SH: 63.0% NA: 69.2%	SH, NA
75.4% NA: 79.5% EA: 69.8%	75.2% NA: 81.6% EA: 67.1%	NA, EA
60.2% SH: 70.3% EA: 46.9%	62.5% SH: 78.9% EA: 43.5%	SH, EA

Table 4.14. Independent and stepwise discriminant function analyses (statistically significant arch dimensions).

Independent	Stepwise	Ancestries Included
47.5% SH: 25.2% NA: 60.8% EA: 43.9% AA: 0.0%	42.1% SH: 37.6% NA: 45.7% EA: 53.9% AA: 0.0%	All
50.3% SH: 46.8% NA: 59.8% EA: 43.9%	49.9% SH: 45.7% NA: 62.7% EA: 41.0%	SH, NA, EA
61.1% SH: 75.0% NA: 42.6%	61.2% SH: 74.6% NA: 43.8%	SH, NA
81.0% NA: 82.5% EA: 79.3%	79.4% NA: 80.5% EA: 78.1%	NA, EA
61.1% SH: 73.9% EA: 43.9%	63.7% SH: 79.3% EA: 42.9%	SH, EA

Table 4.15. Independent and stepwise discriminant function analyses (all statistically significant dimensions).

Independent	Stepwise	Ancestries Included
56.9% SH: 45.7% NA: 75.0% EA: 59.5% AA: 14.3%	50.9% SH: 49.1% NA: 65.0% EA: 50.6% AA: 0.0%	All
66.2% SH: 50.0% NA: 78.6% EA: 67.6%	54.1% SH: 35.2% NA: 74.8% EA: 52.9%	SH, NA, EA
62.0% SH: 62.7% NA: 61.3%	63.2% SH: 57.1% NA: 70.4%	SH, NA
82.5% NA: 84.6% EA: 79.7%	82.0% NA: 85.9% EA: 76.9%	NA, EA
72.3% SH: 78.3% EA: 64.9%	65.9% SH: 76.5% EA: 53.5%	SH, EA

Table 4.16. Independent and stepwise discriminant function analyses (all dental crown dimensions). Sex-specific classification rates.

Independent		**Stepwise**		**Ancestries Included**
Males	Females	Males	Females	
53.6% SH: 67.9% NA: 55.0% EA: 42.9% AA: 14.3%	55.0% SH: 15.8% NA: 85.7% EA: 47.8% AA: 0.0%	41.3% SH: 76.3% NA: 51.3% EA: 0.0% SH: 0.0%	51.3% SH: 13.3% NA: 70.3% EA: 79.5% AA: 0.0%	All
58.1% SH: 67.9% NA: 55.0% EA: 42.9%	55.8% SH: 15.8% NA: 82.9% EA: 47.8%	44.7% SH: 58.6% NA: 42.9% EA: 27.8%	56.1% SH: 13.3% NA: 71.9% EA: 79.5%	SH, NA, EA
68.8% SH: 78.6% NA: 55.0%	70.4% SH: 52.6% NA: 80.0%	70.1% SH: 77.1% NA: 58.6%	61.5% SH: 46.3% NA: 76.5%	SH, NA
67.6% NA: 65.0% EA: 71.4%	84.5% NA: 85.7% EA: 82.6%	75.0% NA: 78.6% EA: 72.5%	83.1% NA: 81.5% EA: 85.7%	NA, EA
59.5% SH: 67.9% NA: 42.9%	47.6% SH: 47.4% EA: 47.8%	57.3% SH: 82.6% NA: 21.5%	60.8% SH: 45.5% EA: 80.0%	SH, EA

Table 4.17. Independent and stepwise discriminant function analyses (all arch dimensions). Sex-specific classification rates.

Independent		**Stepwise**		**Ancestries Included**
Males	Females	Males	Females	
33.3% SH: 55.7% NA: 7.7% EA: 27.0% AA: 0.0%	59.3% SH: 42.0% NA: 84.3% EA: 52.4% AA: 0.0%	40.8% SH: 80.4% NA: 10.9% EA: 16.9% AA: 0.0%	49.4% SH: 28.2% NA: 77.4% EA: 48.4% AA: 0.0%	All
39.5% SH: 60.7% NA: 7.7% EA: 27.0%	63.0% SH: 40.0% NA: 84.3% EA: 54.8%	44.4% SH: 83.5% NA: 6.5% EA: 15.5%	53.4% SH: 26.8% NA: 78.6% EA: 50.0%	SH, NA, EA
63.2% SH: 86.9% NA: 7.7%	76.7% SH: 68.0% NA: 82.9%	67.1% SH: 96.9% NA: 4.3%	81.3% SH: 71.4% NA: 88.5%	SH, NA
71.4% NA: 53.8% EA: 83.8%	86.6% NA: 88.6% EA: 83.3%	72.6% NA: 64.3% EA: 78.1%	81.1% NA: 89.3% EA: 69.5%	NA, EA
55.1% SH: 73.8% NA: 24.3%	67.4% SH: 74.0% EA: 59.5%	54.8% SH: 86.6% NA: 11.3%	63.1% SH: 75.3% EA: 47.9%	SH, EA

Table 4.18. Independent and stepwise discriminant function analyses (all dimensions). Sex-specific classification rates.

Independent		**Stepwise**		**Ancestries Included**
Males	Females	Males	Females	
40.4%	59.4%	35.8%	48.7%	All
SH: 40.0%	SH: 26.7%	SH: 47.3%	SH: 0.0%	
NA: 53.3%	NA: 78.6%	NA: 54.8%	NA: 77.4%	
EA: 36.4%	EA: 63.2%	EA: 17.2%	EA: 81.8%	
AA: 16.7%	AA: 0.0%	AA: 0.0%	AA: 0.0%	
52.2%	58.1%	39.1%	63.2%	SH, NA, EA
SH: 50.0%	SH: 26.7%	SH: 47.3%	SH: 27.3%	
NA: 66.7%	NA: 75.0%	NA: 54.8%	NA: 79.7%	
EA: 36.4%	EA: 57.9%	EA: 17.2%	EA: 75.7%	
62.9%	69.8%	57.0%	77.5%	SH, NA
SH: 65.0%	SH: 53.3%	SH: 58.1%	SH: 62.9%	
NA: 60.0%	NA: 78.6%	NA: 53.3%	NA: 87.0%	
48.1%	83.0%	76.5%	81.4%	NA, EA
NA: 56.3%	NA: 89.3%	NA: 88.9%	NA: 91.5%	
EA: 36.4%	EA: 73.7%	EA: 66.7%	EA: 69.2%	
48.4%	44.1%	52.5%	69.4%	SH, EA
SH: 55.0%	SH: 46.7%	SH: 54.1%	SH: 59.1%	
EA: 36.4%	EA: 42.1%	EA: 50.0%	EA: 81.8%	

Table 4.19. Independent and stepwise discriminant function analyses (statistically significant dental crown dimensions). Sex-specific classification rates.

Independent		**Stepwise**		**Ancestries Included**
Males	Females	Males	Females	
45.3%	51.3%	43.9%	48.8%	All
SH: 65.1%	SH: 25.8%	SH: 71.8%	SH: 14.3%	
NA: 44.4%	NA: 70.8%	NA: 35.1%	NA: 78.1%	
EA: 20.0%	EA: 50.0%	EA: 17.6%	EA: 63.0%	
AA: 27.3%	AA: 37.5%	AA: 21.4%	AA: 7.7%	
53.8%	50.5%	48.6%	54.1%	SH, NA, EA
SH: 69.7%	SH: 29.0%	SH: 65.8%	SH: 18.4%	
NA: 47.8%	NA: 68.8%	NA: 51.3%	NA: 78.1%	
EA: 36.4%	EA: 42.9%	EA: 25.0%	EA: 58.7%	
69.7%	58.3%	70.9%	68.8%	SH, NA
SH: 83.3%	SH: 41.2%	SH: 82.6%	SH: 58.6%	
NA: 46.4%	NA: 70.0%	NA: 47.1%	NA: 77.1%	
62.5%	79.5%	71.7%	80.9%	NA, EA
NA: 62.5%	NA: 79.6%	NA: 66.7%	NA: 87.5%	
EA: 62.5%	EA:79.3%	EA: 75.0%	EA: 71.7%	
55.6%	55.9%	65.2%	61.6%	SH, EA
SH: 69.7%	SH: 61.3%	SH: 89.4%	SH: 68.4%	
EA: 33.3%	EA: 50.0%	EA: 26.4%	EA: 54.5%	

Table 4.20. Independent and stepwise discriminant function analyses (statistically significant arch dimensions). Sex-specific classification rates.

Independent		**Stepwise**		**Ancestries Included**
Males	Females	Males	Females	
35.9% SH: 59.0% NA: 14.8% EA: 27.5% AA: 0.0%	58.1% SH: 42.0% NA: 81.4% EA: 52.4% AA: 0.0%	42.9% SH: 79.4% NA: 10.9% EA: 25.4% AA: 0.0%	48.3% SH: 22.4% NA: 76.4% EA: 58.6% AA: 0.0%	All
41.4% SH: 62.3% NA: 14.8% EA: 27.5%	61.7% SH: 42.0% NA: 80.0% EA: 54.8%	46.7% SH: 80.4% NA: 10.9% EA: 23.9%	53.3% SH: 23.5% NA: 77.5% EA: 58.6%	SH, NA, EA
67.0% SH: 85.9% NA: 50.00%	62.3% SH: 61.4% NA: 63.2%	67.1% SH: 97.0% NA: 4.2%	60.5% SH: 61.0% NA: 60.0%	SH, NA
73.1% NA: 59.3% EA: 82.5%	82.1% NA: 88.6% EA:71.4%	70.9% NA: 58.7% EA: 78.9%	79.9% NA: 84.3% EA: 74.3%	NA, EA
56.4% SH: 73.8% EA: 30.0%	66.3% SH: 72.0% EA: 59.5%	58.3% SH: 85.6% EA: 21.1%	63.1% SH: 75.3% EA: 47.9%	SH, EA

Table 4.21. Independent and stepwise discriminant function analyses (all statistically significant dimensions). Sex-specific classification rates.

Independent		**Stepwise**		**Ancestries Included**
Males	Females	Males	Females	
46.9% SH: 58.3% NA: 50.0% EA: 37.5% AA: 25.0%	58.4% SH: 40.9% NA: 80.0% EA: 42.9% AA: 33.3%	47.5% SH: 54.8% NA: 50.0% EA: 48.3% AA: 0.0%	55.0% SH: 14.6% NA: 87.7% EA: 59.6% AA: 50.0%	All
57.1% SH: 58.3% NA: 62.5% EA: 50.0%	63.9% SH: 36.4% NA: 85.0% EA: 52.4%	50.0% SH: 53.5% NA: 48.5% EA: 46.2%	62.7% SH: 34.9% NA: 83.3% EA: 55.8%	SH, NA, EA
62.1% SH: 76.9% NA: 31.6%	63.4% SH: 48.1% NA: 72.7%	65.2% SH: 80.3% NA: 35.9%	68.4% SH: 47.8% NA: 82.4%	SH, NA
62.9% NA: 64.7% EA: 61.1%	79.0% NA: 80.5% EA: 76.2%	70.9% NA: 75.0% EA: 68.2%	84.8% NA: 87.1% EA: 81.1%	NA, EA
62.5% SH: 75.0% EA: 43.8%	72.1% SH: 68.2% EA: 76.2%	59.3% SH: 69.5% EA: 46.8%	67.9% SH: 66.7% EA: 69.4%	SH, EA

Table 4.22. Discriminant function equations for an individual of unknown sex using statistically significant variables.

Equation 1a. Southwest Hispanics, Native American, European American

UC-BL	UC-MD	UP-BL	UP-MD	UM-BL	UM-MD	LI-BL	LI-MD	LC-BL	LC-MD	LP-MD
-.002	.542	-.512	.957	.080	-.676	.387	-.147	-.427	.378	-1.214
LM-BL	LM-MD	MaxIW	MaxCW	MaxPW	MaxMW	ManIW	ManCW	ManPW	ManMW	
-.841	1.578	.068	.095	-.083	.130	.119	.258	.137	-.153	

Constant -15.001; Wilks' Lambda = 0.294
Functions at Group Centroids: Hispanic = -0.204; Native American = 1.419; European American = -1.730
Prior Probabilities: Hispanic = 0.318; Native American = 0.395; European American = 0.287
Cross-validated classification: 64.3%; Hispanic = 48.8%; Native American = 78.4%; European American = 62.2%

Equation 2a. Southwest Hispanics, Native Americans

UC-MD	UP-BL	UP-MD	UM-BL	LI-MD	LC-MD	LM-BL	LM-MD	MaxCW	MaxPW	ManIW
0.264	-1.068	1.543	-0.411	-0.378	-0.351	0.746	0.620	0.066	-0.043	-0.096
ManCW	ManPW									
0.252	0.127									

Constant -18.634; Wilks' Lambda = 0.791
Functions at Group Centroid: Hispanic = -0.522; Native American = 0.497
Prior Probabilities: Hispanic = 0.488; Native American = 0.512
Cross-validated classification: 62.0%; Hispanic = 62.7%; Native American = 61.3%

Equation 2b. Southwest Hispanics, European Americans

UC-BL	UC-MD	UP-BL	UP-MD	UM-BL	LI-BL	LI-MD	LC-BL	LC-MD	LP-BL	LP-MD
0.627	0.227	-0.057	0.968	-0.527	0.101	0.229	-0.379	-0.325	-0.861	-0.111
LM-BL	LM-MD	MaxIW	MaxCW	MaxPW	MaxMW	ManIW	ManCW	ManPW	ManMW	
-1.369	1.582	-0.157	0.195	-0.252	0.302	-0.013	0.227	0.191	-0.087	

Constant -17.625; Wilks' Lambda = 0.464
Functions at Group Centroid: Hispanic = 0.952; European American = -1.183
Prior Probabilities: Hispanic = 0.554; European American = 0.446
Cross validated classification: 72.3%; Hispanic = 78.3%; European American = 64.9%

Table 4.23. Discriminant function equations for an individual of known sex using statistically significant variables.

Equation 1a. Southwest Hispanics, Native American, European American Males

UC-BL	UC-MD	UP-BL	UP-MD	UM-BL	UM-MD	LI-BL	LI-MD	LC-BL	LC-MD	LP-MD
0.153	0.130	-0.577	1.543	1.160	-1.316	1.063	-0.812	-1.083	1.288	-1.413
LM-BL	LM-BL	MaxIW	MaxCW	MaxPW	MaxMW	ManIW	ManCW	ManPW	ManMW	
-2.302	2.393	-0.054	-0.679	0.159	0.114	-0.386	0.260	0.435	0.238	

Constant -8.975; Wilks' Lambda = 0.085

Functions at Group Centroids: Hispanics = -0.472; Native Americans = 3.224; European Americans = -1.004

Posterior Probabilities: Hispanics = 0.415; Native Americans = 0.283; European Americans = 0.302

Cross-validated classification: 60.4%; Hispanics = 54.5%, Native Americans = 73.3%, European Americans = 56.3%

Equation 1b. Southwest Hispanics, Native American, European American Females

UC-BL	UC-MD	UP-BL	UP-MD	UM-BL	UM-MD	LI-BL	LI-MD	LC-BL	LC-MD	LP-MD
-0.244	0.749	-0.787	0.746	0.018	-0.222	-0.742	-0.687	0.729	0.731	-1.219
LM-BL	LM-BL	MaxIW	MaxCW	MaxPW	MaxMW	ManIW	ManCW	ManPW	ManMW	
-0.577	1.537	0.181	0.053	-0.001	0.074	0.227	0.361	-0.059	-0.199	

Constant = -.14.705; Wilks' Lambda = 0.209

Functions at Group Centroids: Hispanics = -0.134; Native Americans = 1.319; European Americans = -2.076

Posterior Probabilities: Hispanics = 0.253; Native Americans = 0.467; European Americans = 0.280

Cross-validated classification: 64.0%; Hispanics = 42.1%, Native Americans = 77.1%, European Americans = 61.9%

Table 4.23 (continued). Discriminant function equations for an individual of known sex using statistically significant variables.

Equation 2aa. Southwest Hispanics, Native American Males

UC-BL -0.527	UC-MD 0.877	UP-BL -1.100	UP-MD 1.901	UM-BL 1.707	LI-BL 1.107	LI-MD -1.499	LC-BL -0.965	LC-MD 1.260	LP-MD -2.181	LM-BL -2.541	LM-MD 1.268
MaxIW -0.141	MaxCW 0.018	MaxPW 0.246	MaxMW -0.069	ManIW 0.623	ManCW 0.430	ManPW -0.331	ManMW 0.014				

Constant -14.007; Wilks' Lambda = 0.269
Functions at Group Centroids: Hispanics = -1.313; Native Americans = 1.970
Prior Probabilities: Hispanic = 0.600; Native Americans = 0.400
Cross-validated classification: 72.5%; Hispanic = 79.2%, Native American = 62.5%

Equation 2ab. Southwest Hispanics, Native American Females

UC-BL -0.778	UC-MD -0.211	UP-BL 0.570	UP-MD 0.544	UM-BL 0.122	LI-BL -1.523	LI-MD -1.392	LC-BL 1.216	LC-MD 0.664	LP-MD -1.690	LM-BL 0.148	LM-MD 1.142
MaxIW 0.255	MaxCW -0.032	MaxPW 0.002	MaxMW -0.210	ManIW -0.214	ManCW 0.215	ManPW 0.501	ManMW -0.253				

Constant -1.494; Wilks' Lambda = 0.480
Functions at Group Centroids: Hispanics = -1.380; Native Americans = .759
Prior Probabilities: Hispanics = 0.355; Native Americans = 0.645
Cross-validated classification: 72.6%; Hispanic = 59.1%, Native Americans 80.0%

Table 4.23 (continued). Discriminant function equations for an individual of known sex using statistically significant variables.

Equation 2ba. Southwest Hispanics, European American Males

UC-BL	UC-MD	UP-BL	UP-MD	UM-BL	LI-BL	LI-MD	LC-BL	LC-MD	LP-MD	LM-BL	LM-MD
1.092	-2.833	0.344	1.262	-0.617	-0.981	0.344	-0.776	-1.016	1.258	-0.676	1.529
MaxIW	MaxCW	MaxPW	MaxMW	ManIW	ManCW	ManPW	ManMW				
-0.932	0.342	-0.250	0.201	-0.263	0.160	0.379	-0.022				

Constant -7.888 ; Wilks' Lambda = 0.313

Functions at Group Centroids: Hispanic = 1.179; European American = -1.768

Prior Probabilities: Hispanic = 0.600; European American = 0.400

Cross-validated classification: 67.5%; Hispanic = 79.2%, European American = 50.0%

Equation 2bb. Southwest Hispanics, European American Females

UC-BL	UC-MD	UP-BL	UP-MD	UM-BL	LI-BL	LI-MD	LC-BL	LC-MD	LP-MD	LM-BL	LM-MD
0.171	1.047	-1.438	0.733	0.895	0.755	2.056	0.128	-0.841	-1.505	-2.442	1.786
MaxIW	MaxCW	MaxPW	MaxMW	ManIW	ManCW	ManPW	ManMW				
-0.528	0.240	-0.374	0.497	0.369	0.464	-0.421	-0.127				

Constant -21.152; Wilks' Lambda = 0.294

Functions at Group Centroids: Hispanic = 1.478; European American = -1.548

Prior Probabilities: Hispanic = 0.512; European American = 0.488

Cross-validated classification: 72.1%; Hispanic = 68.2%, European American = 76.2%

Table 4.23 (continued). Discriminant function equations for an individual of known sex using statistically significant variables.

Equation 2ca. European American, Native American Males

UC-BL	UC-MD	UP-BL	UP-MD	UM-BL	LI-BL	LI-MD	LC-MD	LP-MD	LM-BL	LM-MD	MaxIW
-0.341	0.916	-0.921	1.455	0.297	0.556	-0.533	-0.055	-1.250	-0.993	1.022	-0.038
MaxCW	MaxPW	MaxMW	ManIW	ManCW	ManPW	ManMW					
0.227	-0.090	0.161	0.238	0.376	0.096	0.175					

Constant -23.328; Wilks' Lambda = 0.276
Functions at Group Centroids: Native American = 1.617; European American = -1.527
Prior Probabilities: Native American = 0.486; European Americans = 0.514
Cross-validated classification: 62.9%; Native American = 64.7%, European American = 61.1%

Equation 2cb. European American, Native American Females

UC-BL	UC-MD	UP-BL	UP-MD	UM-BL	LI-BL	LI-MD	LC-MD	LP-MD	LM-BL	LM-MD	MaxIW
-0.311	0.994	-0.658	0.769	0.376	-0.527	-0.796	0.520	-1.375	-0.119	0.870	0.225
MaxCW	MaxPW	MaxMW	ManIW	ManCW	ManPW	ManMW-					
0.112	-0.052	0.169	-0.174	0.269	0.176	0.131					

Constant -19.391; Wilks' Lambda = 0.269
Functions at Group Centroids: Native American = 0.950; European American = -1.854
Prior Probabilities: Native American = 0.661; European Americans = 0.339
Cross-validated classification: 79.0%; Native American = 80.5%, European American = 76.2%

Table 4.24. ANOVA results of statistically significant variables between Hispanic males and females, including F-values and p-values. * indicates statistical significance.

Variable	F	Sig
Maxillary Incisor Cervical BL*	4.564	.034
Maxillary Incisor Cervical MD*	12.397	.001
Maxillary Incisor Crown BL*	12.397	.001
Maxillary Incisor Crown MD*	5.678	.018
Maxillary Canine Cervical BL*	18.402	.000
Maxillary Canine Cervical MD*	21.094	.000
Maxillary Canine Crown BL*	15.177	.000
Maxillary Canine Crown MD*	13.850	.000
Maxillary Premolar Cervical BL*	9.792	.002
Maxillary Premolar Cervical MD	2.103	.149
Maxillary Premolar Crown BL*	9.306	.003
Maxillary Premolar Crown MD*	7.184	.008
Maxillary Molar Cervical BL*	22.930	.000
Maxillary Molar Cervical MD*	4.569	.034
Maxillary Molar Crown BL*	18.122	.000
Maxillary Molar Crown BL Non-perpendicular*	22.217	.000
Maxillary Molar Crown MD*	13.446	.000
Mandibular Incisor Cervical BL	1.587	.209
Mandibular Incisor Cervical MD	2.320	.129
Mandibular Incisor Crown BL	1.688	.196
Mandibular Incisor Crown MD	2.565	.111
Mandibular Canine Cervical BL*	23.960	.000
Mandibular Canine Cervical MD*	49.369	.000
Mandibular Canine Crown BL*	20.902	.000
Mandibular Canine Crown MD*	52.640	.000
Mandibular Premolar Cervical BL*	17.956	.000
Mandibular Premolar Cervical MD*	4.146	.043
Mandibular Premolar Crown BL*	10.882	.001
Mandibular Premolar Crown MD*	11.003	.001
Mandibular Molar Cervical BL*	8.168	.005
Mandibular Molar Cervical MD*	28.053	.000
Mandibular Molar Crown BL*	6.900	.009
Mandibular Molar Crown MD*	27.787	.000

Table 4.24 (continued). ANOVA results of statistically significant variables between Hispanic males and females, including F-values and p-values. * indicates statistical significance.

Maxillary Incisor Composition*	3.970	.049
Maxillary Canine Composition*	8.984	.003
Maxillary Premolar Composition*	5.976	.016
Maxillary Molar Composition*	8.896	.004
Mandibular Incisor Composition*	4.179	.043
Mandibular Canine Composition*	15.297	.000
Mandibular Premolar Composition*	9.504	.002
Mandibular Molar Composition*	15.839	.000
Maxillary Arch Depth	.863	.354
Maxillary Incisor Width	1.774	.184
Maxillary Canine Width*	6.129	.014
Maxillary Premolar Width*	5.533	.020
Maxillary Molar Width*	7.745	.006
Mandibular Arch Depth	1.071	.302
Mandibular Incisor Width	.016	.899
Mandibular Canine Width	2.283	.132
Mandibular Premolar Width	3.614	.059
Mandibular Molar Width*	11.784	.001

Table 4.25. ANOVA results of statistically significant variables between Native American males and females, including F-values and p-values. * indicates statistical significance.

Variable	F	Sig
Maxillary Incisor Cervical BL*	17.193	.000
Maxillary Incisor Cervical MD*	18.114	.000
Maxillary Incisor Crown BL*	13.398	.000
Maxillary Incisor Crown MD*	13.967	.000
Maxillary Canine Cervical BL*	10.381	.002
Maxillary Canine Cervical MD*	11.116	.001
Maxillary Canine Crown BL*	8.750	.004
Maxillary Canine Crown MD*	11.074	.001
Maxillary Premolar Cervical BL*	10.449	.002
Maxillary Premolar Cervical MD*	4.079	.045
Maxillary Premolar Crown BL*	8.164	.005
Maxillary Premolar Crown MD*	4.210	.042
Maxillary Molar Cervical BL*	14.866	.000
Maxillary Molar Cervical MD*	8.629	.004
Maxillary Molar Crown BL*	18.377	.000
Maxillary Molar Crown BL Non-perpendicular*	19.314	.000
Maxillary Molar Crown MD*	6.415	.013
Mandibular Incisor Cervical BL	.624	.431
Mandibular Incisor Cervical MD*	10.306	.002
Mandibular Incisor Crown BL	.058	.811
Mandibular Incisor Crown MD*	9.109	.003
Mandibular Canine Cervical BL*	6.981	.009
Mandibular Canine Cervical MD*	41.102	.000
Mandibular Canine Crown BL	2.547	.113
Mandibular Canine Crown MD*	20.778	.000
Mandibular Premolar Cervical BL*	13.421	.000
Mandibular Premolar Cervical MD	1.093	.297
Mandibular Premolar Crown BL*	14.284	.000
Mandibular Premolar Crown MD	2.110	.148
Mandibular Molar Cervical BL*	7.313	.008
Mandibular Molar Cervical MD*	24.002	.000
Mandibular Molar Crown BL*	8.616	.004
Mandibular Molar Crown MD*	11.884	.001

Table 4.25 (continued). ANOVA results of statistically significant variables between Native American males and females, including F-values and p-values. * indicates statistical significance.

Maxillary Incisor Composition*	7.651	.008
Maxillary Canine Composition*	12.514	.001
Maxillary Premolar Composition*	5.952	.016
Maxillary Molar Composition*	5.629	.020
Mandibular Incisor Composition*	6.807	.010
Mandibular Canine Composition*	12.415	.001
Mandibular Premolar Composition	3.411	.067
Mandibular Molar Composition*	5.824	.018
Maxillary Arch Depth*	10.510	.001
Maxillary Incisor Width	1.388	.241
Maxillary Canine Width	.485	.488
Maxillary Premolar Width	3.448	.065
Maxillary Molar Width*	7.752	.006
Mandibular Arch Depth	.236	.628
Mandibular Incisor Width	2.789	.097
Mandibular Canine Width	.882	.349
Mandibular Premolar Width	.807	.370
Mandibular Molar Width*	12.028	.001

Table 4.26. ANOVA results of statistically significant variables between European American males and females, including F-values and p-values. * indicates statistical significance.

Variable	F	Sig
Maxillary Incisor Cervical BL*	5.902	.016
Maxillary Incisor Cervical MD*	8.388	.004
Maxillary Incisor Crown BL*	2.289	.023
Maxillary Incisor Crown MD*	6.351	.013
Maxillary Canine Cervical BL	3.199	.076
Maxillary Canine Cervical MD*	18.528	.000
Maxillary Canine Crown BL	2.114	.148
Maxillary Canine Crown MD*	31.246	.000
Maxillary Premolar Cervical BL*	8.654	.004
Maxillary Premolar Cervical MD	2.795	.097
Maxillary Premolar Crown BL*	5.588	.020
Maxillary Premolar Crown MD	3.868	.052
Maxillary Molar Cervical BL*	16.674	.000
Maxillary Molar Cervical MD*	10.147	.002
Maxillary Molar Crown BL*	21.835	.000
Maxillary Molar Crown BL Non-perpendicular*	25.462	.000
Maxillary Molar Crown MD*	14.600	.000
Mandibular Incisor Cervical BL	1.410	.237
Mandibular Incisor Cervical MD	2.156	.144
Mandibular Incisor Crown BL	1.201	.275
Mandibular Incisor Crown MD*	15.409	.000
Mandibular Canine Cervical BL	.768	.382
Mandibular Canine Cervical MD*	25.768	.000
Mandibular Canine Crown BL	.071	.790
Mandibular Canine Crown MD*	26.187	.000
Mandibular Premolar Cervical BL*	6.130	.015
Mandibular Premolar Cervical MD*	7.877	.006
Mandibular Premolar Crown BL*	9.067	.003
Mandibular Premolar Crown MD*	5.881	.017
Mandibular Molar Cervical BL*	15.753	.000
Mandibular Molar Cervical MD*	12.673	.001
Mandibular Molar Crown BL*	10.060	.002
Mandibular Molar Crown MD*	17.693	.000

Table 4.26 (continued). ANOVA results of statistically significant variables between European American males and females, including F-values and p-values. * indicates statistical significance.

Maxillary Incisor Composition*	6.344	.013
Maxillary Canine Composition*	6.068	.015
Maxillary Premolar Composition*	16.823	.000
Maxillary Molar Composition*	5.922	.017
Mandibular Incisor Composition*	6.407	.013
Mandibular Canine Composition*	18.058	.000
Mandibular Premolar Composition*	11.140	.001
Mandibular Molar Composition*	6.421	.014
Maxillary Arch Depth*	10.675	.001
Maxillary Incisor Width*	16.268	.000
Maxillary Canine Width*	3.957	.049
Maxillary Premolar Width	1.555	.215
Maxillary Molar Width*	8.413	.004
Mandibular Arch Depth*	5.508	.020
Mandibular Incisor Width*	5.139	.025
Mandibular Canine Width*	13.412	.000
Mandibular Premolar Width*	4.239	.041
Mandibular Molar Width*	12.537	.001

Table 4.27. ANOVA results of statistically significant variables between Asian American males and females, including F-values and p-values. * indicates statistical significance.

Variable	F	Sig
Maxillary Incisor Cervical BL	.303	.586
Maxillary Incisor Cervical MD	2.366	.132
Maxillary Incisor Crown BL	.054	.818
Maxillary Incisor Crown MD	1.141	.292
Maxillary Canine Cervical BL	.705	.406
Maxillary Canine Cervical MD*	9.592	.004
Maxillary Canine Crown BL	.840	.365
Maxillary Canine Crown MD*	8.463	.006
Maxillary Premolar Cervical BL*	5.252	.028
Maxillary Premolar Cervical MD	2.586	.117
Maxillary Premolar Crown BL	1.470	.233
Maxillary Premolar Crown MD	3.461	.071
Maxillary Molar Cervical BL*	13.675	.001
Maxillary Molar Cervical MD*	5.936	.020
Maxillary Molar Crown BL*	11.029	.002
Maxillary Molar Crown BL Non-perpendicular*	8.779	.005
Maxillary Molar Crown MD	1.399	.248
Mandibular Incisor Cervical BL	1.371	.249
Mandibular Incisor Cervical MD	.046	.832
Mandibular Incisor Crown BL	1.492	.229
Mandibular Incisor Crown MD	.320	.575
Mandibular Canine Cervical BL	.236	.630
Mandibular Canine Cervical MD*	8.615	.006
Mandibular Canine Crown BL	.017	.897
Mandibular Canine Crown MD	1.247	.272
Mandibular Premolar Cervical BL*	12.397	.001
Mandibular Premolar Cervical MD*	7.579	.009
Mandibular Premolar Crown BL*	9.586	.004
Mandibular Premolar Crown MD*	9.498	.004
Mandibular Molar Cervical BL*	8.584	.006
Mandibular Molar Cervical MD*	10.001	.003
Mandibular Molar Crown BL	.477	.495
Mandibular Molar Crown MD*	8.229	.008

Table 4.27 (continued). ANOVA results of statistically significant variables between Asian American males and females, including F-values and p-values. * indicates statistical significance.

Maxillary Incisor Composition	1.195	.283
Maxillary Canine Composition*	12.858	.001
Maxillary Premolar Composition*	7.048	.013
Maxillary Molar Composition	2.993	.098
Mandibular Incisor Composition	.389	.537
Mandibular Canine Composition*	9.365	.004
Mandibular Premolar Composition*	11.241	.002
Mandibular Molar Composition	2.251	.156
Maxillary Arch Depth*	8.137	.007
Maxillary Incisor Width	1.524	.224
Maxillary Canine Width*	6.980	.012
Maxillary Premolar Width*	14.320	.001
Maxillary Molar Width*	8.604	.006
Mandibular Arch Depth	2.632	.114
Mandibular Incisor Width	.176	.677
Mandibular Canine Width	1.817	.185
Mandibular Premolar Width*	7.675	.009
Mandibular Molar Width*	7.842	.009

Table 4.28. Classification accuracies of ancestry-sex pairs between Hispanic, Native, and European Americans.

Ancestry-Sex	**Hispanic-Female**	**Native American-Female**	**European American-Female**	**Hispanic-Male**	**Native American-Male**	**European American-Male**
Hispanic-Female	6.7%	26.7%	26.7%	33.3%	0.0%	6.7%
Native American-Female	7.1%	60.7%	3.6%	10.7%	14.3%	3.6%
European American-Female	15.8%	5.3%	57.9%	15.8%	0.0%	5.3%
Hispanic-Male	20.0%	15.0%	10.0%	45.0%	5.0%	5.0%
Native American-Male	0.0%	53.5%	0.0%	6.7%	40.0%	0.0%
European American-Male	18.2%	0.0%	36.4%	36.4%	0.0%	9.1%

Table 4.29. Sex classification rates for Hispanic, Native, and European Americans.

Ancestry	**Sex**	**Dental Crown**	**Dental Arcade**	**Pooled**
Southwest Hispanic	Male	64.3%	70.5%	90.0%
	Female	47.4%	36.0%	66.7%
Native American	Male	60.0%	38.5%	46.7%
	Female	74.3%	88.6%	75.0%
European American	Male	42.9%	51.4%	73.7%
	Female	73.9%	54.8%	72.7%

Table 4.30. Interobserver error results for dental crown dimensions.

Variable	N	T value	Sig
Maxillary Incisor BL	48	.229	.820
Maxillary Incisor MD*	42	-2.620	.012
Maxillary Canine BL	34	1.839	.075
Maxillary Canine MD	37	1.207	.235
Maxillary Premolar BL	39	-1.856	.071
Maxillary Premolar MD	38	-1.175	.247
Maxillary Molar BL	42	-.757	.454
Maxillary Molar BL*	41	-3.305	.002
Maxillary Molar MD*	37	-2.689	.011
Mandibular Incisor BL*	47	5.055	.000
Mandibular Incisor MD	46	1.078	.287
Mandibular Canine BL*	38	2.235	.035
Mandibular Canine MD	41	-.436	.665
Mandibular Premolar BL	43	.907	.370
Mandibular Premolar MD	44	1.544	.130
Mandibular Molar BL	36	-1.143	.261
Mandibular Molar MD	31	-.158	.876

Table 4.31. Interobserver error results for cervical measurements.

Variable	N	T value	Sig
Maxillary Incisor BL*	45	-4.599	.000
Maxillary Incisor MD	26	1.864	.074
Maxillary Canine BL*	34	4.573	.000
Maxillary Canine MD*	22	3.974	.001
Maxillary Premolar BL*	37	4.838	.000
Maxillary Molar BL	45	.885	.381
Mandibular Incisor BL*	50	4.026	.000
Mandibular Incisor MD*	21	-2.875	.009
Mandibular Canine BL*	38	6.249	.000
Mandibular Canine MD*	24	2.573	.017
Mandibular Premolar BL*	42	3.594	.001
Mandibular Molar BL*	37	4.499	.000

Table 4.32. Interobserver error results for dental composition.

Variable	N	T value	Sig
Maxillary Incisor	19	2.867	.010
Maxillary Canine	22	3.229	.004
Maxillary Premolar	23	-.697	.493
Maxillary Molar	19	4.305	.000
Mandibular Incisor	26	2.699	.012
Mandibular Canine	36	3.196	.003
Mandibular Premolar	26	2.879	.008
Mandibular Molar	11	6.035	.000

Table 4.33. Interobserver error results for arcade dimensions.

Variable	N	T value	Sig
Maxillary Arch Depth	36	-1.937	.061
Maxillary Incisor Width	36	.271	.788
Maxillary Canine Width	29	.546	.590
Maxillary Premolar Width	31	1.672	.105
Maxillary Molar Width*	35	3.601	.001
Mandibular Arch Depth*	33	-4.146	.000
Mandibular Incisor Width	38	.683	.499
Mandibular Canine Width	38	1.166	.251
Mandibular Premolar Width*	33	2.415	.022
Mandibular Molar Width*	28	4.272	.000

Table 4.34. Intraobserver error results for all measurements.

Variable	N	T value	Sig
Maxillary Incisor Cervical BL	50	1.202	.235
Maxillary Incisor Cervical MD*	53	4.388	.000
Maxillary Incisor Crown BL	50	-.377	.708
Maxillary Incisor Crown MD	44	.434	.667
Maxillary Canine Cervical BL	50	1.287	.204
Maxillary Canine Cervical MD*	51	6.230	.000
Maxillary Canine Crown BL	50	1.948	.057
Maxillary Canine Crown MD	51	-1.045	.301
Maxillary Premolar Cervical BL	48	-1.522	.135
Maxillary Premolar Crown BL	48	-.608	.546
Maxillary Premolar Crown MD	47	-1.239	.222
Maxillary Molar Cervical BL*	54	-2.843	.006
Maxillary Molar Crown BL	48	1.577	.121
Maxillary Molar Crown BL Non-perpendicular	48	.936	.354
Maxillary Molar Crown MD	32	.627	.535
Mandibular Incisor Cervical BL	56	-1.055	.296
Mandibular Incisor Cervical MD	56	1.662	.102
Mandibular Incisor Crown BL*	54	2.730	.009
Mandibular Incisor Crown MD	50	.521	.605
Mandibular Canine Cervical BL	49	1.325	.192
Mandibular Canine Cervical MD*	52	2.925	.005
Mandibular Canine Crown BL	48	.851	.399
Mandibular Canine Crown MD	53	1.471	.147
Mandibular Premolar Cervical BL	55	-1.898	.063
Mandibular Premolar Crown BL*	55	-4.060	.000
Mandibular Premolar Crown MD	52	.613	.543
Mandibular Molar Cervical BL	43	-.054	.957
Mandibular Molar Crown BL*	29	-2.749	.010
Mandibular Molar Crown MD	24	1.825	.081

Table 4.34 (continued). Intraobserver error results for all measurements.

Maxillary Incisor Composition	16	.155	.879
Maxillary Canine Composition	34	-.137	.892
Maxillary Premolar Composition	38	1.007	.320
Maxillary Molar Composition*	22	-2.333	.030
Mandibular Incisor Composition	36	-.646	.523
Mandibular Canine Composition	34	-.137	.892
Mandibular Premolar Composition	35	-1.397	.172
Mandibular Molar Composition*	13	-2.201	.048
Maxillary Arch Depth	53	-1.192	.239
Maxillary Incisor Width	51	-1.549	.128
Maxillary Canine Width	38	.029	.977
Maxillary Premolar Width*	46	2.027	.049
Maxillary Molar Width	47	-1.788	.080
Mandibular Arch Depth	48	.511	.612
Mandibular Incisor Width	57	-1.689	.097
Mandibular Canine Width	56	-1.859	.068
Mandibular Premolar Width	50	-.205	.838
Mandibular Molar Width*	33	-2.456	.020

APPENDIX B: Figures

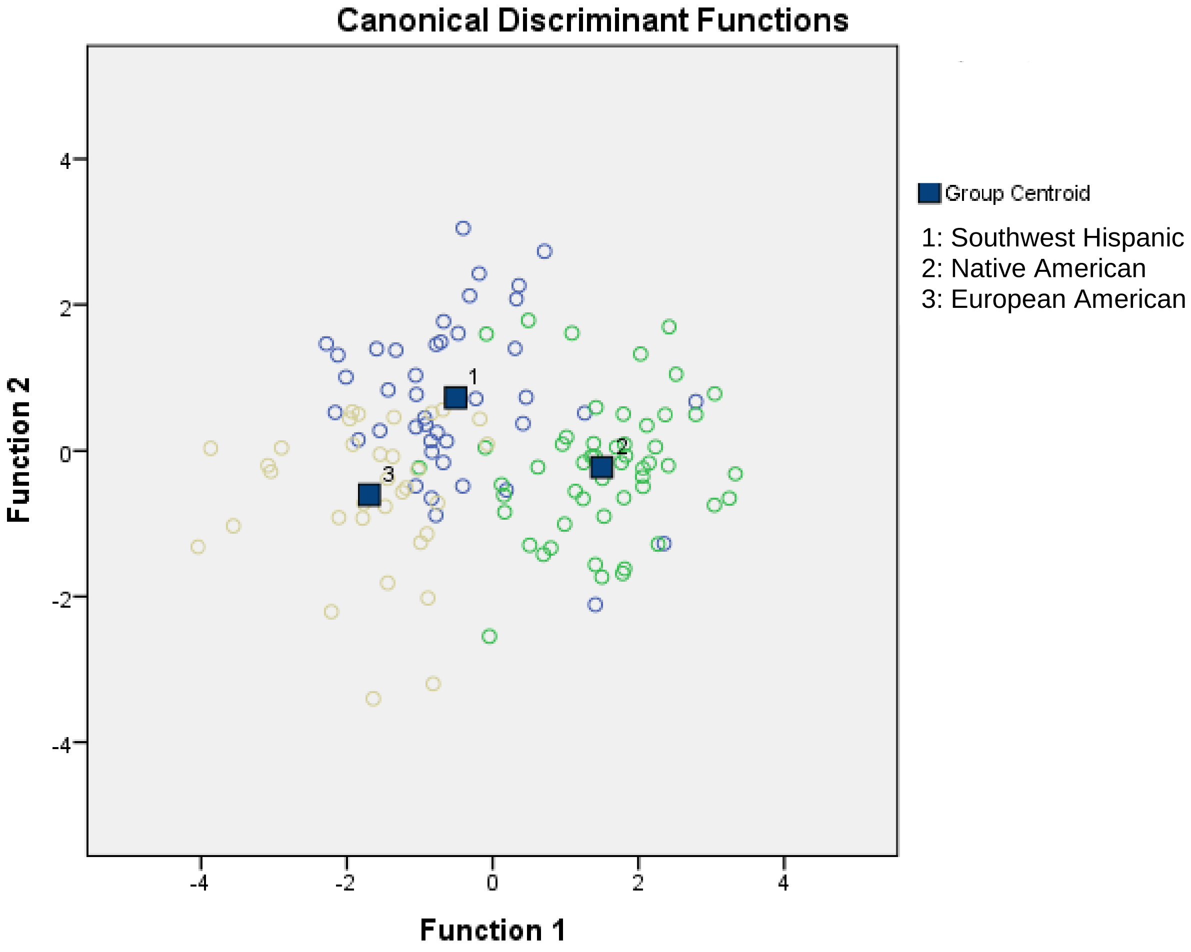

Figure 4.1. Discriminant function analysis group centroids – includes males and females (1: Southwest Hispanic, 2: Native American, 3: European American)

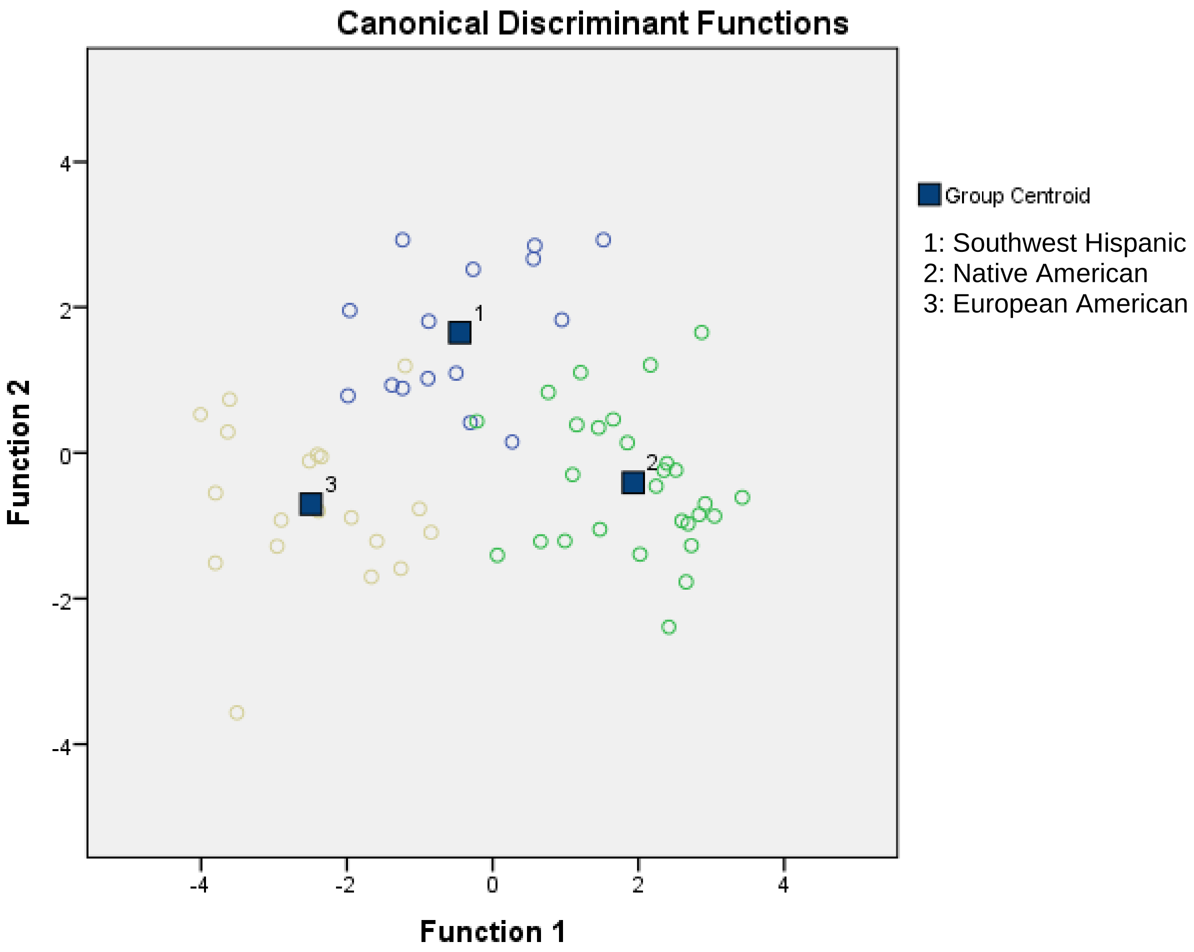

Figure 4.2. Discriminant function analysis group centroids – includes males (1: Southwest Hispanic, 2: Native American, 3: European American)

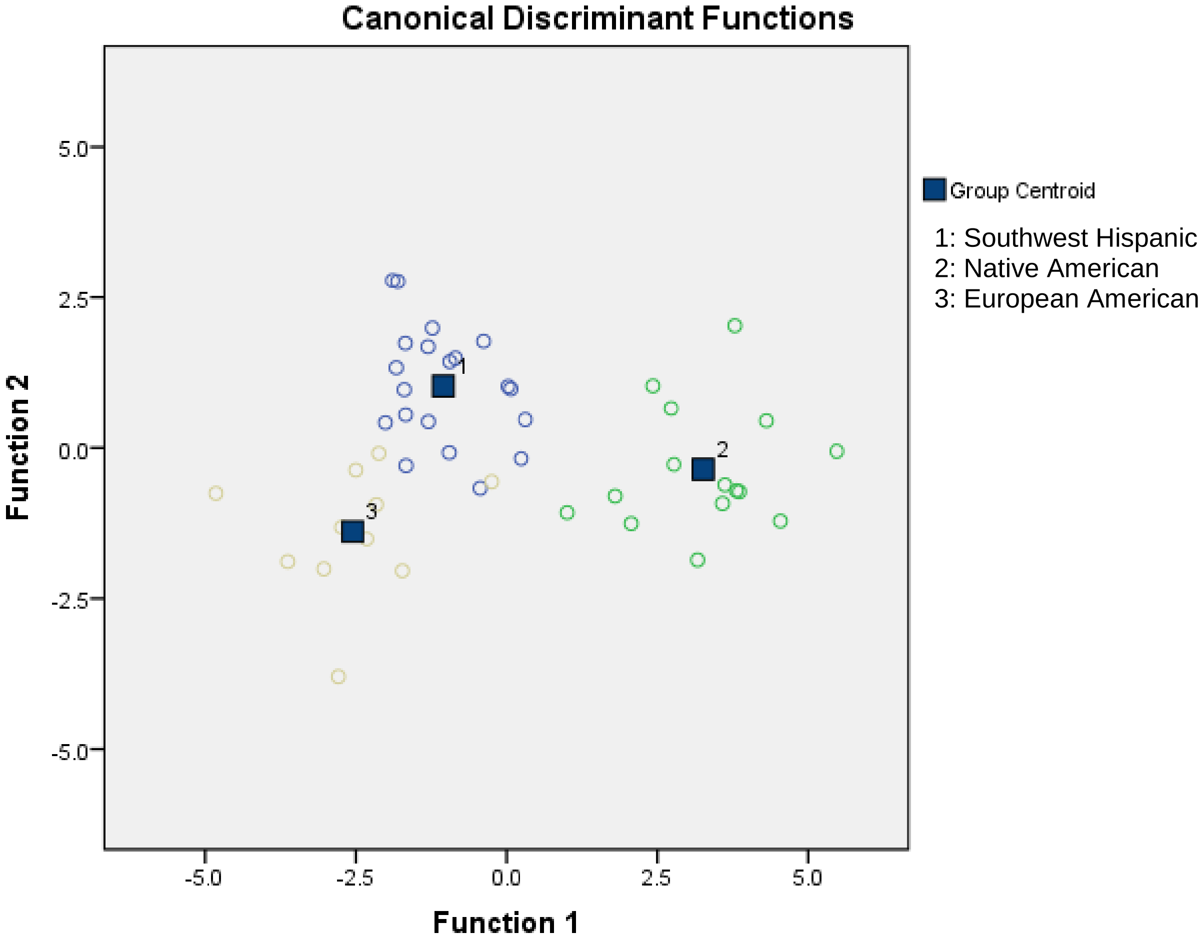

Figure 4.3. Discriminant function analysis group centroids – includes females (1: Southwest Hispanic, 2: Native American, 3: European American)

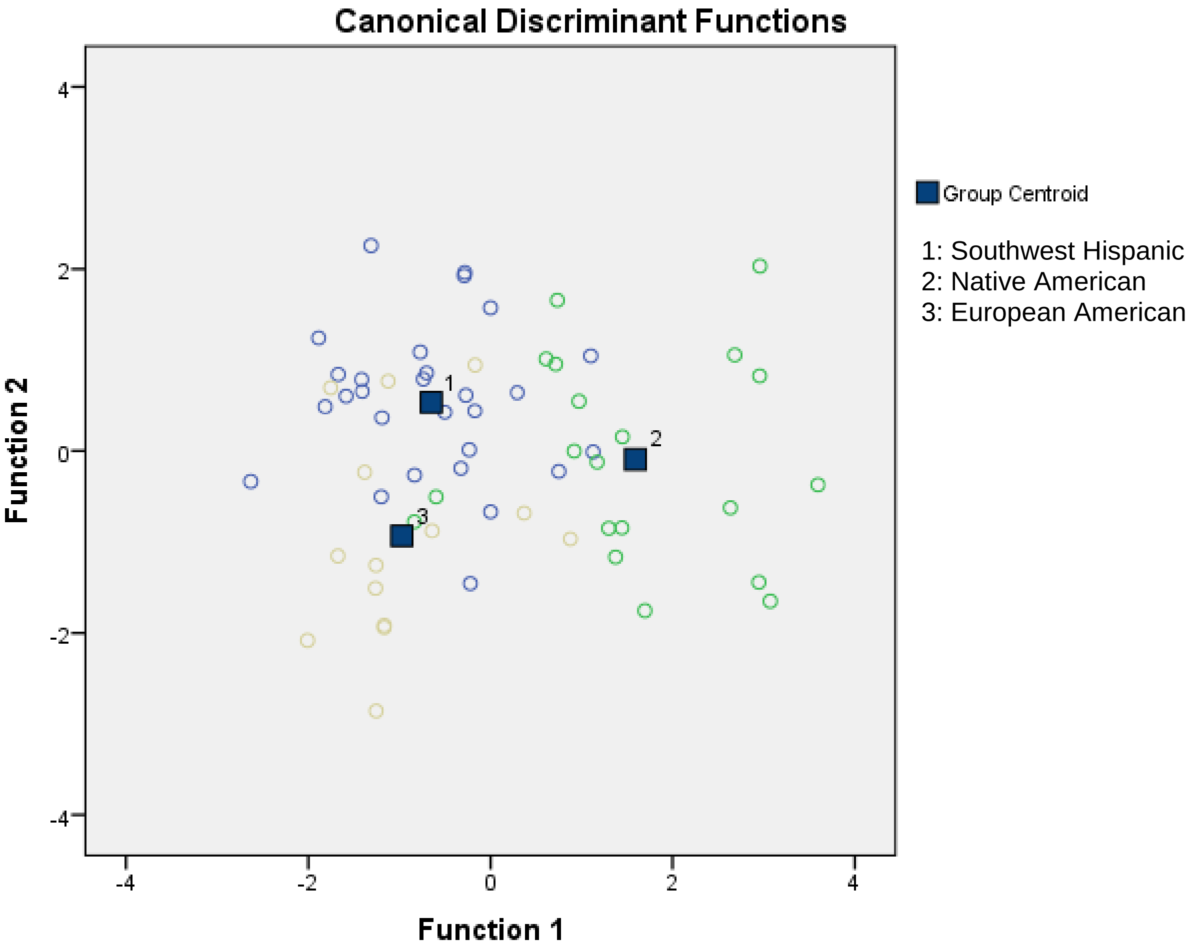

Figure 4.4. Discriminant function analysis group centroids – includes males (1: Southwest Hispanic, 2: Native American, 3: European American). Dental crown variables only.

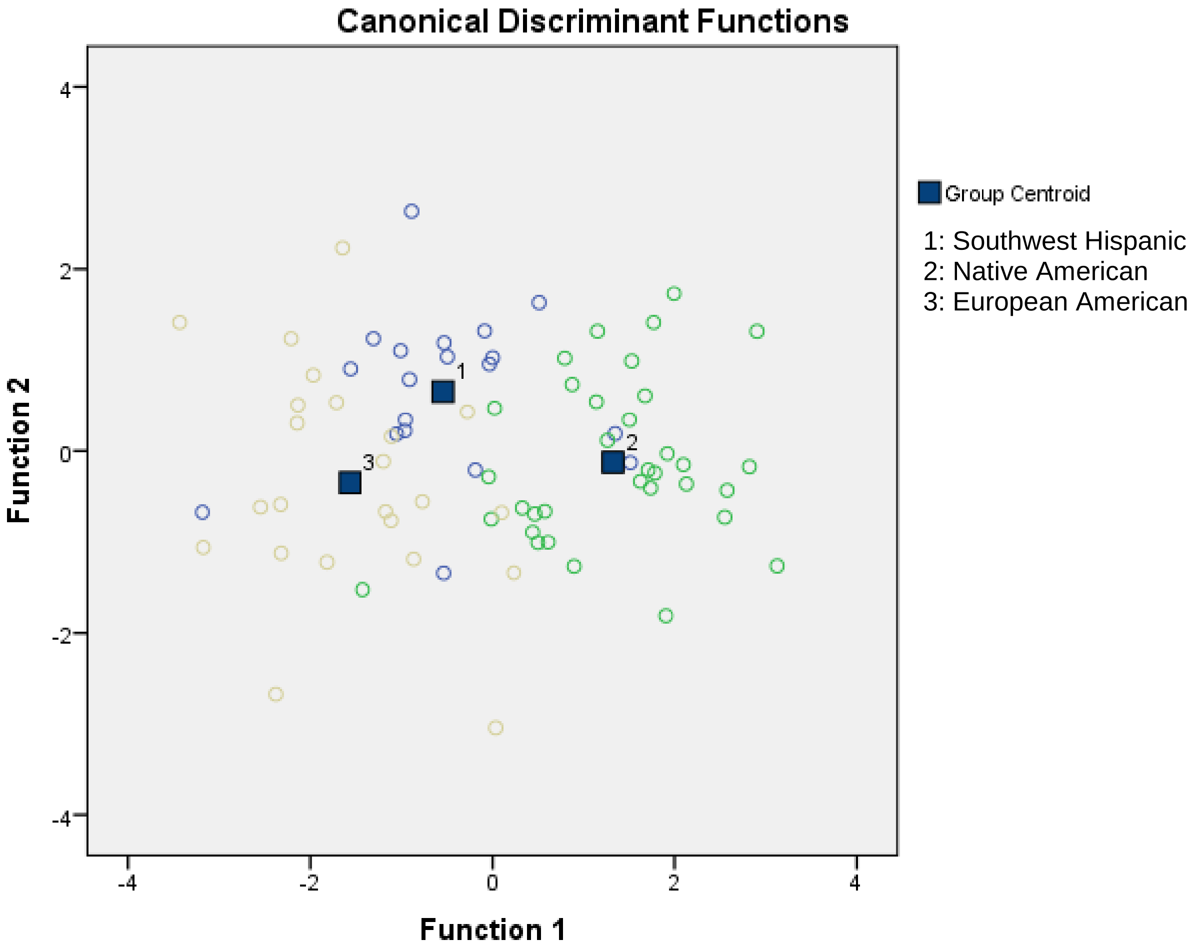

Figure 4.6. Discriminant function analysis group centroids – includes females (1: Southwest Hispanic, 2: Native American, 3: European American). Dental crown variables only.

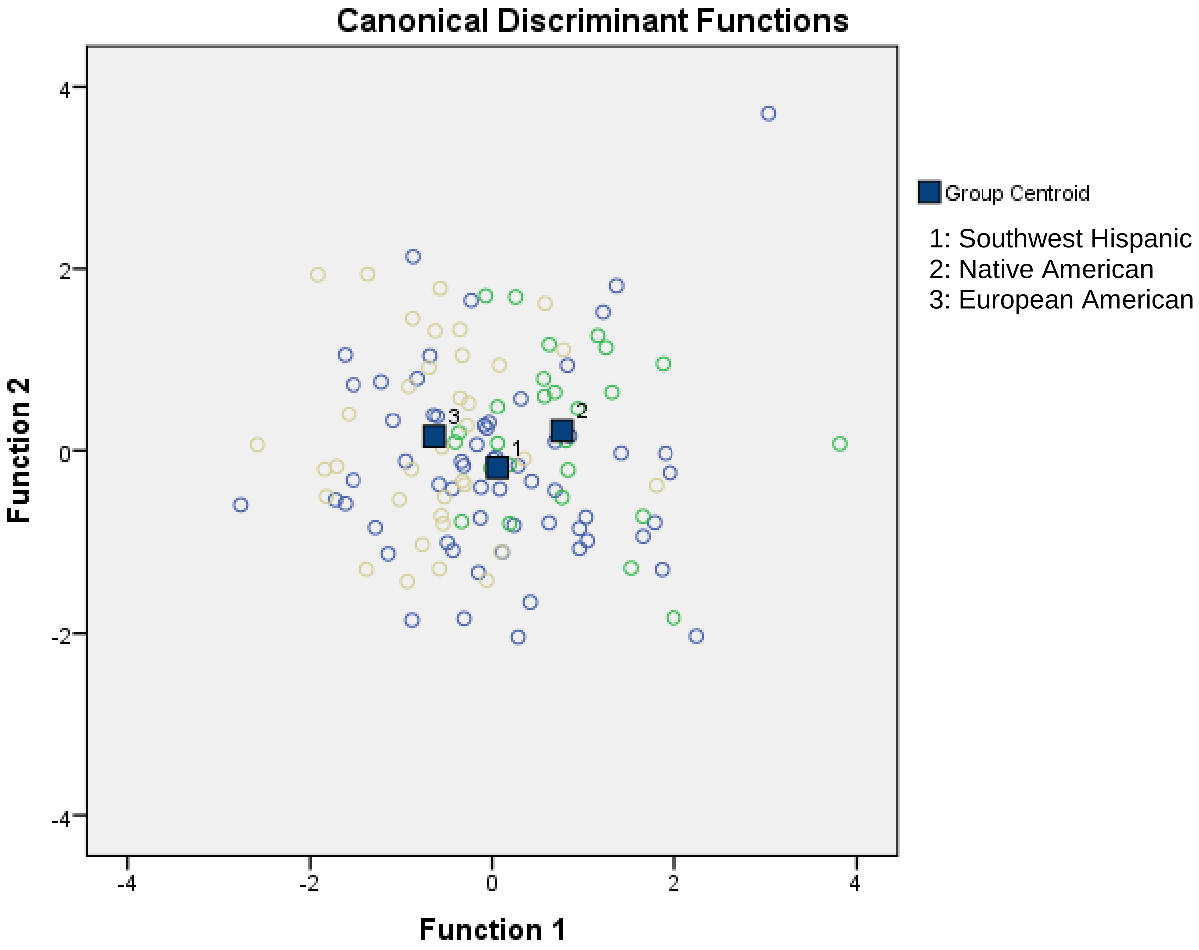

Figure 4.6. Discriminant function analysis group centroids – includes males (1: Southwest Hispanic, 2: Native American, 3: European American). Dental arcade variables only.

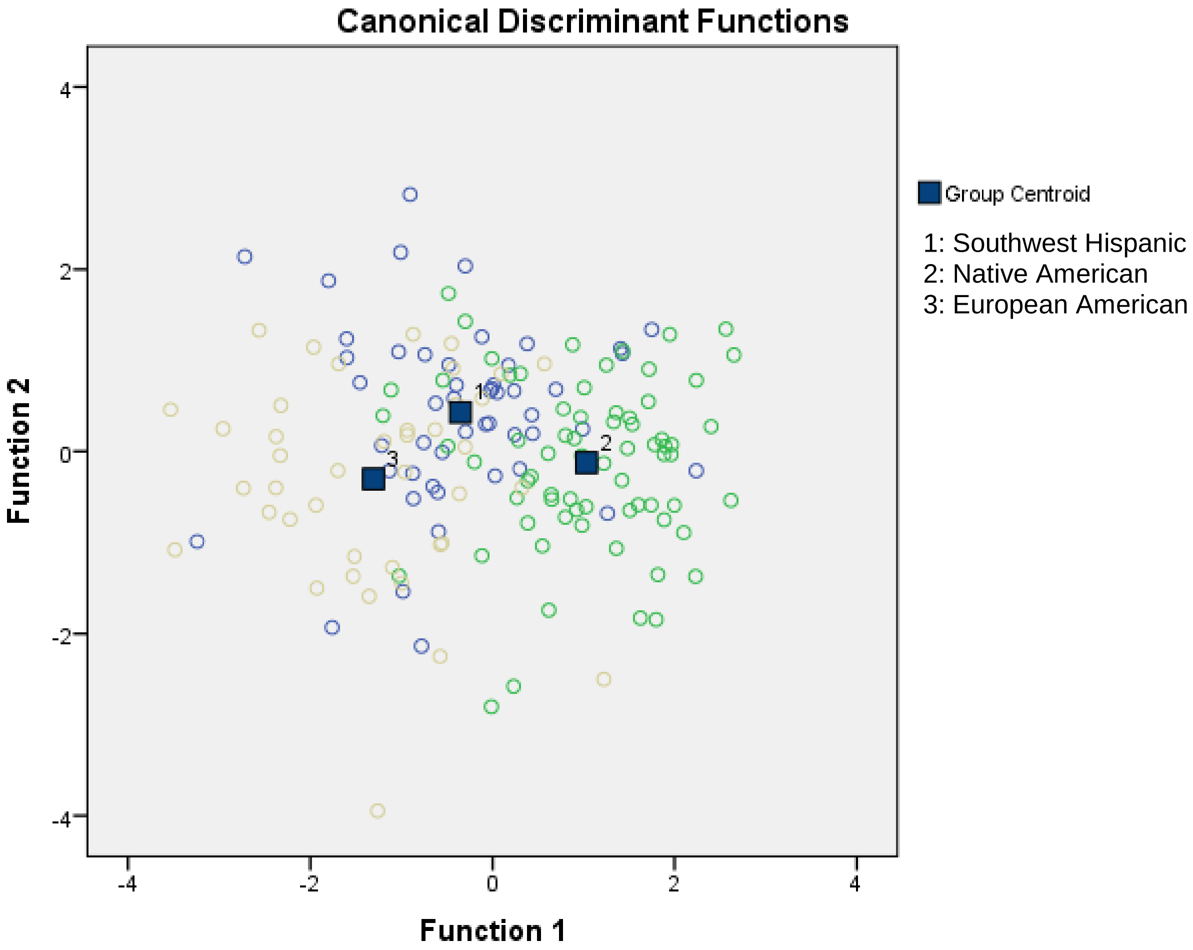

Figure 4.7. Discriminant function analysis group centroids – includes females (1: Southwest Hispanic, 2: Native American, 3: European American). Dental arcade variables only.

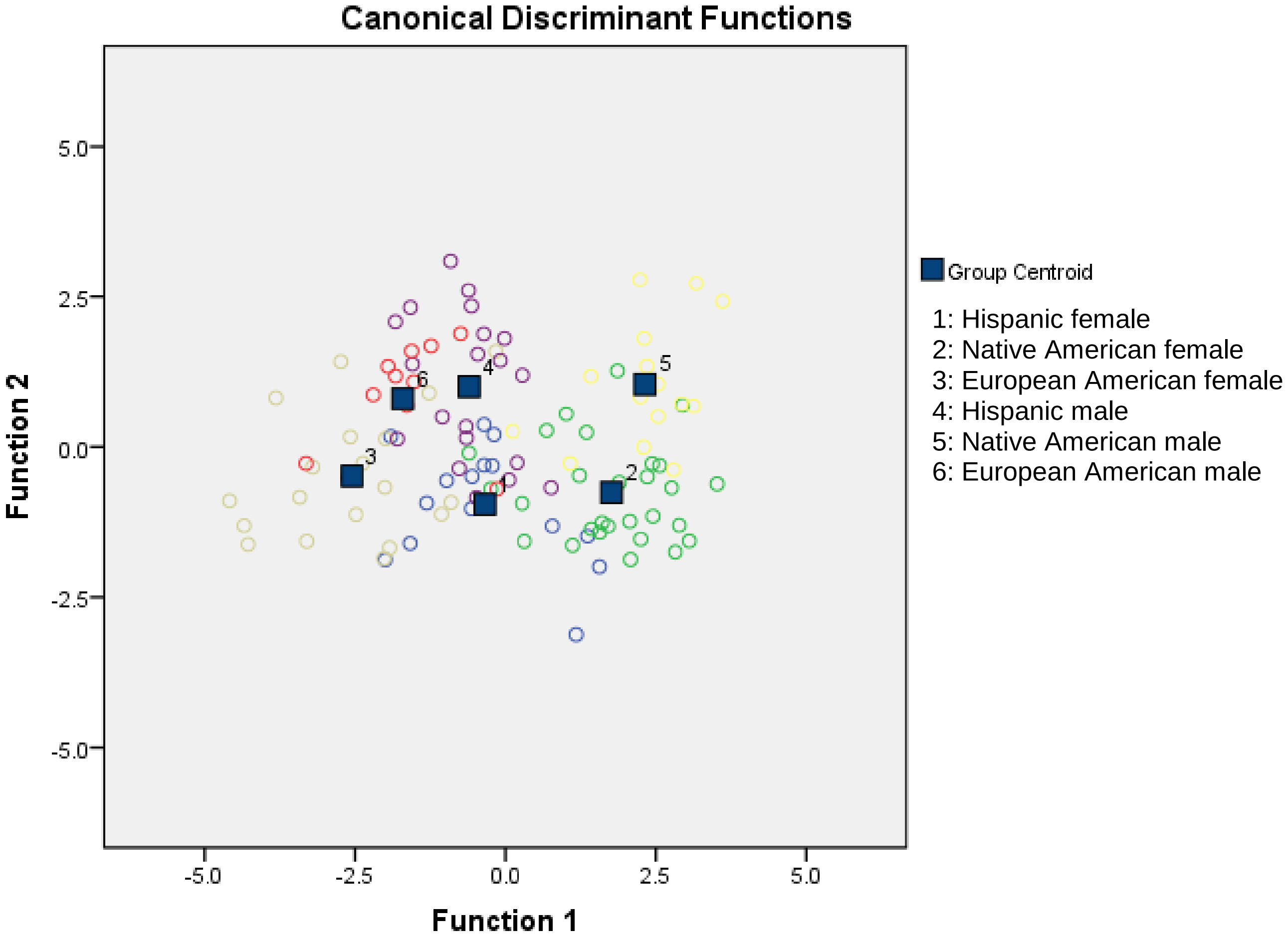

Figure 4.8. Discriminant function analysis group centroids – includes males and females (1: Hispanic female, 2: Native American female, 3: European American female; 4: Hispanic male; 5: Native American male; 6: European American male). Pooled variables.

LIST OF JOURNAL ABBREVIATIONS

Am J Phys Anthropol	American Journal of Physical Anthropology
Angle Orthod	The Angle Orthodontist
Aust Orthod	Australian Orthodontic Journal
Caribbean J Sci	Caribbean Journal of Science
Dental Anthropol	Dental Anthropology
Euro J Orthod	European Journal of Orthodontics
Forensic Sci Int	Forensic Science International
Front Oral Biol	Frontiers of Oral Biology
Hum Biol	Human Biology
J Am Dent Assoc	The Journal of the American Dental Association
J Archaeol Sci	Journal of Archaeological Science
J Craniofac Genet Dev	Journal of Craniofacial Genetics and Developmental Biology
J Dental Res	Journal of Dental Research
PLoS ONE	Public Library of Science ONE
PNAS	Proceedings of the National Academy of Sciences
Proc Zool Soc Lon B	Proceedings of the Zoological Society of London B

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