MOLAR SIZE AND SHAPE IN THE ESTIMATION OF BIOLOGICAL AFFINITY: A COMPARISON OF RELATIVE CUSP LOCATIONS USING GEOMETRIC MORPHOMETRICS AND INTERLANDMARK DISTANCES

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A

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Abstract

The study of teeth has been a central tenet in biological anthropology since the inception of the field. Teeth have been previously shown to have a high genetic component. The high heritability of teeth has allowed researchers to use them to answer a myriad of anthropological questions ranging from human origins to modern variation due to microevolution. Traditionally, teeth have been studied either morphologically, through the assignment of nonmetric character states, or metrically, through mesiodistal and buccolingual crown measures. Increasingly, geometric morphometric techniques are being used to answer anthropological questions, especially dentally. However, regardless of analytical technique utilized, the biological affinity of modern U.S. individuals has often been limited to examination under a forensic lens (classification of either American Asian, black, Hispanic, or white) without consideration of parent populations. The current study uses geometric morphometric techniques on human molars for two main goals: 1) to examine biological affinity of each of the four largest population groups in regard to population history; and 2) examine the variation within and among the four modern groups as a means of classification.

A total of 1,225 dentitions were digitized. Each of the four modern U.S. groups was compared to possible parental groups via discriminant function analysis (DFA). Additionally affinity was examined using Mahalanobis generalized distances (D^2) wherein significance of distances between groups was calculated via permutation tests. Furthermore, the D^2 values were subjected to principal coordinate analysis, or classical multidimensional scaling, to visualize group similarity and dissimilarity. Each group demonstrated affinity with potential parental groups and geographically similar groups as expected given population histories; however, each was also significantly unique from the comparison groups. The four modern U.S. groups were then compared to one another using the same statistical tests. Total among-group correct classifications ranged from 33.9-55.5%, indicating a greater classification than random chance (25%). These classifications were negatively correlated with the reported intermarriage rates for each group: American whites and blacks have the lowest intermarriage rates, which resulted in the highest correct classifications. Conversely, American Asians and Hispanics have the highest intermarriage rates, which resulted in the lowest total correct classifications. Still, the DFA model created from the modern U.S. sample was able to accurately classify a holdout sample. Lastly, a comparison of the three most abundant groups in the U.S. (black, Hispanic, and white), achieved a total correct classification of 72.3%, which is comparable to other studies focusing on the same populations. Restricted gene flow through sociologically constructed barriers and positive assortative mating are the likely factors in the observed variation.

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CHAPTER 1: INTRODUCTION

Few dental anthropological studies have focused on the biological affinity of modern American populations (Edgar, 2005, 2013; Lease and Sciulli, 2005; Kenyhercz et al., 2014a). More broadly, no physical anthropological studies to date have examined the variability within and between the four largest modern U.S. groups (American Asian, black, Hispanic, and white), as labeled by the U.S. Census Bureau. Further, little has been written concerning the biohistory of each of the four modern American groups, with some notable exceptions for American black (Spradley, 2006; Edgar, 2009), white (Edgar, 2009), Hispanic (Ross et al., 2002; Willermet and Edgar, 2009), and Asian (Schmidt et al., 2011). Given the variation in biological affinity in the U.S., in conjunction with the stringent laws concerning the admissibility of evidence in court via the Daubert rulings (Daubert v. Merrell Dow Pharmaceuticals, Inc., 1993), how can variation be identified and measured when only the teeth remain? The following hypotheses were derived in relation to modern U.S. biological affinity:

1. American Asians will demonstrate intermediacy between East Asians and American whites.
2. American blacks will demonstrate intermediacy between West Africans and American whites.
3. American Hispanics will demonstrate intermediacy with historic Mexicans, historic Spanish, and American whites.
4. American whites will be the most similar to historic European groups.

5. The modern groups with lower intermarriage rates will demonstrate less within group variation, i.e. lower misclassification rates, than groups with higher intermarriage rates.

Statistical hypotheses will be used to evaluate each of the abovementioned qualitative hypotheses. For example, the differences between two groups' Mahalanobis distances will be different from zero, or null, which implies that each of the groups is significantly distinct.

Geometric morphometrics (GMM) has been defined as "the study of shape variation and its covariation with other variables" (Adams et al., 2004; p. 5). In the proposed usage, the shape in question will be the relative location of molar cusp apices and the other variables will be biological affinity, or ancestry (which will be detailed in Chapter 2). Geometric morphometric techniques allow for landmarks, which in this case are biological locations with names, to be compared directly in the same shape space to examine the effects of size-free shape. Since Morris (1986) first published on a pseudo-morphometric dental technique he termed occlusal polygons, many studies have utilized morphometric techniques to analyze teeth, though these have primarily focused on paleoanthropological questions (Hartman, 1989; Hlusko, 2002; Bailey, 2004; Martinón-Torres et al., 2006; Gómez-Robles et al., 2007; Bailey et al., 2008; Gómez-Robles et al., 2008). More recently, Kenyhercz et al. (2014a) used geometric morphometrics to investigate variability within and between American blacks and whites, though no study has been conducted on each of the big four U.S. groups, or examined their individual biohistories.

Irish (1993) identified six attributes that have contributed to the continued use of dental data within anthropology:

1. Teeth are hard so they will survive longer and in better condition than other tissues.

2. There is a link between teeth and behavior in mammals.
3. Teeth have a high genetic component, up to 80%.
4. Environmental conditions have less impact on teeth than other tissues.
5. Teeth are evolutionarily stable, i.e., they evolve slowly.
6. Teeth can be examined and compared on both living and dead individuals and populations.

Given the advantages of analyzing teeth, as outlined by Irish (1993), the high genetic component of inheritance of both size and shape (Alvesalo and Tigerstedt, 1974; Harris and Bailit, 1980; Townsend et al., 2003; Townsend et al., 2009), and the recent publications on dental morphometrics of molars showing their significance at discriminating between groups in a paleoanthropological context (Bailey, 2004; Gómez-Robles et al., 2007; Bailey et al., 2008), dental morphometrics also offer a means to investigate microevolutionary processes, such as the biohistory and comparison of variation of modern U.S. populations (Kenyhercz et al., 2014a).

1.1 DENTAL DEVELOPMENT

Much work has been done within anthropology using dental dimensions, morphology, and lately, morphometrics. Many of these aforementioned analyses have used groups both spatially and temporally to examine within and between group similarities and differences to answer questions of biological affinity (Hrdlicka, 1920; Hanihara, 1967; Harris and Bailit, 1988; Harris and Rathbun, 1989; Turner, 1990; Irish, 1993, 1997, 2006; Lukacs and Hemphill, 1993; Bailey 2004; Edgar, 2005, 2007, 2013; Harris and Lease, 2005; Lease and Sciulli, 2005; Bernal, 2007; Bailey et al., 2008; Kenyhercz et al., 2014a), peopling and migration (Turner, 1985; Irish and Hemphill, 2004; Scott and Turner, 2008), and paleoanthropology (Robinson, 1956; Brace, 1963; Brace and Mahler, 1971; Sperber, 1974; White et al., 1981; Wood et al., 1983; Wood and Uytterschaut, 1987; Wood and Engleman, 1988; Wood et al., 1988; Hartman, 1989; Zubov, 1992a; Zubov, 1992b; Irish, 1998; Hlusko, 2002; Irish and Guatelli-Steinberg, 2003; Bailey, 2004; Martinón-Torres et al., 2006; Gómez-Robles et al., 2007; Bailey et al., 2008; Gómez-Robles et al., 2008; Irish, 2013). Even if significant molar morphometric differences are found between modern U.S. populations, it is necessary to understand dental development and theoretical developmental models to place the results in a theoretical context. Additionally, an overview of previous dental anthropological work, including metric, morphological, and morphometric, is necessary to place any potential results in a relatable context.

All dental studies, be them morphological, metric, or morphometric, are dependent upon a firm theoretical understanding of dental development. The ontogeny of molars, and all teeth, result from the following stages: bud, cap, bell, formation, and deposition (Hillson, 1996). Even though each tooth goes through the same stages, over 300 genes have been found to regulate odontogenesis with various interactions between ectodermal cells and ectomesenchymal tissues (Thesleff, 2006; Townsend et al., 2012). The bud and cap stages start the initiation of odontogenesis by proliferating cells and will ultimately regulate the number and form of teeth within the arcade (Townsend et al., 2009; Townsend et al., 2012). Differentiation, both histologically and morphologically, occur during the early and late bell stages, respectively. Lastly, the formation and deposition of enamel and dentin matrices occurs.

The following description of odontogenesis is paraphrased from Hillson (1996) unless otherwise noted. The “bud” stage occurs around the 6th week of fetal development.

Epithelium is under laid by mesenchymal stem cells. The mesenchymal cells proliferate into an arch of the developing jaw. At this stage, Dlx homeobox genes have been shown to initiate dental fields (Jernvall and Thesleff, 2000). The epithelium grows into a condensed arch to form the primary epithelial band, thus becoming the dental lamina. By 10 weeks, 10 small swellings of mesenchyme develop on the dental lamina creating the enamel organs of deciduous teeth that will later give rise to the enamel of the tooth crowns. The enamel organs for the permanent teeth are later formed starting near the 16th week of development through birth. The bud stage comes to an end with the formation of the primary enamel knot (Brook, 2009).

The "cap" stage continues the proliferation of cells with the enamel organ "bud" hollowing out and filling with the dental papilla, which was derived from the mesenchyme. In teeth with multiple cusps, a secondary enamel knot is formed and controls subsequent folding in the inner enamel epithelium (Townsend et al., 2012). Outside of the dental papilla, mesenchyme also forms the dental follicle. In late cap stage, the enamel organ differentiates into the internal enamel epithelium, which will become the enamel matrix. The cap stage is increasingly influenced epigenetically by folding of the enamel knots in the inner enamel epithelium (Townsend et al., 2003).

The early "bell" stage concerns mainly histodifferentiation, in which the cells differentiate into three distinct layers (Nanci, 2013):

1. Inner enamel epithelium – a single layer of cells that will eventually differentiate into ameloblasts (enamel laying cells);
2. Stratum intermedium – a dew layers of squamous cells that exist between the inner and outer enamel epithelia;

3. Outer enamel epithelium – this layer will fold into complex layers of capillary networks and differentiate into cuboidal cells that will later give rise to dentin.

The late "bell" stage focuses on morphodifferentiation, in which mineralization of the tooth starts and root formation begins, essentially shaping the teeth into their future structures. The formation of dentin is deposited along what will be the dentinoenamel junction. After the dentin is deposited, the enamel is laid down in the future cusp areas and then finishes depositing on the crown by moving both apically and towards the neck of the tooth.

Lastly, the crown stage continues the appositional deposition of dentin and enamel. Apposition of the dentin matrix and enamel continues with sequential bands being added that result in the appositional growth of the tooth. Dentin is formed from the odontoblasts and starts at the dentinoenamel junction and moves inward. Meanwhile, the enamel is being mineralized by ameloblasts starting at the dentinoenamel junction and moving outward. Again, Dlx homeobox genes have been shown to influence the overall morphogenesis and patterning in both ameloblasts and odontoblasts (Robinson and Mahon, 1994).

1.1.1 Molar eruption timing

The permanent molars develop consistently, and complimentary (upper and lower) teeth, aka isomeres, experience the same developmental and eruption timing (Nelson and Ash, 2009); however, as indicated by Tompkins (1996), there are slight population differences in dental development. The following development and eruption timings are paraphrased from Nelson and Ash (2009). The permanent first molars both initiate at birth; the crown is complete between 2.5 and 3 years; gingival eruption occurs consistently between 6 and 7 years; and the root apex is complete between 9 and 10 years. The permanent second molars initiate formation between 2.5 and 3 years; the crown completes between 7 and 8 years; gingival eruption occurs between 12 and 13 years in the maxilla, and 11 and 13 years in the mandible; and the apex is complete between 14 and 16 years in the maxilla and 14 and 15 years in the mandible. The permanent third molar is the most variable tooth and initiates formation between 7 and 9 years in the maxilla and between 8 and 10 years in the mandible; the crown is complete between 12 and 16 years; eruption occurs between 17 and 21 years; and the apex is complete between 18 and 25 years.

1.2 DENTAL DEVELOPMENT MODELS

1.2.1 The Field Concept Model

The biologically stable and consistent development of teeth lends them perfectly to evolutionary studies. The human dental complex exhibits dental fields comprised of incisors, canines, premolars and molars that exhibit a metameric relationship from one field to the next. For example, the first premolar (PM3) has more characteristics of a canine, while the more distal premolar (PM4) has more of a molar appearance. However, how each of the dental fields develops has not been historically agreed upon. Three main models exist in the field to describe the developmental fields: the Field Concept model (Butler, 1939; Dahlberg, 1945), the Clone model (Osborn, 1973), and the homeobox model (Cobourne and Mitsiadis, 2006).

Percy Butler (1939) first developed the Field Concept model for the mammalian dentition when he recognized that, “almost every detail on a tooth can be compared with corresponding details on adjacent teeth, and only a common morphogenetic cause acting on more than one tooth germ could create such similarity” (1939, pp. 1). The gradation between teeth indicated that the morphogenetic fields within the embryonic jaw influenced teeth to develop uniquely in different areas. Butler asserted that some coordinated agency was at work resulting in equilibrium, or the fields, as we know them. Any change to the intensity of the agency within the fields would disrupt the entire complex. In sum, each field is acted upon as an entire dental unit; individual fields could not be affected without disrupting other fields. Butler's concept of agency was borrowed from Huxley and de Beer (1934) who surmised that chemo-differentiation was the factor in field formation due to regionally specific chemical gradients. Additionally, Butler postulated that the morphogenetic fields had an anteroposterior axis because the posterior end of the field demonstrated no return to form of the anterior end, but instead showed a constant gradation from anterior to posterior. However, each field is independent of one another in regards to the anteroposterior gradation. Butler concluded that, "this study makes very improbable the view that individual teeth are independent of each other in variation and evolution" (1939, pp. 39).

Later, Albert A. Dahlberg (1945) adapted Butler's field theory to the human dentition. Dahlberg propounded that, "a field may be defined loosely as a sphere of influence. It manifests itself in decreasing strength as the distance is increased from the hypothetical pole located within the field. It might be compared to a magnetic field" (1945, pp. 687). Dahlberg very eloquently translated Butler's original Field theory and also introduced the concept of a "polar" tooth that, within each field, had the most "strength" or complexity and teeth further away from the polar tooth would demonstrate less complexity. Additionally, Dahlberg included premolars as a fourth field. Dahlberg posited that less morphological variability is found within each polar tooth. In Dahlberg's view, timing of dental development was crucial and that there are critical points of field activity that are instrumental in the differentiation of particular tooth germs. Dahlberg continued that the fields are at their peak activity when the first (pole) tooth, within each field, is differentiating and receives the most genetic information. Polar teeth then have the strongest trait expressions and also demonstrate the lowest coefficients of variability (i.e., were more morphologically stable than other teeth within the same field). Dahlberg concluded that, "the changes [in the dentition] are present and inheritable. The general trend of tooth character is toward a reduction in size, form and number" (1945, pp. 690).

1.2.2 The Clone Model

Osborn (1973) developed a separate model for dental field development known as the clone model. Osborn, like Dahlberg, noted that there is a primary tooth within each field. In the clone model, Osborn described the primary tooth as the "determinant" tooth for each specific region that held the "paradigm tooth shape" (1973, pp. 558). The information for each determinant tooth is then cloned, through mitosis, for the remainder of the teeth within each specific field, generally moving anteriorly to distally within the jaw. Each subsequent clone receives less genetic information, thus explaining why there is a general cline towards less complex teeth in the distal regions of each field, similar to a facsimile effect. Embryonically, each determinant tooth appears in each of the developmental regions around the same time of development. Each region creates a zone of tissue around the region that it inhibits. In reference to the reduction in complexity for clones, Osborn stated that, "successive dental papillae derived from a single colony of jaw mesoderm retain successively less ability to generate the paradigm molar shape, with the result that they are less complex" (1973, pp. 559). Support for the clone model came from

A. G. S Lumsden (1988) during an experimental study when a presumptive first molar germ was isolated and moved and then continued to grow and form all three molars in their normal sequence.

1.2.3 The Homeobox Model

The homeobox model, as described by Cobourne and Mitsiadis (2006) focuses more on the histological aspects of dental field development. First the ectoderm of the first branchial arch and the ectomesenchymal cells migrate from the neural axis. The mixing of genes in the ectomesenchymal cells produces distinct fields with certain overlap among them. Ectoderm initiates the development and ectomesenchymal cells impact the morphological aspects of the respective fields. The initiation is time specific and is regulated by the ectoderm. Morphologically speaking, the germs are plastic initially but become rapidly fixed in time. There is reciprocal signaling between the ectoderm and the ectomesenchyme that signals specific homeobox genes at specific times and gradients to solidify crown and root morphology of teeth within their respective fields. The homeobox signaling molecules include fibroblast growth factor (FGF) and bone morphogenetic proteins (BMP). The BMP are responsible for the anterior teeth, while the FGF are responsible for the posterior teeth; however, there is considerable overlap between BMP and FGF leading to the gradation in tooth form throughout the palate.

1.2.4 Combined models

Mitsiadas and Smith (2006) contended that each of the models are not mutually exclusive and could be used in conjunction with one another. The chemo-differentiation and timing explained in the Field Concept model were found in the homeobox theory with the fact that the mesenchymal and ectodermal cells in combination with signaling and homeobox genes will contribute to the overall patterned tooth. Further, each tooth is time depended, based on its tooth position and different teeth within the same field will be time-dependent, but, "different signals and combinations of homeobox genes will contribute to different tooth shapes" (Mitsiadas and Smith, 2006, pp. 180), thus corroborating Osborn's clone model.

1.3 STUDIES OF DENTAL MORPHOLOGY

Hrdlicka (1920) first published on morphological characteristics, specifically, shovel-shaped teeth, in the dentition and their relative frequencies between populations. Hrdlicka noticed that, "subdeveloped and transitional forms of shovel-shaped incisors are coming. In a large series of teeth of perhaps any race there may probably be found all forms, from the complete absence of a fossa and enamel frame to their most typical development" (1920, pp. 448). Hrdlicka devised a four-scale system:

1. Shovel
2. Semi-shovel
3. Trace-shovel
4. No shovel

Hrdlicka found high levels of shoveling in American Indian and Asiatic peoples, specifically Chinese and Japanese. The lowest frequency of shoveling was found in American whites, followed by American blacks. The Hawaiian sample was intermediate, with about 1/3rd of the sample containing shoveling.

Following Hrdlicka, Albert Dahlberg saw the need for standardization in dental morphological traits, which he described in detail in 1957 (Scott and Turner, 2008). To adequately examine the range of variation in morphological traits, and to improve interand intra-observer error, Dahlberg created reference plaques (the Zoller Lab plaques) representing the variation gradient expressed in dental morphological traits, including expressions in size of specific cusps. The intermediate morphological expressions now observable due to the dental plaques allowed for fine-grained studies in populations that were previously not possible (Turner, 1967). The standards set in place by Dahlberg would be paramount in the establishment of further standards in documenting dental morphology.

Inspired by Dahlberg's development of dental plaques for the permanent dentition, Hanihara (1967) developed reference plaques of deciduous teeth and introduced the idea that different populations exhibit different frequencies of various dental traits and thus dental complexes, or suites of traits, could be used to describe populations. Hanihara (1967) examined deciduous crown characteristics of Japanese, Pima Indian, Eskimo, and American white and blacks and developed two dental complexes, "Mongoloid" and "Caucasoid".

A standardized set of dental traits and corresponding type specimens organized on reference dental plaques, which were a refinement and elaboration on Dahlberg's Zoller dental plaques, were organized at Arizona State University and first published upon by Turner et al. (1991). The ASUDAS system includes 27 references plaques showing an ordinal expression of between 30-40 traits depending on the completeness of the dentition under observation. Turner et al. (1991) reported that there is little to no sexual dimorphism in morphological traits and that the sexes in samples can be pooled. Additionally, the authors recommended the individual count method, in which in the presence of asymmetry, the antimere with the greatest expression is used in the analysis because it is believed that the greater trait expression reflects the underlying genetic potential. Previously, Nichol and Turner (1986) examined the intra- and interobserver concordance in scoring dental morphology. They found that there were no significant differences in scoring dental morphology both within and between observers. However, four traits were found to be more difficult, i.e., less concordant both within and between observers. The four difficult traits included: the tuberculum dentale, canine distal accessory ridge, PM1 marginal accessory cusps, and LM1 anterior fovea (Nichol and Turner, 1986).

With the development of a standardized scoring system and comparative reference plaques, researchers could collect comparable and consistent data. Using the ASUDAS system, different anthropological questions could be addressed such as paleoanthropological (Robinson, 1956; Sperber, 1974; Wood et al., 1983; Wood and Uytterschaut, 1987; Wood and Engleman, 1988; Wood et al., 1988; Zubov, 1992a; Zubov, 1992b; Irish, 1998; Irish and Guatelli-Steinberg, 2003; Irish, 2013) migration and peopling (Turner, 1985; Scott and Turner, 2008), and biological affinity (Turner, 1990; Irish, 1993, 1997, 2006; Edgar, 2005, 2007, 2013).

1.4 STUDIES OF ODONTOMETRY

Henry Flower (1885) first tried to examine molar dental length by measuring from the mesial aspect of the maxillary 1st premolar to the distal aspect of the maxillary 3rd molar. Flower noted that larger individuals generally displayed larger dentitions, and through this, he posited that there must be some way to standardize the size between individuals. To achieve standardization, Flower also recorded basio-nasal length from basion to nasion. With the two measurements, Flower formulated the dental index: Dental

Index = $\frac{Dental\ Length\ x\ 100}{Basio-nasal\ length}$. From the results of samples from many world populations, Flower established three classes: microdonts with a dental index <42, mesodonts with dental indices between 42 and 44, and megadonts with dental indices >44. Due to the nature of Flower's dental index, women of each population group exhibited consistently greater dental indices because their basio-nasal lengths were shorter than males. While examining group means, Flower described European white groups as microdonts, Asians as mesodonts, and Australian aborigines and American blacks as megadonts. However, on the subject of overall tooth dimensions, Brace (1963) and Brace and Mahler (1971) found a reduction in overall tooth size throughout evolution from Australopiths through current *H. sapiens.* Brace (1963) and Brace and Mahler (1971) posited that it was not simply natural selection that would account for the overall dental reduction, but likely what was referred to as the probable mutation effect, which is explained in more detail later.

Due to the weak analytical nature of Flower's dental index, the only information still used from his study were his terms for dental size classes. A more straightforward method to measure teeth was developed by Moorrees (1957) in which maximum mesiodistal (MD) and buccolingual (BL) values are collected for each tooth. The MD value is recorded as being the greatest mesiodistal value of the tooth crown measured parallel to the occlusal and buccal surfaces, while the BL value is the greatest distance between the buccal and lingual surfaces of the tooth crown in a plane perpendicular to that of the mesiodistal measure. However, Moorees and Reed (1964) noted that the MD and BL diameters of each of the 32 permanent teeth were highly correlated. Multicollinearity is problematic, analytically, because the information being gained from the measures is redundant and does not offer any useful discriminating information between populations. Additionally, multicollinearity violates many statistical assumptions when using continuous data to investigate differences between populations.

That is not to say that raw dental measures are not of value. Ditch and Rose (1972) used maximum MD and BL values to derive discriminant functions to estimate an individual's sex and achieved results as high as 95+%. However, Harris (1997) noted that odontometrics demonstrated a unimodal distribution among world populations, with a positive skew due to the megadonty found in Australian aborigines. To test the efficacy of odontometrics, Falk and Corruccini (1982) tested a set number of craniometrics versus a set number of odontometrics and tested how well each method sorted human populations. Falk and Corruccini (1982) concluded that raw odontometrics alone are not effective at differentiating between population groups.

Penrose (1952) introduced a new distance metric that accounted for both size and shape of teeth, based solely on odontometrics measures. Essentially, Penrose (1952) proposed a mean squared distance measure with two components: size and shape. To further examine odontometrics in meaningful ways, Wolpoff (1971) introduced the dental robusticity index (RI) by multiplying maximum MD and BL measures together. Wolpoff (1971) suggested that the RI would approximate total occlusal area. Following suit, many other indices were created in an attempt to better quantify the shape of teeth. Lukacs (1985) demonstrated the use of several dental indices, which included: the incisor breadth index, the molarization index, and the step-index. The incisor breadth index divides the MD diameter of the lateral incisor by the MD diameter of the central incisor. The molarization index examined the relative size of the lower second premolar by dividing its BL diameter by the BL diameter of the lower first molar. Lastly, the step-index examined the relative size of the second molar to the first by diving the BL diameter of M2 by the BL diameter of M1, and could be applied to both maxillary and mandibular molar series. Despite the improvement of raw measures with indices, Schmidt et al. (2011) concluded that indices, specifically the robustness index, overestimate occlusal areas in molars with pronounced hypocones or hypoconulids, as determined by utilizing the ASUDAS reference casts, and that an adjusted regression equation was necessary to better approximate actual occlusal area.

To further refine odontometrics analyses, Harris and Bailit (1988) introduced dental apportionment analysis by subjecting odontometrics to a PCA to negate the effects of too many highly intercorrelated variables. Along with the traditional MD and BL diameters, Harris and Bailit (1988) also included summary summation measures of each of the MD and BL lengths, respectfully, and also the sum of the MD x BL lengths. The PCA was able to reduce the number of variables for analysis by including only the PCs that contributed eigenvalues greater than one. Principal component one was considered to be the effect of overall size as demonstrated by each variable contributing positive loadings. However, each consecutive PC represented shape information by examining the relative size of each tooth in the dental arcade without the influence of gross size. Wherein odontometrics were too varied within populations because of the effects of gross size, apportionment analysis allows the relative size of teeth to be directly compared.

The same types of studies addressed by dental morphological analysis can be conducted using odontometrics and dental apportionment analysis. Using dental apportionment analysis, studies have been conducted in paleoanthropology (Brace, 1963;

Brace and Mahler, 1971; White et al., 1981), migration and peopling (Irish and Hemphill, 2004), and biological affinity (Harris and Bailit, 1988; Harris and Rathbun, 1989; Lukacs and Hemphill, 1993; Harris and Lease, 2005; Lease and Sciulli, 2005).

1.5 STUDIES OF DENTAL GEOMETRIC MORPHOMETRICS

Bookstein (1982) first introduced geometric morphometrics (GMM) as the integration of geometry and biology. The most common morphometric technique is a Procrustes Superimposition, in which, landmark coordinate data are translated, scaled, and rotated to minimize the differences between landmark pairs to remove the influence of size. However, other morphometric techniques such as elliptical Fourier analysis (EFA) and sliding semi-landmarks are also used. Elliptical Fourier analysis examines shape outlines through the addition of ovals of known properties termed harmonics (Iwata and Ukai, 2002). The subsequent addition of each harmonic better describes the outline shape. Sliding semi-landmarks are points along a smooth surface or contour whose position cannot be defined by homology and must be approximated between other landmarks (Mitteroecker and Gunz, 2009).

During the 1980s, a pseudo-geometric morphometric technique known as occlusal polygons was developed to directly measure the lengths, angles, and areas between cusps to investigate biological affinity in modern population groups (Morris, 1986). The impetus for occlusal polygons was from an earlier study undertaken by Morris (1981) in which he determined the angular measures of the first maxillary premolar. The method, revived and expanded upon by Morris (1986), designated the four cusps of the maxillary first molar as A (protocone), B (paracone), C (metacone), and D (hypocone). The letter designation of the cusps allowed for the creation of a polygon, ABCD, with the tip of each cusp representing a vertex. Distances between cusps were each measured using needle-tipped calipers. The polygon was then separated into two oblique triangles, ABD and ACD. From the two triangles, angles were calculated from the linear measures using the cosine operation instead of attempting to utilize a protractor. Next, the areas of each triangle were calculated using the following formula:

$$Area\ ABC = \sqrt{\frac{P}{2}}\left(\frac{P}{2} - AB\right)\left(\frac{P}{2} - AC\right)\left(\frac{P}{2} - CB\right)$$

The abovementioned process of analyzing occlusal polygons according to Morris (1986) resulted in 11 variables: linear measures of four sides, perimeter, area, and four angles. Morris then used simple descriptive statistics (mean and standard deviations) to compare the population groups. Morris (1986) found more variation in molar widths as compared to lengths, with only one group demonstrating differences in angular data.

Bailey (2004) and Bailey et al. (2008) offered a revamped version of occlusal polygons with the use of high definition photography and modern computer software to calculate the variables presented by Morris (1986), though angles were recorded as radians instead of degrees for statistical analyses. The use of newer technology allowed Bailey to calculate all of the variables without the need to separate the polygon into two oblique triangles, and the use of high-definition photography was believed to reduce the method error by further removing the human element. Additionally, Bailey (2004) and Bailey et al. (2008) included cusp base areas, which determined the area of each cusp by using the molar's natural fissures to divide the tooth into quadrants. The cusp base areas were summed to produce a total cusp area. Lastly, the relative cusp areas were calculated by dividing the cusp base areas by the total cusp area. The relative cusp areas were generated to negate the influence of size based solely on the occlusal polygon generated through cusp apices because of the cusps general internally facing orientation, which was thought to give a false representation of the actual size of the tooth.

1.6 SUMMARY

The consistency of odontogenesis, the rich theoretical backbone for the development of dental fields, and heritability of both metric and morphological dental traits make teeth well suited for anthropological research, both in modern and ancient populations. Using dental data has allowed for research into biological affinity, migration and peopling, and paleoanthropology. In both morphological and metrical analyses, techniques have been developed and refined throughout the years to allow for consistent and repeatable testing, which has resulted in richer datasets and more fine-grained analyses. In comparison, geometric morphometric analyses are relatively new and have not been adequately used to their full potential. While geometric morphometrics have been utilized in research similar to both morphological and metrical analyses, the volume of studies to corroborate findings, or expand upon previous morphometric literature is lacking.

Many nonmetric and metric studies have been done for modern human populations, but there is a gap in the morphometric literature, especially concerning multiple teeth. The inheritance of dental morphology and overall size has been adequately described in the literature by several of the abovementioned authors; it then follows that if both nonmetric shape and gross size are inheritable, so then should morphometric variables. Geometric morphometrics offer a means to bridge the gap between purely morphological or metrical studies, and also circumvent limitations of the traditional methods by examining both size and shape together in high fidelity. Lastly, given Bernal's (2007) assertion that dental morphometric techniques are better at discriminating between closely related populations than traditional metric techniques, the current study will explore whether morphometrics can be used in modern peoples of the U.S. to examine microevolutionary processes.

1.7 DISSERTATION OUTLINE

To conceptualize the aims of the current study, Chapter 2 will provide theoretical information on the concept of "race" (here used interchangeably with biological affinity and ancestry), social identity and individual population histories in the U.S. that has led to each of the groups under analysis to be unique entities. Even though "race" has been thoroughly debunked within anthropology as no more than a sociological construct, the idea social race has permeated American culture and has been continually collected by the U.S. Census Bureau. However, there has been a shift in collecting more descriptive data, such as ancestry, which details the ancestral origins of a person rather than a sociologically constructed label.

Once each group has been thoroughly defined theoretically, Chapter 3 will discuss the materials and methods that the current study has used. First, there will be a review of the collections used in the study followed by a breakdown of the individuals that comprise each group. Next, the methodology will include the use of a three-dimensional digitizer as a data collection tool to collect consistent and accurate data to represent the molar cusp apices. Additionally, several different statistical analyses will be used to examine group similarities and differences and to trace biological affinity from potential parental groups. Ultimately, the variation observed will serve as a means for classification in a modern, forensic sense.

Chapter 4 will then discuss the results of measures of repeatability, sexual dimorphism, and asymmetry in the molars. Pearson's product moment and intraclass correlations and different t-tests were used to determine if the proposed methodology could supply a consistent means of data collection where the sexes can be pooled and antimeres can be used interchangeably.

Chapters 5-8 will examine each of the four modern groups individually with reference to possible parental populations. Each chapter will start with hypotheses concerning the biological affinity of the particular group within question based upon individual population history and known intermarriage rates. The descriptive statistics will be used for each molar individually, and combined molar models wills be subjected to a discriminant function analysis (DFA) wherein Mahalanobis' generalized distance (D^2) was calculated as a measure of biological similarity. Furthermore, the relationships of the D^2 were subjected to principal coordinate analysis (PCO), aka classical multidimensional scaling, to visualize both similarity and dissimilarity between groups.

Chapter 9 will compare each of the four modern U.S. groups, again with hypotheses related to population history and intermarriage rates. Additionally, Chapter 9 will analyze each molar individually, as well as in combined models with the aforementioned analytics. Further, Chapter 9 will provide an applied example of classification. Lastly, Chapter 9 will include a three-group analysis focusing on the three most prevalent population groups in the U.S. (American Asian, black, Hispanic, and white) as a means of comparison to recent literature focusing on these groups.

Chapter 10 will discuss the results and compare them to available literature as a means to corroborate results. Overarching trends between group analyses will be discussed with special attention to theoretical implications of molar variability through the lens of developmental processes and ultimately the implications of restricted gene flow through cultural barriers and positive assortative mating.

Finally, Chapter 11 will serve as a summary to the major points and provide concluding remarks, as well as recommendations for future considerations utilizing geometric morphometrics within dental anthropology.

CHAPTER 2: CONCEPT OF RACE, BIOLOGICAL AFFINITY, SOCIAL IDENTITY, AND POPULATION HISTORIES IN THE UNITED STATES

In the pursuit of any study that aims to examine within and between group variations, it is necessary to have a definition of said groups. In many analyses, group membership is considered mutually exclusive and defining the groups can become problematic. In humans, how does one arrange groups? According to Ousley et al. (2009), there are no groups, only populations; however, how does the U.S. population fit into this distinction? It has long been known that in humans there is no biological race, pure and simple. However, social race is a very real construction that is constantly reinforced in day-to-day life. According to the U.S. Census Bureau, there are four main ancestral groups in the United States, whites, blacks, Asians, and Hispanics (2013). However, the aforementioned population groups are not natural populations. Each of the broad ancestral categories is the product of consistent migration, admixture, and unique population history. Thus, samples may not be strongly representative of the overall populations from which they are derived, particularly the Hispanic sample, as will be made apparent later. As will be shown, the concept of which types of peoples are included within particular groups has been in constant flux. To consider each of these groups distinctive enough to warrant the labels, it is necessary to look at the concept of race, unique population histories, and theoretical underpinnings of why these groups are homogenous.

The concept of "race," specifically, the practice of categorizing peoples into groups is not new in anthropology. In fact, it could be argued that through cladistics and phylogeny, a large part of biological anthropology has involved identifying groups, either spatially, temporally, or both. However, two major associations in biological anthropology, the American Association of Anthropologists (AAA) and the American Association of Physical Anthropologists (AAPA) released statements decrying race (AJPA, 1996; AAA, 1998). The AAPA's position on biological race added to the 1964 UNESCO report on race, while the AAA's statement is largely based on a monograph by Smedley (1993). The foundation for each of the arguments is rightly based on the fact that there is no "biological race" in humans; variation among populations is a complex interplay of environment, culture, and biology. Further, each statement argued that there is more variation within "groups" than between them (AJPA, 1996; AAA, 1998). Armelagos and Van Gerven (2003) stated that "across the millennia of recorded history, race has been an amalgamation of observed biological differences interpreted through the lens of cultural prejudice." Further, Smay and Armelagos (2000) noted that 85% of variability is within a person, while only 6-12% is between people; they asserted that labeling people as particular races does nothing in the aims of identification. Earlier, Relethford (1994) demonstrated through craniometrics that more variation was inherent within geographic regions than between them.

Conversely, several researchers have argued that, while biological races do not exist, there is enough patterned variation between geographic populations that can be measured and used for means of identification (Sauer, 1992; Kennedy, 1995; Brace, 1995; Ousley et al., 2009). To test the notion of greater variability within-than-between groups, Ousley et al. (2009) used Howells craniometric dataset to demonstrate that while there is more variation within population groups, the range of variation is specific to each group and can be used to separate groups. In America, especially, Ousley et al. (2009) asserted that positive assortative mating was a likely factor in the group separation.

It is well known in anthropology that, generally, groups located more closely to one another geographically will be more similar genetically and phenetically. The concept of proximity lending itself to similarity, as formally addressed by Wright (1943), has today become the isolation by distance model; it was originally developed in the field of genetics to examine evolutionary questions centering on factors that could result in speciation. Similarly, ecology has used the notion of spatial autocorrelation to describe how ecological variables located closer to one another are statistically more similar than those farther away -- solely based on proximity (Cliff and Ord, 1970; Legendre, 1993). In a practical sense for a modern population, constrained access to other individuals is more appropriate than spatial autocorrelation as presented by Cliff and Ord (1970) and Legendre (1993). The isolation by distance model has influenced concepts of biological, geographical, and temporal affinity studies in the areas of dental anthropology (Turner, 1971, 1983, 1985, 1986; Irish, 1997, 1998, 2005; Hanihara, 2008), and craniometry (Szathmary, 1979; Howells, 1973, 1989; Ross et al., 2002; Relethford, 2004; Ousley and Jones, 2010).

Additionally, genome-wide studies have contributed to studies of population variation geographically. Li et al. (2008) examined over 650,000 single-nucleotide polymorphisms from 51 populations across the globe and found distinct differences in haplotype heterozygosity between populations. Similarly to the previously reported studies discussing within-versus-between group variation, Li et al. (2008) also concluded that there was more variation within geographic populations than between populations;

however, the variation between populations was of high enough resolution to detail population structures. Specifically, haplotype heterozygosity decreased proportionally to the distance from sub-Saharan Africa, thus reaffirming the notion of an out-of-Africa migration model in addition to multiple founder effects on frequent migration events (Li et al., 2008; Hunley et al., 2009). Using the same dataset, Pickrell et al. (2009) demonstrated positive selection in skin pigmentation, and perhaps also in type II diabetes. Putative selection signals were found among biologically similar populations such as European, Middle Eastern, and Central Asian, where sub-Saharan African, and New World populations demonstrated distinct differences in putative selection signals (Pickrell et al., 2009). Both of the aforementioned studies corroborate earlier report from Rosenberg et al. (2002) who surveyed 52 world populations and found five major groups: (1) sub-Saharan Africans; (2) European and Central Asians; (3) East Asians; (4) Pacific Islanders; and (5) New World Native Americans, which is consistent with the positive selection signals observed by Pickrell et al. (2009).

Further, Rosenberg et al. (2002) noted that with enough genetic markers, local populations could be teased apart from one another. Lastly, Tang et al. (2005) used 326 microsatellite data from over 3,200 individuals from 15 different locations across the Unites States that contained self-identified ancestry as: white, African American, East Asian, or Hispanic. Using genetic cluster analysis, four major clusters were identified and corroborated the self-identified ancestry nearly perfectly (99.86%). Further, Tang et al. (2005) calculated the allele-frequency differences between the four U.S. groups wherein smaller differences in allele-frequency indicates greater admixture. American Asians had the least difference with Hispanics, followed by whites, and then blacks; American blacks had the least difference with Asians, followed by whites, and then blacks; American Hispanics had the least difference with whites, then Asians, then blacks; and lastly, American whites had the least difference with Hispanics, followed Asians, and then blacks. Tang et al. (2005) concluded that "older geographic ancestry" is highly correlated with self-identified ancestral categories, contrary to previous researchers' claims (p. 274).

To address the negative connotation of "race" in relation to human groups, Sauer (1992) proposed use of the term "ancestry" instead. Since his suggestion, ancestry has been recorded by the U.S. Census Bureau, and is defined by the agency as:

> a person's ethnic origin or descent, "roots," or heritage, or the place of birth of the person or the person's parents or ancestors before their arrival in the United States. Some ethnic identities, such as "German" or "Jamaican," can be traced to geographic areas outside the United States, while other ethnicities such as "Pennsylvania Dutch" or "Cajun" evolved in the United States. The intent of the ancestry question is not to measure the degree of attachment the respondent had to a particular ethnicity…A person's ancestry is not necessarily the same as his or her place of birth; i.e., not all people of German ancestry were born in Germany (U.S. Census Bureau, 2013).

However, as noted by Boas (1912), using only craniometrics, descendants of immigrants in the U.S. demonstrate differences from their parent populations born abroad; such variation brings to light environmental impacts, at least in craniometrics, and perhaps reinforces the isolation by distance model.

The first modern census took place in 1790 and consisted of 3,929,214 persons; of these, 3.1 million were recorded as whites and 750,000 as blacks (Daniels, 2002). As of 2011, the U.S. Census Bureau reported an almost 10 fold increase in population of 311,591,919 persons; over 230 million are self-identified as white, over 39 million as black, more than 15 million as Asian, and over 51 million as Hispanic (U.S. Census Bureau, 2013).

Alba and Golden (1986) demonstrated that intermarriage is of fundamental importance as a measure of social distance and structural assimilation; for the purposes of anthropology, these factors can be used as points of discussion in observable differences between groups, be it cultural or physical. Of course, the genetic and phenotypic assumptions based upon intermarriage are dependent on the belief that intermarriage also means intermating. Since there are no credible resources that have examined intermating preference or practice within the U.S., the rates of intermarriage are used as a proxy for gene flow. Still, it should be made exceedingly clear that intermarriage rates do not explicitly imply intermating and vice versa. Intermarriage rates for the big four groups in the United States have been relatively low. As of 2010, American whites had the lowest intermarriage rate of 9.4%, followed by blacks at 17.1%, then Hispanics with 25.7% and lastly Asians with 27.7% (Taylor et al., 2012a). Additionally, as of 2010, 15.1% of all new marriages are intermarriage, though only 8.4% of are intermarriages (Taylor et al., 2012a).

The aforementioned intermarriage rates are consistent with the allele-frequency differences noted by Tang et al. (2005) in American Hispanics and whites, though conflicting in American Asians and blacks. American Asians consistently have the lowest allele-frequency differences with each of the groups and also the highest rate of intermarriage (27.7%). Of the groups, American Asians share the lowest allele-frequency difference with Hispanics (48%), followed closely by whites (49%) (Tang et al., 2005). However, American Asians have a preference to intermarry with whites at 75.1% compared to Hispanics at 11.8% (Passel et al., 2010). American blacks share the lowest allele-frequency difference with Asians (54%), followed by whites (57%) and have the highest rate of intermarriage with whites (57.5%), followed by Hispanic (22.5%), and lastly Asian (6.6%) (Passel et al., 2010; Tang et al., 2005). American Hispanics have the least allele-frequency differences with whites (41%), which also is the group with which they most commonly intermarry (80.5%) (Passel et al., 2010; Tang et al., 2005). Lastly, American whites have the least allele-frequency differences with Hispanic (41%), followed by Asian (49%), and lastly black (57%), which is consistent with the intermarriage rates with Hispanics (48.8%), Asians (18.1%), and blacks (13.6%).

2.1 MODERN U.S. POPULATION HISTORY

2.1.1 Population History of American Whites

It is long been taught that America was a "melting pot" of different peoples and cultures. However, over 60 million immigrants are from Europe (Daniels, 2002). In fact, using the 1992 General Social Survey, 92% of white American respondents could name a specific country or region of the world their ancestors had hailed from; of that, over 89% named a European country (Hout and Goldstein, 1994). Today, 76.4% of the population identifies as white, and again, ancestries are primarily derived from European origins (U.S Census Bureau, 2013). Broadly, more than half of European immigrants that came to the United States did so through indentured servitude and were labeled either as such or as redemptioners (Smith, 1971). In the end, migrations of all kinds resulted from the concepts of push, pull, and means. Push refers to circumstances in a home country that acts a catalyst for people to move (religious persecution, for example); pull refers to some enticing reason to leave (e.g., wealth and lands); and lastly, means simply entails having the ability to do so (advanced transportation technology) (Daniels, 2002).

Between 1820 and 1930, almost 36 million people emigrated from Europe, starting with just over 100 thousand between 1820 and 1830 and peaking at nearly 9 million between 1901 and 1910 (Daniels, 2002). However, post 1930, European immigration fell drastically due to new government policies (Massey, 1995). The influx remained low for over 60 years, a lag in which Massey (1995) believes led to the assimilation of European groups into a more homogenized unit because of the lack of reinforced "ethnicity" being constantly supplied from the ancestral homes. Additionally, Daniels (2002) pointed out that even during the highest influx of immigrants (1901-1910), the proportion of foreign born people to those born in America only peaked at 14.7%; thus, the growing "intermixed" American born population increased at a greater rate than via immigration. Further, Alba and Goldstein (1986) noted that European groups had extremely high rates of intermarriage with other European groups in America, with rates as high as 86%. It is thus clear that an intermarriage divide existed between Europeans and non-Europeans. As of 2000, whites marry other whites at a rate of about 93%; however, geographic origin of the different white European groups is not a significant factor (Waters, 2000). As Hout and Goldstein (1994) reported, overlapping religious beliefs have a stronger effect on intermarriage than ethnicity.

2.1.1.1 English

Today, nearly 26 million, or 8.2% of the American population claim English ancestry (U.S. Census Bureau, 2013). The first immigrant group to colonize the U.S. was from England in 1607. It consisted of 104 men in Jamestown, Virginia, which was named through a combination of the Virginia Company founding the colony, and as homage to King James I

(Stebbins, 2011). However, by the end of the first year, roughly two-thirds of the original population died (Daniels, 2002). Over the next few years, the population rose to over 500 before a period of great starvation claimed the lives of around 80% of the population, reducing it to 60 persons (Daniels, 2002). To combat the dwindling population, and to continue to grow the profitable tobacco, the Virginia Company transported over 3,750 people to Jamestown between 1619 and 1622 (Daniels, 2002). The number of immigrants rose to over 8000 by 1644 due to the continued influx of workers brought over (Stebbins, 2011).

As the Virginia colonies grew, English immigrants began to move to surrounding areas, namely Maryland and New England. The big movement in Maryland involved the Calvert family establishing tobacco trade in 1634 (Daniels, 2002). Contemporaneously, New England was being colonized in the 17th century by several families, which included a minority composed of Pilgrims and Puritans (Daniels, 2002). Arrival of the Mayflower at Plymouth Rock in 1620 included some 100 individuals, mostly indentured servants. Plymouth would later become part of Massachusetts, which, in the 1630s, saw a major immigration of over 21,000 people (Daniels, 2002). By 1700 over 90 thousand people were living in New England, most of which were English (Daniels, 2002). The English in New England were a distinctly homogenized group, and were considered to be the most homogenous in America through the 18th century (Daniels, 2002).

2.1.1.2 Irish

As of 2011, the number of U.S citizens claiming Irish ancestry is over 34 million, or >11% of the reported ancestries (U.S. Census Bureau, 2013). The 19th century saw the peak of Irish immigration when 4 million people emigrated to the United States, concentrated mainly in urban centers of Massachusetts, New York, Pennsylvania, and Illinois (Sowell, 1981). Irish immigrants not only came in large numbers, but also had one of the lowest return migration rates of any of the European group (Daniels, 2002). The Irish settled basically where they had landed due to extreme poverty; in fact, Irish Americans paid the majority of the fares for passage to the U.S., where between 1848 and 1864, over 65 million dollars was sent to Ireland (Sowell, 1981). After the peak immigration of the 19th century, between 200,000 and 300,000 came after 1920 (Hout and Goldstein, 1994). The Irish always made up a substantial percentage of European immigrants, contributing up to half of all European immigrants throughout the 19th century (Daniels, 2002).

Irish Americans were ostracized and segregated in the cities they resided, and were of the lowest economic class -- financially worse off than free blacks in the same regions (Sowell, 1981). Segregation, in conjunction with homogeneity in religious belief (Catholicism), led to a high degree of within group marriages, arguably, the highest of any European population (Hout and Goldstein, 1994). Homogeneity in Irish marriage preference is likely a factor in the nine-fold population increase with reported Irish ancestry between initial immigrant populations of 4 million to the >34 million today (Hout and Goldstein, 1994). Further, Kennedy (1973) reported on the positive effect on fertility on being considered a “minority” group, specifically concerning the Irish.

2.1.1.3 German

German ancestry is the most commonly claimed European ancestry in America, with 15.2%, or over 47 million Americans (U.S. Census Bureau, 2013). However, much of the immigration to the United States happened before Germany became a unified country in 1871 (Sowell, 1981). The first Germans settled in current day New York City, then New Amsterdam, in the 1620s; later, several German families moved throughout Pennsylvania seeking religious freedoms in the forms of Mennonites, Calvinists, Amish, Quakers, and Lutherans – in fact, the term "Pennsylvania Dutch" is a bastardized mispronunciation of Pennsylvania Deutsch (Daniels, 2002). The first large influx of German immigrants came in 1709 with roughly 2,500 moving through the port of Philadelphia (Grubb, 1990). In a few years, however, there was an increase in immigration to nearly 60,000 between 1727 and 1756 (Grubb, 1990). By 1760, Germans accounted for up to 60% of the population of Pennsylvania and 30% of the colonies' total population (Grubb, 1990). Further, like the Irish, Germans accounted for a substantial proportion of all immigrants during the 19th century -- peaking at over 36% (Daniels, 2002). Between Waterloo and World War I, about 90% of German emigration was to the United States; between 1850-1860, about 1 million individuals arrived (Sowell, 1981). Throughout the 19th century, over 5 million Germans immigrated to the United States; however, this drastic increase was likely due to the switch to steam-powered ships, making the journey quicker, easier, and more frequently available (Daniels, 2002).

Largely, pre-World War I German immigrants did not face the same stigmas that the Irish endured. For one, people of German descent represented a significant proportion of the U.S. and were also more widespread geographically than the Irish (Sowell, 1981). Traditionally, through the 18th and early 20th centuries, Germans married other Germans; the reason was likely because of intense cultural retention, as evidenced by over 500

German-language publications available daily, weekly, or monthly (Sowell, 1981). Within group marriage was as high as four-fifths in the early 20th century, but quickly diminished to one-third by the 1970s (Sowell, 1981).

2.1.1.4 Jewish

Unlike the previous groups, Jews are not from one specific geographic location, but are dispersed throughout Europe and the Middle East. As of 2011, over 6.5 million Americans claim Jewish ethnicity, representing 2.1% of the total population (Sheskin and Dashefsky, 2011). The earliest immigrants to the U.S. were Sephardic Jews from Spain, Portugal, and later Holland (Sowell, 1981). The first synagogue was established in New York in 1695. By the late 18th century, there were nearly 2000 Jews in America, generally within small communities (Sowell, 1981). Within 100 years of the Revolutionary War over 500,000 Jews emigrated to the U.S., mostly from Germany (Sowell, 1981). The next, and one of the largest migrations, began in the late 1880s through the 1920s; it involved movement of over 2 million Eastern European Jews from Poland and, especially Russia due to anti-Semitic policies (Sowell, 1981). Unlike the German Jews, Eastern European Jews did not spread as far geographically with most residing in New York (Sowell, 1981).

The rate of intermarriage in Jews was extreme, specifically within a particular sect of Judaism; for example, in the 1940s it was unheard of for German Jews to marry Eastern European Jews (Sowell, 1981). Today, the rate of intermarriage is nearly 50% (Dashefsky et al., 2013). Compared to the 1900s when the intermarriage rate was only 2%, it rose considerably to 31.7% by the late 1960s (Massarik, 1971). Today, while New York has retained the highest concentration of Jewish people, California has the second highest population, with the Midwestern and Southern U.S having lower population distributions (Sheskin and Dashefsky, 2011).

2.1.1.5 Italian

As of 2011, there are 17.5 million Americans claiming Italian ancestry, i.e., 5.6% of the total population (U. S. Census Bureau, 2013). Italians did not come to the U.S. in great numbers, as had the previously mentioned groups. Between 1820 and 1850 less than 5,000 Italians immigrated to the U.S. (Perlmann, 2000). Between 1880 and 1920 over 4.1 Italians million entered the U.S., representing the greatest single influx of any population in the shortest amount of time (Daniels, 2002). Just before World War I and post-war to 1921, over 200,000 Italians were immigrating per year (Sowell, 1981). However, the Italians had the greatest rate of return migration to Italy, generally within the first five years of arrival (Perlmann, 2000). Sowell (1981) surmised that the return was because the initial migration was exploratory due to the disproportionate amount of males (80%).

Italians, more than previously discussed European groups, were heavily segregated in areas of cities that were sometimes specific to the Italian village from which they came (Sowell, 1981). The relative displacement to form the previously mentioned close-knit communities led to extreme rates of endogamy. Rates of intermarriage fluctuated between 1% and 5% from the 1860s through 1940s (Perlmann, 2000). Early on, Italian in-marriage was based on localities as specific as immigration from the same province in Italy, and then later by either northern or southern regions (Sowell, 1981). However, by the 1970s, intermarriage rates rose as high as 70%, demonstrating assimilation into an American identity (Perlmann, 2000).

2.1.2 Population History of American Blacks

In more than two centuries of bondage, their many ancestral languages and cultures faded away, and their genetic differences were amalgamated (together with substantial mixture of Caucasian genes) to produce the American Black—a cultural and biological product of the New World, rather than a direct descendant of any given African nation or culture.

– Thomas Sowell, 1981

As of 2011, there were over 42 million persons in the United States claiming “Black” or African American ancestry, which represents 13.7% of the total population (U.S. Census Bureau, 2013). However, 20% of Americans were either from Africa, or ancestor to an African at the end of the colonial period (Daniels, 2002). The overwhelming majority of blacks came directly from the slave trade, which focused on transport out of West Africa (Daniels, 2002). In total, over 11 million people were kidnapped and forced into the slave trade (Sowell, 1981). The trade focused around Angola in the 17th century and had spread to Mozambique by the 19th; however, the vast majority (approximately 8 million) was from western Africa, with west-central Africa (Cameroon and Angola) contributing much of the rest (Salas et al., 2004).

Of the estimated 11 million Africans abducted, around 420,000 were brought to America, with many more brought to Brazil and the West Indies (Daniels, 2002). The first Africans brought to the New World were brought to Virginia in 1619 as indentured servants, same as previously described for European groups, complete with entitlement to lands once their contracts were fulfilled (Sowell, 1981). However, the first law that perpetually enforced slavery, extending toward slaves and their children, was passed in Virginia in 1661 (Sowell, 1981). The apex in slave trade and transport came between 1721 and 1820, which accounted for 60% of the total number of slaves in the New World (Daniels, 2002). The increase was largely due to advancements in the Industrial Revolution, specifically, the steamship -- which made transport of slaves easier, and the cotton gin -- which intensified growing and production of cotton in the United States (Sowell, 1981). In 1750 there were an estimated 250,000 blacks in America; by the first census in 1790 there were over 750,000, of which over 690,000 were enslaved; of these, only about 150,000 were African born (Daniels, 2002). By 1820, the black population had grown to nearly 2 million, with 90% living in the South (Daniels, 2002). By the time of Lincoln's passing of the famous Emancipation Proclamation in 1863, the black population was nearly 4 million, with 3.1 million now freed from slavery; this freedom, in turn, led to a great northward migration from the south (Sowell, 1981).

Between the end of the Civil War and 1920, about a quarter of the black population migrated to the Northeastern United States, stimulated by worsening race relations in the post-bellum South, dwindling economy from boll weevil infestation, and the pull of the more liberal and industrialized North, with better relations and financial opportunities (Sowell, 1981). The Great Depression paused migrations from the South, but between 1940 and 1970, 4 million blacks moved to the North (Sowell, 1981). Not all of black migrants came from the South. Freed slaves from the British West Indies also migrated north; however these migrants only accounted for about 1% of the total black population in the United States (Sowell, 1981).

The massive migration of blacks, in tandem with natural population increase, corresponded with forced segregation (i.e., Jim Crow laws spanning 1876-1965). Until the benchmark *Loving v. Virginia* Supreme Court decision in 1967, intermarriage between blacks and whites was illegal. Since then, intermarriage rates for black Americans has been low, with only 6-7% of blacks marrying exogamously in 1979 (Alba and Golden, 1986) and, as of 2010, 17.1% (Taylor et al., 2012a). In each case, black males more often had a preference to intermarry than females (Alba and Golden, 1986; Taylor et al., 2012a).

2.1.3 Population History of American Asians

As of 2011, approximately 5%, or just over 15 million citizens claimed Asian ancestry (U.S. Census Bureau, 2013). The largest demographic group is the Chinese, with over 3.5 million U.S. citizens having Chinese heritage, followed by Filipino with over 2.5 million, Vietnamese with 1.6 million, Korean with 1.4 million, and Japanese with 756 thousand. In the 1940s, American Asians accounted for less than 2/5ths of 1% of the population, making the growth of American Asians to the 5% today one of the greatest population increases in American history (Daniels, 2002). The immigration boom came with the passing of the Immigration Act of 1965, lifting a long time ban on all Asian migration, in conjunction with the loss of the Vietnam War and fall of U.S. backed governments in Southeast Asia (Massey, 1995). American Asians have the highest rate of intermarriage at 27.7%, with the highest incidence of intermarriage between Asian females and white males (Taylor et al., 2012a).

2.1.3.1 Chinese

Today there are over 3.5 million Chinese Americans (U.S. Census Bureau, 2013). However, Chinese only really migrated to the U.S. since the California Gold Rush beginning in 1849; like many immigrant groups, Chinese came to the U.S. as contract workers or on borrowed money (Daniels, 2002). The initial influx was overwhelmingly from the Kwangtung province in southern China (Sowell, 1981); most spoke Cantonese (Daniels, 2002). By 1851, there were over 25,000 Chinese in the U.S., almost exclusively in California (Sowell, 1981). In just 20 years, the population had grown to over 63,000 with most Chinese being sojourning males looking to build a nest egg in the gold rush and return to China (Daniels, 2002). In fact, about half of the Chinese who came to the U.S. did not stay; more left the U.S. than entered in the 1880s (Sowell, 1981). Furthermore, two pieces of legislature continued to hinder Chinese population growth: 1) the Naturalization Act of 1870, which limited naturalization to whites and blacks, thus keeping Chinese a separate class; and 2) the Chinese Exclusion Act of 1882 that made the Chinese the only population that could not freely immigrate (Daniels, 2002). The Chinese Exclusion Act of 1882 was effectively repealed in 1943 and was modified to allow limited immigration of Chinese; generally these immigration slots were limited to wives of Chinese Americans still in China to help counteract the sex ratio that, at times, favored men to women 20 to 1 (Sowell, 1981). Further, the Immigration Act of 1965 effectively dismantled limitations on Chinese (and all Asian) immigration. To put the weight of the passing the Act of 1965 into perspective, there were reportedly 106,000 Chinese in America in 1940; by 1980 the number was over 800,000 (Daniels, 2002).

Chinese populations became urbanized quite rapidly, establishing enclaves that would become known as Chinatowns; the first was established in San Francisco in the 1850s (Daniels, 2002). The sex imbalances in the late 19th and early 20th centuries caused high rates of intermarriage of Chinese men (Sowell, 1981). However, in the 1980s intermarriage of Chinese was 15.7% with 22.2% being within other Asian ethnic groups; intermarriage rates continued to fall to 12.1% in the 1990s with interethnic Asian marriage rates growing to 32.7% (Lee and Fernandez, 1998).

2.1.3.2 Japanese

United States citizens of Japanese ancestry comprise 0.2% of the total population, or just over 750,000 (U.S. Census Bureau, 2013). The first emigration came during the Meiji Era was in 1868, when 148 contract workers were brought to Hawaii to work in the plantations (Sowell, 1981). In 1884, over 30,000 Japanese workers were brought to Hawaii. When Hawaii was annexed by the U.S. as a territory in 1898, many Japanese migrated to California (Daniels, 2002). By 1900, there were over 24,000 Japanese in the continental U.S., most of whom were farm laborers like the steadily urbanizing Chinese who were the majority of California farm workers a generation prior (Daniels, 2002). Due to hostility geared towards Japanese farm workers, which was catalyzed by the similar American disdain for the previous Chinese, the U.S. struck the "Gentlemen's Agreement" of 1907-1908 with Japan that effectively ended Japanese labor immigration. Japan refused to issue passports to any Japanese with the intent to travel to America (Daniels, 2002). The Gentlemen's Agreement resulted in stagnation of the Japanese population, who, like the Chinese, had an incredibly biased sex ratio, i.e., >24 males to 1 female in 1900 (Sowell, 1981). However, the Gentlemen's Agreement included a provision that allowed passports to workers already in America, and extended passport access to their families overseas (Daniels, 2002). The Gentlemen's Agreement effectively balanced the sex ratio of Japanese men to women to less than 2:1 by 1920 (Sowell, 1981). By 1940, there were nearly 300,000 Japanese Americans, mainly in California, and over 2/3rd of them were native born in the U.S (Daniels, 2002).

Just as with the Chinese, the Immigration Act of 1965 opened the proverbial floodgates on Japanese immigration. When the act was passed in the 1960s, there were 464,000 Japanese in America; in just 20 years, there were over 700,000 (Daniels, 2002). However, with the economic rebound of Japan, immigration has steadily declined. While the Japanese were the largest Asian ethnic group between 1910 and 1970, they had dropped to 3rd in the 1980s; today they have fallen to 6th largest (Daniels, 2002; U.S. Census Bureau, 2013). Exogamy of ethnic Japanese in the U.S. followed the same trend as the Chinese; there were higher rates in the 1980s at 34.2%, dropping in the 1990s to 25.6%, with interethnic Asian marriages rising from 11.9% in the 1980s to 20.3% in the 1990s (Lee and Fernandez, 1998).

2.1.3.3 Filipinos, Koreans, and Vietnamese

Filipinos, Koreans, and Vietnamese comprise the remaining large proportion of Asian ethnicity in the U.S. Their population history is relatively brief compared to that of the Chinese and Japanese. As above, the Immigration Act of 1965 reopened immigration to the U.S., specifically for Asian countries. Filipinos had been in the U.S. and Hawaii for some time, beginning in the early 20th century with a wave of students due to the 1898 American annexation of the Philippines; however, the number was small (Daniels, 2002). Post WWII, Filipinos who had served for the American Armed Forces could legally become citizens; as a result, there was an increase in Filipino citizenship. However, the biggest influx of Filipinos was due to the Immigration Act of 1965, where in just 30 years the Filipino population rose from 181,000 to nearly 1.5 million (Daniels, 2002). In 20 years, the number of Filipinos in America rose to over 2.5 million (U.S. Census Bureau, 2013). Intermarriage of Filipinos was high in 1980 at 30%, but fell to 18.9% in 1990; interethnic Asian marriage rose to 12.2% in 1990 from 6.9% in 1980 (Lee and Fernandez, 1998).

Today, over 1.4 million Americans claim Korean ancestry (U.S. Census Bureau, 2013), but many arrived after the Korean War and most are descendants of that population (Daniels, 2002). A unique feature of the original Korean immigration cohort was the fact that over 70% were women, due to the numerous marriages to American G.I.'s during the war (Daniels, 2002). Another sizeable influx of immigrants came as orphan adoptions, generally to American white parents (Daniels, 2002). The Korean population in the U.S. totaled under 70,000 in 1970, had a 417% increase to over 350,000 in the 1980s, and saw another sizeable increase to 798,000 in the 1990s, before becoming the 1.4 million of today (Daniels, 2002). In 1980 intermarriage was 31.8%, with only 8.7% interethnic Asian intermarriage. Intermarriage dwindled to 6.5% in the 1990s, while interethnic Asian intermarriage increased to 23.1% (Lee and Fernandez, 1998).

Unlike the previously mentioned recent Asian immigrants, Vietnamese have been described as mainly a "push" immigrant as war refugees (Daniels, 2002). Today, there are over 1.6 million Vietnamese Americans (U.S. Census Bureau, 2013). Prior to 1970, there were less than 10,000 in the U.S. As the United State's involvement in Vietnam grew, so did the number of immigrant refuges, which reached over 245,000 by 1980 (Daniels, 2002). War refugees also included several other Southeast Asian groups including 149,000 Laotians, 147,000 Cambodians, and 91,000 Thai (Daniels, 2002). In 1980, the intermarriage rate for Vietnamese was 19.8% with only 6.7% intermarrying interethnic Asian, but by 1990, exogamy had fallen to 8% and interethnic Asian intermarrying had grown to 39.1% (Lee and Fernandez, 1998).

2.1.4 Population History of American Hispanics

Currently, American Hispanics comprise 16.7% of the total U.S. population, which equates to nearly 52 million individuals. The majority claim Mexican ancestry at 10.8%, followed by Puerto Rican at 1.6%, Cuban at 0.6% and a mix of ancestries at 3.7% (U.S. Census Bureau, 2013). Hispanics have the second highest incidence of intermarriage at 25.7% and the exogamy is evenly split between males and females -- with a slightly higher tendency for males at 25.9% opposed to females at 25.4% (Taylor et al., 2012a). Contrary to trends of the American Asian groups, Hispanic rates of intermarriage increased from the 1980s through today, with 12.7% exogamy in 1980, 18.6% in 1990, and stabilizing between 2008 and 2010, which had 25.5% and 25.7% respectively (Lee and Fernandez, 1998; Taylor et al., 2012a). Furthermore, the most common intermarriage with Hispanics is with American whites at 43.3% (Taylor et al., 2012a).

2.1.4.1 Mexican

There are over 33.5 million U.S. citizens claiming Mexican heritage (U.S. Census Bureau, 2013). Contemporary Mexicans are descendants primarily of Spanish and indigenous tribes that were largely decimated after Cortes' arrival in 1519 (Sowell, 1981). By the 1800s, the number of Mexicans born of mixed Spanish and indigenous tribes, known as mestizos, outnumbered Spaniard nationals, imported slaves, and indigenous peoples (Sowell, 1981). During the westward expansion of American immigrants in the 1820s, there were Mexican settlements throughout the southwestern U.S. as far west as California.

There were three major waves of Mexican immigration to the United States. The first (roughly between 1820 and 1930) saw the bulk of immigrants, 720,000 out of the total 750,000 of the period, arrived after the 1909 Mexican Revolution; conditions in Mexico worsened while there was promise of higher pay in the U.S. (Daniels, 2002). The Great Depression, in conjunction with aggressive deportation policies of the U.S. surrounding that period (with over 200,000 Mexicans deported) acted as deterrents for further immigration (Sowell, 1981). The second wave of Mexican immigration came during WWII when a majority of the available labor was overseas fighting, and historically agriculturally active Japanese were kept in internment camps (Daniels, 2002). Due to the drastic need for labor, the U.S. and Mexico struck an accord known as the bracero program in 1942 where contract laborers were brought to the U.S. (Sowell, 1981). Originally 50,000 workers were brought in under the program in 1945, but by the 1950s, over 400,000 per year arrived due to the program; these numbers were compounded by the regular immigration that saw 60,000 in the 1940s exploded to almost 650,000 in the 1970s. There were over 2 million Mexican-born individuals in the United States by 1980 (Daniels, 2002). Between the end of WWII and 1954, almost 4 million Mexicans were deported (Sowell, 1981). The third wave began in the 1980s and is ongoing. In the 1987 census, it was estimated that there were 12 million individuals in the U.S. with Mexican ancestry; the number has nearly tripled to the 33.5 million today (Daniels, 2002; U.S. Census Bureau, 2013).

2.1.4.2 Puerto Rican

Individuals of Puerto Rican ancestry comprise the second largest Hispanic group at 1.6% of all Hispanics, totaling nearly 5 million individuals (U.S. Census Bureau, 2013). Puerto Rico was annexed to the United States in 1898 after the Spanish-American War. In 1917, the Jones Act proclaimed that all Puerto Ricans were naturalized United States citizens (Daniels, 2002). To put the population growth of Puerto Rico in perspective, in 1800 there were an estimated 150,000 individuals, by 1900 over 1 million, and, in just 25 years, there were 2 million individuals (Sowell, 1981). Migration to the continental United States was slow, with no substantial migration until post-WWII when air travel became inexpensive, specifically non-stop flights from San Juan to New York City (Daniels, 2002). In the continental U.S., mainly New York City, there were over 300,000 citizens with Puerto Rican ancestry; by 1960, this number nearly tripled to 887,000; and lastly, by 1980, there were over 2 million Puerto Ricans in the U.S., exceeding the number living in Puerto Rico (Daniels, 2002).

2.1.4.3 Cuban

Cuban ancestry is the last group of Hispanics recorded by the 2011 U.S. Census. Cubans comprise 0.6% of the total Hispanic population, which equates to almost 1.9 million persons (U.S. Census Bureau, 2013). Like Puerto Rico, Cuba was essentially “liberated” in the Spanish-American War and was a protectorate of the U.S. until Fidel Castro’s revolutionary rise in 1959 (Daniels, 2002). Post-liberation saw little immigration.

Substantial numbers of Cubans only came during the political unrest of Castro's ongoing revolution. In 1950, there were 30,000 Cubans in the United States. By 1960, there were over 120,000 —both first and second generation—in the U.S. (Daniels, 2002). When Castro came to power in 1962, an additional 150,000 Cubans, mainly political refugees, immigrated to the U.S. (Daniels, 2002). Additionally, in 1965, President Johnson made an agreement with Cuba to enable one plane per day between Miami and Cuba. Throughout the entirety of the arrangement, which lasted until 1973, an estimated 250,000 Cubans immigrated and stayed (Daniels, 2002). Since the end of the agreement in 1973, the population reached nearly 2 million individuals through natural increase and clandestine boat travel (Daniels, 2002).

2.2 DISCUSSION

Qian and Lichter (2007) proposed the use of intermarriage rates as a measure of social distance. Given the low intermarriage rates in the United States between groups, the four social groups have remained socially distant. Furthermore, classical assimilation theory states that assimilation is "a process of interpenetration and fusion in which persons and groups acquire the memories, sentiments and attitudes of other persons and groups and, by sharing their experience and history, are incorporated with them in a common cultural life" (Park and Burgess, 1969:735). By Park and Burgess's (1969) definition, the big four social groups in the U.S. have not fully assimilated, which is likely a reason for the retention of endogamy, in fact, according to Rosenfeld (2008), members of a particular social group are 100 times more likely to marry within their group than outside of their group.

Kalmijn (1998) detailed three possible causes for endogamy: (1) marriage candidates have preferences for similar spouses; (2) "third parties" such as family and other members of the same social group interfere with exogamous practice; and (3) constrained access to different social groups. Previously in discussing racial formation theory, Omi and Winant (1994) proposed that different social groups shared a "racial common sense" that was essentially a collective consciousness for each particular group. As a consequence of "racial common sense", different groups have grown "racial expectations", or perceptions of what is and is not acceptable of members of a particularly perceived group (Omi and Winant, 1994; Winant, 2000). The "racial common sense and expectations" would then account for the first two causes for endogamy by limiting the agency within particular groups to certain expectations, which are reinforced by the third party, or, in this instance, other members of the same social group. The third cause of endogamy could be explained by proximity alone, and also the racial bias in housing patterns, wherein social groups stay in relatively homogenous geographic clusters (Massey and Denton, 1993). As an example from before of the racially biased housing patterns, the "Chinatown" phenomenon described under the American Asian population history shows the unique clusters that social groups form.

Though race does not exist biologically, it is an undeniable Durkheimian social fact. Omi and Winant (1994) viewed race formation as a sociopolitical consequence that is constantly in flux. Support for Omi and Winant was demonstrated by the various legislatures passed throughout U.S. population history that barred entry into the country, dictated working privileges, and the ability to own land was all due to changing concepts of race. For example, the population history of the U.S. whites is riddled with instances wherein one European group was chastised and segregated before they could fully assimilate in the classical sense as defined by Park and Burgess (1969).

The paucity of available ancestries prescribed by the U.S. census in conjunction with the "racial common sense and expectations" (Omi and Winant, 1994; Winant, 2000), leads to a reinforced and, in some cases, limited idea of agency (Ortner, 2006). The racial common sense, that led to the expectations laid a theoretical framework that Ortner (2006) would describe as "agentic" (pp. 151). Furthermore, Ortner (2006) described agency in conjunction with power, wherein some people are prescribed more than others. Using agency in conjunction with the fluidity of the race concept and also ideas from demographic transition theory can then be used to understand the prevalence of social race in the United States. Graham (2000) noted that initially populations are characterized by high fertility and mortality rates leading to low population growth; next a few intermediate stages occur where mortality begins to decline and then is followed by fertility, almost always producing a population boom before the final phase in which there are both low birth and mortality rates, essentially causing a population plateau, stagnation, or even slight population decline. In the last 20 years, each of the population groups has seen a decline in fertility rates (Mather, 2012), which indicates that each of the populations has entered into the final demographic transition phase and have settled and stabilized. In conjunction with endogamy, racial common sense and expectations, assimilation into the prescribed group would, theoretically, garner each individual of that group greater agency through a greater support structure and political presence.

2.3 SUMMARY

American whites, or those of European based ancestries, account for the majority of the U.S. population at over 76% of the total population demographic. The most common European ancestries recorded in the U.S. are the English at over 85% of the total population, Irish at over 11%, German at over 15%, Jewish at 2%, and Italian at almost 16% (U.S. Census Bureau, 2013). However, the American white population group, based primarily on the above mentioned amalgamation of several European groups, has interdigitated into a homogenous population with high rates of intermarriage to other European ancestral groups, but low rates of intermarriage outside of a common European origin.

The American black population group is a coalescence of West African groups and American white influence. Indeed, immigration of West African blacks was essentially limited to the slave trade with the current population being the product of natural increase, as opposed to constant migration. However, due to racial stigmas and legislation, intermarriage rates between blacks and whites has been historically low, which is not to say that intermating always has been. Even post civil rights movement, intermarriage rates between American blacks have been consistently low at 17%, with a preference for black males to more frequently out-marry (Taylor et al., 2012a).

The current American Asian population accounts for 5% of the total U.S. population (U.S. Census Bureau 2013). Of the 5%, the majority (1.1%) is Chinese, followed by Filipino at 0.8%, Korean and Vietnamese both at 0.5%, and Japanese at 0.2% (U.S. Census Bureau, 2013). The Asian groups have remained homogenous due to the constant influx of new immigration post 1965 (Daniels, 2002). Though originally having the highest rates of intermarriage due to immigration restrictions prior to 1965, American Asians have been increasingly intermarrying other interethnic Asians as opposed to the other big four groups (Lee and Fernandez, 1998).

American Hispanics constitute nearly 17% of the total U.S. population and are overwhelmingly represented by immigrants from Mexico at nearly 11%, followed by Puerto Rico at 1.6% and then Cuba at 0.6% (U.S. Census Bureau, 2013). Intermarriage rates for Hispanics is the highest of any group at approximately 25%, most commonly with American whites (Taylor et al., 2012a). Of any group, Hispanics, primarily Mexicans, have the largest constant influx of new immigration, primarily on the Mexican-American border, which would offset the seemingly high levels of intermarriage between Hispanics and American whites (Daniels, 2002).

As mentioned earlier, intermarriage is also being used as a proxy for intermating, and thus gene flow. Given the socio-politically imposed ancestry system by the government through the census, the big four groups (Asian, black, Hispanic, and white) have remained relatively homogenous, as measured through the low rates of intermarriage between the four groups, which was approximately 8% of all marriages in 2010 (Taylor et al., 2012a). Even though it has been shown that intermarriage has declined throughout time, Rosenfeld (2008) explained that "what has not always emerged so clearly from the literature on racial intermarriage is the extent to which racial barriers are still, even after decades of decline, dramatically more powerful than any other kind of social barriers in the marriage market" (pp. 31). Lastly, intermarriage rates have shown similar trends as genetic distances in modern U.S. groups as shown by Tang et al. (2005).

Given the relatively low rates intermarriage in conjunction with racial formation theory and demographic transition theory members of the big four groups should, in theory, demonstrate similarities both genotypically and phenotypically with other members of their respective group, while also exhibiting differences between members of other groups. While Boas (1912) demonstrated that, anthropometrically, descendants of immigrants showed significant differences from their parent populations, less environmentally plastic traits, such as dental morphology, would be more impervious to environmental influence and could thus be used as a measure of biological affinity between modern U.S. populations and compared to parent populations.

CHAPTER 3: MATERIALS AND METHODS

3.1 SAMPLES

Molar data from a total of 1,267 individuals were collected for the study. Outliers were removed from the current study if the Mahalanobis distances based on the morphometric variables were greater than two standard deviations outside of the mean in the program MorphoJ (Klingenberg, 2013). After the removal of outlier, a total of 1,225 specimens remain. The statistical program R (R Core Development Team, 2013) was used to perform a power test using the package "pwr" (Champely, 2012). The linear model power test, as outlined by Cohen (1988), was used with a small effect size (0.02), significance level of 0.05, and a power of 0.95. A power test looking for a small effect size resulted in a proposed sample of at least 144 individuals for each group. Sufficient data were available to meet the requirements of the power test for the modern groups. The number of suitable dentitions for the possible parental groups was limited. Thus, as many specimens as possible were recorded for each parental group.

3.1.1 Modern American

The modern American samples were collected at four institutions across the United States: the Economides Orthodontic collection at the Maxwell Museum of Anthropology at the University of New Mexico (UNM), the Hamann-Todd Osteological Collection at the Cleveland Museum of Natural History (CMNH), the William M. Bass donated skeletal collection at the University of Tennessee Knoxville (UTK), and the dental anthropology casts housed at the University of Alaska Fairbanks (UAF) (Table 3.1). The Economides Orthodontic collection consists of over 5,000 dental casts collected between 1972-1999 from a private practice in Albuquerque, NM (Edgar et al., 2011). The Hamann-Todd Osteological Collection contains over 1,000 modern American skeletons collected and curated by T.W. Todd between 1912 and 1938 ("Hamann-Todd Osteological Collection", 2014). The William M. Bass donated skeletal collection consists of nearly 1000 donated skeletons, primarily from Tennessee, who were born between 1940 and 2011 ("WM Bass Donated Skeletal Collection", 2014). Dr. Joel D. Irish collected the dental casts from the University of Alaska Fairbanks' Department of Anthropology throughout the years as part of his on-going dental anthropology courses (circa 2000 – present).

Each institution assigned ancestry differently. The specimens of the Economides collection had their ancestry assigned post-hoc by a panel of individuals after the University of New Mexico acquired the collection in 2005. The assignment of ancestry was based on: patient name, patient address, skin color, facial features, and hair form and color (Edgar et al., 2011). A full description of the classification criteria and rationale for ancestry assignment at UNM is available through Edgar et al. (2011). The Hamann-Todd Osteological Collection was mostly comprised of donated bodies of vagrants whose ancestry as assigned during autopsy based primarily on skin color ("Hamann-Todd Osteological Collection", 2014). The Bass collection at UTK is comprised of donated bodies wherein their ancestry was self-prescribed prior to death ("WM Bass Donated Skeletal Collection", 2014). Lastly, each individual that produced a dental cast at UAF prescribed their own self-identified ancestry. While it would be ideal to include only self-identified individuals in the study, there is a paucity of material available to generate large samples.

The post-hoc assignment of ancestry is inherently flawed because of the wide range of variation and substantial overlap between groups, specifically the UNM sample.

Table 3.1. Demographic information for each of the modern groups.

Group	Collections and Sample Sizes	Sex	Total Number
Asian	UNM – 152 UTK – 3	F = 86 M = 69	155
Black	UNM – 102 CMNH – 77	F = 105 M = 99	204
Hispanic	UNM – 204 UTK – 14	F = 137 M = 82	219
White	UAF – 108 UTK – 82 UNM – 39	F = 112 M= 117	229

3.1.2 Historic Parental Groups

A total of 399 individual dentitions were collected at the American Museum of Natural History (AMNH) in New York City to be used as the parental population groups (Table 3.2). Primarily, the dentitions were recorded from the Felix von Luschan collection (n = 308). Von Luschan collected crania from around the globe between 1883-1906 and his collection was purchased by the AMNH where it is currently curated. The remaining individuals are from various collections with no other provenience other than geographic region and, if available, country of origin. The data were pooled according to broad geographic region, i.e. European, North Africa, Southeast Asia, etc. Additionally, 19 historic Native Alaskan crania were recorded at the University of Alaska Fairbanks, Department of Anthropology. Each of the samples has a sex bias in favor of males; the African samples contain 76 females and 123 males, the Asian samples have 17 females and 49 males, the European has 22 females and 43 males, and the Mexican sample has 15 females and 28 males. The Native Alaskan sample is not provenienced and lacks any additional elements to estimate sex.

3.1.3 Modern Comparison Groups

Additionally, two modern comparison groups were recorded: American Indian and modern Thai. The two groups were recorded to serve as out-group comparisons. The American Indian out-group was used for comparison with American Asians, Hispanics, and whites, while the modern Thai sample was used as a comparison with the Asian samples. Given what is known about migration into the New World (Turner, 1990; Scott and Turner, 2008), the American Indian group should compare to the American Asian and East Asian samples, as they all belong to the dental family known as Sinodonts (Turner, 1990). The American Indian group contains 20 individuals (F = 14; M = 6) and was collected from the Economides Orthodontic collection, which has been previously described. The modern Thai collection comes from an osteological collection at the medical school of Khon Kaen University (KKU), Thailand. The KKU collection contains over 700 individuals of known identity born in the 20th century. For the current study, data was recorded from 48 individuals (F = 16; M = 32).

Table 3.2. Demographic information for each of the comparison groups.

Group	Region and Sample Size	Total Number
East African	Burea – 2 Kenya – 5 Rwanda – 3 Tanzania – 14	24
North African	El Hesa – 27 Gizeh – 4 Thebes – 39	70
South African	-	18
West African	Benin – 12 Cameroon – 14 Congo – 2 Ghana – 40 Liberia – 3 Nigeria – 12 Togo – 4	87
East Asian	China – 12 Japan – 18 Korea – 2 Mongolia – 1	33
Southeast Asian	Borneo – 9 Indonesia – 4 Malaysia – 9 Philippines – 3 Singapore – 8	33
European	Austria – 10 Germany – 14 Hungary – 19 Italy – 7 Poland – 3 Spain - 12	65
Mexican	Huichol – 7 Ihuatzio – 2 Northern Mexico – 11 Mexico City – 3 Sonora – 12 Tarasco – 9	43
Native Alaskan	-	19

3.2 THREE-DIMENSIONAL DATA COLLECTION

W. W. Howells (1973) mentioned seven potential sources of error in measuring crania with traditional calipers. Most issues noted by Howells (1973) focused on human error (i.e., application of the technique, or unfamiliarity with methods, intra- and inter-observer error, instrument reading error, recording error, and data entry error). Yet, only one of the potential sources of error focused on the instrument (e.g., intrinsic error in the calibration of calipers). Further, while linear measures are informative on their own, they rarely have spatial context or relationship with other dimensions (Ousley and McKeown, 2001). For example, if one were to measure intercusp distances in molars, calipers could be used to measure distances between cusps; however, these measurements have no information on relative cusp location without additional information and geometric transformations (e.g., use of angles and cosines). Further, the calipers must be accurate enough to precisely capture small intercusp distances. Moreover, if digital calipers are not used, the scale must measure to an appropriate degree, and the recorder must know how to properly read the output. From there, error is possible in transcription of the readout either on paper, or directly into a computer. Still, as noted by Ousley and McKeown (2001), use of 3D digitizers minimizes many of Howells (1973) concerns.

Three-dimensional coordinate digitizers consist of a base, which rests on a fixed space, and an arm with multiple joints and a stylus attached at the end (Fig. 3.1). This instrument is connected to a computer via a USB or serial connection port. The base must remain stationary, as that spot will be designated as the arbitrary zero point, or datum. The stylus is placed on an object of interest that is also in a fixed space. Once the stylus is positioned on a landmark, either a button or foot pedal is pressed to record that point's coordinates. It is paramount that neither the base nor object being digitized is moved until all landmarks under study are recorded. If either the instrument or specimen moves, then the landmarks are no longer in the same relational space. Information is recorded directly into a computer spreadsheet or database program, thus eliminating potential human error in data transcription. Further, only one landmark is collected at a time, as opposed to two landmarks in linear measures; as such, the recorder can focus on the specific definition of just one location. Finally, the MicroScribe series of digitizers have a positional accuracy of 0.23mm, which eliminates unknown caliper calibration errors (Immersion, 2002). However, data collected are in an arbitrary coordinate system with no direct relationship with one another; thus, special treatment of these data is needed through geometric morphometrics techniques.

Fig. 3.1. Coordinate digitizer set-up.

3.2.1 Geometric Morphometrics

Geometric morphometrics were first described as "the empirical fusion of geometry with biology" (Bookstein, 1982: pp.2). To adequately retain the geometry of relative objects, it is necessary to have clearly defined landmarks, which are simply "loci with names" (Bookstein, 1991). The use of homologous landmarks is necessary so that forms, and importantly, their underlying biological properties, can be directly compared as being "pulled together" or "pushed apart" (Bookstein, 1991).

Shape refers to "the geometric properties of an object that are independent of the object's overall size, position, and orientation, where as the form of an object comprises both its shape and size" (Mitteroecker and Gunz, 2009). In practical terms, a golf ball and soccer ball have the same basic shape, but widely different forms due to isometric scaling of the differences in gross size. Bookstein (1991) discussed the three types of landmarks to be used in geometric morphometrics within biology:

Type 1: intersection of sutures or other biological structures. e.g., bregma;

Type 2: maximal or minimal lengths, e.g., maximum cranial breadth (euryon left – euryon right);

Type 3: composite landmarks based on estimates, e.g., orbital breadth (ectoconchion left – ectoconchion right).

The use of landmark-based homologies is central in morphometrics because, oftentimes, homologies are difficult to define via linear measures alone (Adams et al., 2004). To paraphrase Adams et al. (2004), if one were to compare the shapes of evenly sized ovals and teardrops -- the linear dimensions based on homologies (i.e., Type II landmarks of maximum length and width) -- “shape” information would be the same; however, ovals and teardrops are very different shapes visually. Yet, if coordinate information for the location of these landmarks could be analyzed, with proportions between all landmarks within a specimen retained, then information is gained about the differing shapes (Bookstein, 1986).

The direct comparison of multiple forms was made possible by the use of biological homologies. The study of geometric morphometrics has progressed to involve the co-variation of shape with other variables (Adams, 1999; Adams et al., 2004) and has come to include outline analyses, such as elliptical Fourier analysis (EFA), in addition to traditional landmark analyses. Biologically, the most common methods are based on a Generalized Procrustes Analysis (GPA) (Slice, 2007; Mitteroecker and Gunz, 2009; Klingenberg, 2010, 2011).

A Generalized Procrustes Analysis, or Generalized Procrustes Superimposition, scales all of the coordinate information in a sample to a common shape space and derives a consensus shape from each of the specimens. The first step is to calculate centroid size for each specimen. The centroid size is calculated through the squared root of the summation of the squared distances between all landmark pairs (Bookstein, 1991). Due to the calculation of centroid size, it is an appropriate measure of gross size because it accounts for information from each set of coordinates. Due to the nature of the calculation, the centroid will become the “gravitational center” (Rosas and Bastir, 2002) of each specimen; its location in the geometric center has been found to be uncorrelated with shape (Bookstein, 1991). Once centroid size has been calculated, each specimen is translated, or aligned according to their centroid position. Next, each specimen is scaled to the mean centroid size, thereby removing the influence of gross size. By convention, the mean centroid size is adjusted to 1.0 (Mitteroecker and Gunz, 2009). Lastly, each specimen is rotated around its centroid to minimize the squared differences between homologous landmarks in Euclidean distance, a technique known as partial least squares. Once the landmarks have been translated, scaled, and rotated, they are independent of size and are directly comparable as Procrustes shape coordinates. A mean, based on the least summed squared differences, is then generated from each specimens' Procrustes coordinates for every landmark. Thus, through the generation of each landmark mean, a consensus shape is derived. Deviations from the mean shape, known as Procrustes residuals, can be quantified for each specimen. The direction and magnitude of shape changes can be visualized and further refined through principal components analysis (PCA). Many researchers have used these aforementioned techniques to investigate the influence of size-free shape both within and between populations (Rosas and Bastir, 2002; Lockwood et al., 2004; Harvati and Weaver, 2006; Perez and Monterio, 2009; Weisensee and Jantz, 2011; among others).

Additionally, thin-plate splines can be used to interpolate deformation in shape between two objects. D'Arcy Thompson (1915) created the concept of deformation grids by describing how homologous landmarks between two biological specimens "deformed" from one shape to another through the use of Cartesian coordinates. A deformation grid is "laid" on the coordinate points simulating the topography, and relative deformation between two or more objects, known as partial warps, can be used as shape variables and subjected to statistical tests (Bookstein, 1996). Similar to GPA, partial warps can be further analyzed through PCA to describe overall shape variation within a sample (Adams et al., 2004). Thin-plate splines can also be used after processing coordinate information through GPA to analyze shape deformation from a mean shape instead of simply the difference between two shapes.

In addition to the oval and teardrop example, the advantages of morphometric analyses over linear distances are numerous. Many researchers surmised that a principal advantage is the visualization of shape changes beyond the more abstract plots [e.g., scatter plots (Bookstein, 1991; Adams et al., 2004; Mitteroecker and Gunz, 2009; Klingenberg 2010, 2011)]. So, morphometrics offer a means to analyze shapes as a complex, in terms of their overall configurations. Once the morphometric data has been generated, it can then be subjected to analytical techniques to identify and quantify variation both within and between groups.

3.2.2 Data Collection and Preparation Protocol

The data collection protocol used in the current study was the same followed by Kenyhercz et al. (2014a). The current study used a MicroScribe G2 digitizer in which each specimen was aligned so that the molars were face up in plane view; the stylus of the digitizer was positioned at the tip of each molar cusp and the coordinate point for each landmark was recorded (Fig. 3.2). Molars were only included in the study if they only demonstrated slight wear, or, showed no more than a pinpoint apex of dentine according to Smith (1984). In the event of slight wear, no greater than stage 2 according to Smith (1984), the digitizer stylus was placed at the center of the dentine exposure and that point was collected. Only the primary cusps were recorded for each molar. The primary cusps include the protocone (cusp 1), paracone (cusp 2), metacone (cusp 3), and hypocone (cusp 4) on the maxillary molars and the protoconid (cusp 1), metaconid (cusp 2), hypoconid (cusp 3), entoconid (cusp 4), and hypoconulid (cusp 5) on the mandibular molars. No accessory cusps, such as Carabelli's trait, were recorded. Whenever available, the left molars were used to collect the data. A custom version of 3Skull (Ousley, 2004) was used to collect the coordinate data.

The coordinate data for each molar were kept separate due to inconsistent spatial relationships between teeth and between individuals, especially in regards to modern orthodontic intervention. The *z* value, which corresponds to elevation, was removed from the coordinate files to negate the effects of worn versus non-worn teeth. The raw coordinate data were entered into MorphoJ (Klingenberg, 2013) where they were subjected to a GPA to produce Procrustes coordinates, principal components of shape, and centroid size. Since the PCA of the Procrustes coordinates is based on the variance-covariance matrix instead of a correlation matrix, the cut-off for effective PCs was based on using the mean eigenvalues as a cut-off point as opposed to the convention of only including PCs contributing eigenvalues greater than one, as in PCA based on a correlation matrix (Jolliffe, 2002).

Additionally, the raw coordinate data were used to generate interlandmark distances (ILDs) through a simple Euclidean distance function. The interlandmark distances were then subjected to a principal components analysis (described in detail below). Contrary to the PCA of the morphometric variables, the PCA of the ILDs used the correlation matrix. Thus, only ILD PCs that contributed eigenvalues greater than one were retained for analysis. Each molar had four datasets associated with it: 1) principal components of shape; 2) principal components of shape with centroid size; 3) ILDs; and 4) PC of ILDs. The four different datasets allowed for the investigation of both shape and size separately and together.

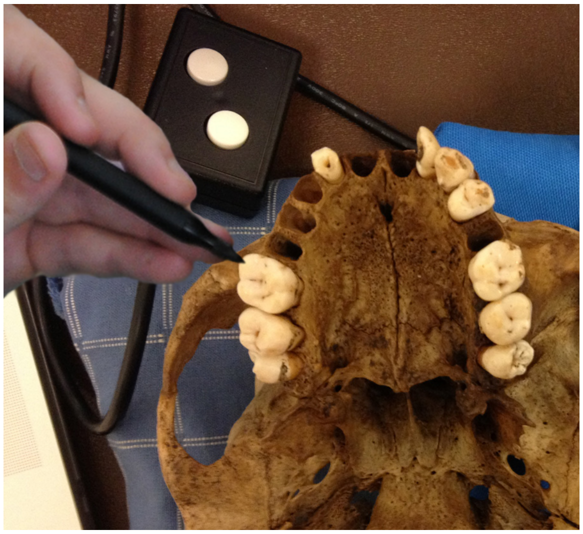


Fig. 3.2. Close-up of molar cusp digitization

3.3 STATISTICS

Each of the variables generated through data collection were used to examine the relationships between the groups under study. The population biohistory analyses include descriptive statistics for each of the variables for each tooth. The group mean for each individual molar variable was tested against one another via an independent samples two-tailed t-test. In the modern group analysis, in which each of the four U.S. group means were tested for each variable, an ANOVA was used. Next, the combined molar dataset was subjected to a linear discriminant function analysis (DFA) to maximize the variation between groups. The Mahalanobis generalized distance (D^2) was calculated for each group as a measure of similarity. The D^2 were further visualized through principal coordinates analysis (PCO), or classical multidimensional scaling (MDS), to examine trends in biological affinity. All statistical analyses were conducted in R (R Core Team, 2013).

3.3.1 Descriptive Statistics

Once the landmark coordinates have been transformed into a common shape space via the GPA, statistical analyses can be performed on the data. Basic descriptive statistics summarize the data in terms of central tendency (mean, mode, median) and variability (range, variance, standard deviation, kurtosis). Used in conjunction, the previously mentioned summary statistics, describes the central tendency of the data, as well as variability around the mean, which will become important in later analyses as many statistical techniques require normally distributed data and approximately equal variances (homogeneity of the variance-covariance matrices in linear discriminant function, for example).

3.3.2 Principal Components Analysis

Principal components analysis (PCA) is a form of factor analysis that takes a combination of correlated continuous variables, in this instance *x* and *y* coordinates and ILDs, and linearly transforms them into a smaller subset of uncorrelated variables, or principal components (Jolliffe, 2002). Weights from each of the original variables are included in each PC, which are known as loadings. The influence of a particular variable in a PC is based on the greatest loading, either positive or negative. Thus, PCA creates a smaller subset of variables that are uncorrelated and from which one can examine the influence of particular variables on observed variation.

Principal components analysis examines variation within the entire sample through use of either the variance-covariance or correlation matrix of a dataset (Kachigan, 1991). While there will be just as many principal components derived as variables present, the components derived are ordered so that the first few represent the majority of variation in the sample; therefore, dimensionality of the data is reduced while keeping the components uncorrelated (Kachigan, 1991). The decision on how many PCs to be retained will depend on whether a correlation or covariance matrix was used in the PCA (Jolliffe, 2002). In the event that a correlation matrix was used, only PCs that contributed eigenvalues greater than one are retained. In other words, a PC with an eigenvalue of one is as useful as one of the original variables in the analysis (Harris, 1997). In the event of a covariance matrix, as is standard in morphometric analyses, there is no rule-of-thumb in selecting the appropriate number of PCs; however, Jolliffe (2002) has suggested that using the mean of the eigenvalues as a cut-off is acceptable, and has been used in the current study. The aforementioned rules for accepting PCs in the analyses were chosen over the use of a scree plot to keep analyses consistent and to avoid heuristic practice.

In the instance of using PCA with coordinate data, shape and direction changes in the sample can be visualized as deviations from the landmark centroid instead of merely differences in a single *x* or *y* coordinate value. The use of the variance-covariance matrix allows for the overall shape variation by examining how each coordinate point within a landmark influence one another. Figure 3.3 shows an example of a lollipop graph created in the program MorphoJ (Klingenberg, 2011). The circle of the lollipop represents the negative extreme, while the stem of the lollipop shows the incremental change in shape it would take to alter each of the landmarks by one principal component score unit; thus the longer the lollipop stem, the more marked the shape change inherent in the sample. In sum, each PC represents actual shapes based on the coordinate data.

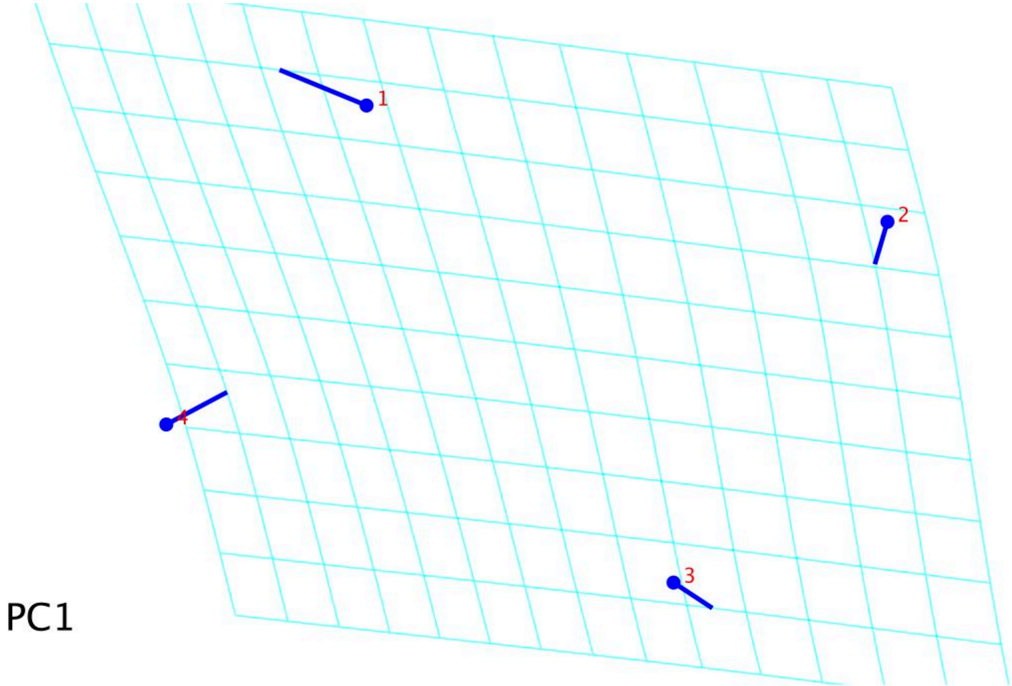


Fig. 3.3. Lollipop graph showing shape changes associated with the maxillary first molar from Kenyhercz et al. (2014a). The landmarks are in order of cusp numbers: (1) protocone; (2) paracone; (3) metacone; (4) hypocone.

Once the PC scores have been generated, it is then necessary to decide whether or not to rotate the data. Rotating PCs has been traditionally used to allow for easier interpretation of the variables by distributing the variance across the derived components (Kachigan, 1991). Further, Harris (1997) has described rotation of PCs as pushing the loadings to either zero or one, which, again, allows for an easier interpretation of loadings.

In the case of the coordinate data, rotation was not used because it would offer an unrealistic representation of the shape variation (Klingenberg, 2013). However, rotation was used on the PCA of the ILDs. Several different rotation protocols have been developed, but the orthogonal varimax rotation is generally applied (Harris, 1997) and was used in the current study. The program MorphoJ (Klingenberg, 2011) was used to perform the non-rotated PCA on the Procrustes coordinates and the package "psych" (Revelle, 2014) was used in R to generate the varimax rotated principal components for the ILDs. While PCA describes variation inherent within the entire sample, different methods are necessary to describe variation among groups.

3.3.3 Discriminant Function Analysis

Sir Ronald Fisher (1936) was the first to introduce the applications of DFA, using *Iris* petal lengths and widths. This statistical god proposed that a linear combination of variables ($x_1 - x_n$) could be used to discriminate between groups with a categorical expression, in this instance the taxonomic classification of plants. Rencher (1995) described two main goals in the separation of groups: 1) description of the group separation, i.e., which variables are best discriminating groups, and how these variables explicate the observed differences (x is larger than y, etc.); and 2) use of these linear discriminant functions to classify an unknown individual into the known samples. Further, Albrecht (1980) noted that the linear combination of variables, or descriptors, should maximize differences between populations.

The linear combination of variables is reduced to discriminant functions, or canonical variates, that, "maximize, or most efficiently summarize, the overall differences among the population groups" (Albrecht, 1980: pp. 680). However, the following assumptions (Klecka, 1980) must be met. First, and most importantly, it is assumed that each specimen is part of a mutually exclusive group. Second, the variables must be measurable at the ratio or interval level. Third, variables in the analysis should not be highly correlated; if they were, no new information would be gained as only redundant information is analyzed. Fourth, multicollinearity of variables must be avoided, as it reduces reliability; that is, in addition to redundancy (which does not refine the analysis), the degrees of freedom are reduced and unnecessary noise is introduced to the data (Alin, 2010). Fifth, the variance-covariance matrices between samples must be equal, or assumed equal, due to the linear combination equations used in the analysis. Lastly, it must be assumed that each sample population has a multivariate normal distribution. However, Lachenbruch and Goldstein (1979) noted that comparing non-parametrically distributed populations is still possible if proper precautions were taken in the interpretation. Likewise, Hand (1981) demonstrated that a cross-validation procedure does make use of the normality assumption. Nonetheless, the abovementioned assumptions are all related to the mathematical properties of the discriminant function.

In practice, the groups under analysis are not mutually exclusive (Kenyhercz et al., 2010a, 2010b). As a result, care must be taken in assignment of group names to populations. However, ascertainment bias is an inherent issue in discriminant function because individuals are forced into categories based on prescribed group assignment. Obviously, sample size will affect the variable means that are used in discriminant function wherein larger sample sizes will have a larger ascertainment bias (Rogers and Jorde, 1996).

The discriminant function, following Kachigan (1991), is expressed as:

$$L = b_1 x_1 + b_2 x_2 \ldots + b_n x_n$$

where L is the discriminant function, b is the weight associated with the variable (unstandardized coefficient), and x is the actual predictor variable. The equation is used in conjunction with a cutoff score selected to maximize group differences, but minimize overlap, or misclassifications. Similarly, weights for each variable are chosen with the same criteria: maximize differences between groups by minimizing misclassifications. The number of discriminant functions, or canonical variates, necessary for an analysis depends upon the number of groups. Generally, there is one less discriminant function than criterion groups; however, if there are fewer variables under analysis than groups, the number of discriminant functions will be equal to the number of variables (Kachigan, 1991). Thus, discriminant scores can be plotted on several axes in n-dimensional space, which depends upon the number of discriminant functions generated.

To avoid problems associated with multicollinearity, stepwise selection of variables is often necessary. The most common stepwise procedure is a forward selection method, in which addition of each variable increases the F-statistic, or fit to the regression line. Generally, Wilks' lambda (λ) is utilized for the forward selection with the addition of the variables being accepted as long as they pass a predefined alpha (α), which by convention, $\alpha = 0.05$ (Rencher, 1995). Conversely, a backward elimination approach can be used, in which variables that contribute least are iteratively removed with the same goal of maximizing group separation.

Albrecht (1980) outlined the steps of DFA as follows. Once the functions have been derived, the scores can be used as coordinates and plotted in a scatter plot. The first step in plotting is to rotate the original axes to be parallel to the major and minor axes of variation in the plots. The x-axis will be kept parallel to the major axis of variation of the data, while the y-axis will be parallel to the minor axis of the data. The next step is to rescale the transformed variables to standardize the axes. Then, another rotation is made to keep the transformed and scaled variables' major and minor axes parallel to the x and y-axes, respectfully. Albrecht (1980) stressed that no new mathematical operations are introduced in the transformations and scaling procedures; instead, the goal is to display the data in such a way that shows the greatest statistical separation while maintaining the integrity of individual and centroid distances. Transformed and scaled plots offer a good visual explanation for classification purposes; an individual will classify to a group based on proximity to the nearest centroid. However, due to the transformation and scaling, the distance cannot be measured as Euclidean distance. Instead, Mahalanobis' generalized distance (D^2) must be used (Mahalanobis, 1936).

The Mahalanobis D^2 essentially examines the squared distance from an individual case to the group centroid and contains the same properties of a chi-square test; as Klecka (1980) stated, the measurement of distance is in "chi-square units". Thus, an individual will be classified into the group with which it has the lowest D^2. However, an individual will be forced to classify into a group, even if the actual group is not in the reference data. The Mahalanobis D^2 is also used as a measure between group centroid distances. According to

Mahalanobis (1936), the D^2 statistic is an appropriate measure of biological similarity, and the closer groups are to one another, the more similar they are, and vice versa.

The first step in evaluating a discriminant function and, indeed, one of the main goals of the analysis, is to examine the total correct classification (actual versus expected outcomes based on discriminant cut-off score). However, because the model is derived from the same sample it is tested against, simply relying on total correct classification may yield misleadingly optimistic classification results. There are two ways to negate unrealistically biased results from a standard discriminant function: 1) Partitioning of the sample; and 2) leave-one-out cross-validation (LOOCV), or the hold out method (Rencher, 1995).

Partitioning simply refers to dividing the sample into a training set used to derive discriminant functions, and a validation sample to test the functions independent of the training set. Furthermore, the roles of the training set and validation sample can be reversed to further refine error estimates. However, as Rencher (1995) pointed out, it must be assumed that the training set is adequately representative of the sample, and partitioning requires much larger sample sizes.

Perhaps a more pragmatic approach to estimating realistic error rates is to use the LOOCV, or holdout method (Rencher, 1995). In LOOCV, upward bias toward greater classification accuracy is avoided as the individual under evaluation is removed from the reference group; instead, it is tested against the discriminant function based upon all other members of the new reference group, which is essentially n-1. Equations are recalculated and the individual is then classified into one of the reference groups, thus giving a realistic evaluation of model performance and unbiased error rates. As mentioned, Hand (1981) demonstrated that cross-validated models do not make use of the normality assumption in discriminant function analysis.

To examine the relative effect of the variables, it is necessary to standardize the variable coefficients used to construct the model (Rencher, 1995). Standardized coefficients are needed because some variable measures in a discriminant function might be much larger than other variables; as such, the unstandardized coefficients would appear to contribute more to the analysis, when in actuality, it is an issue of scale (Rencher, 1995). To standardize coefficients, one takes the square root of the sum of squares for a particular variable and divides it by the total number of cases in the group, minus the number of groups in the analysis (Klecka, 1980). Once each variable has been standardized, the relative magnitude of the variable contribution, regardless of sign, indicates greater contribution to the function, similar to PCA loadings.

For the current study, the “MASS” package (Venables and Ripley, 2002) was used for DFA utilizing forward stepwise selection of variables and leave-one-out cross-validation and the prior probabilities were set equally among the groups.

3.3.4 Principal Coordinate Analysis/Classical Multidimensional Scaling

Principal coordinate analysis (PCO), or classical multidimensional scaling, analyzes and visualizes group relationships based on any number of distance measures. According to Cox and Cox (2001), PCO searches for the lowest dimensional space between points based on a combination of variables, though retains the distance relationships. Gowler (1966) outlined the necessary steps in the PCO. First, a distance matrix is transformed and centered by multiplying the distance matrix by -1/2. Next the eigenvalues and eigenvectors are tabulated and the eigenvectors are scaled to the square roots of their respective eigenvalues. Lastly, the eigenvectors are retained as columns and can be graphed in *n*-dimensional space. However, an eigenanalysis is performed on each of the dimensions, and only dimensions with eigenvalues greater than zero can be retained and visualized. Lastly, a goodness-of-fit is returned, which is essentially an R^2 value and determines how well data fit a model (Kachigan, 1991).

Graphically, the points represent objects, or groups, that are separated by Euclidean distance in a perceptual plot (Kachigan, 1991). The further objects are from one another in the multidimensional space, both horizontally and vertically, represent greater dissimilarities, while closer objects are more related (Cox and Cox, 2001). One can infer relatedness of objects in the two or three-dimensional space because even though the objects are projected in a Euclidean space, the original distance measures have been preserved (Anderson and Willis, 2003). The package "cmdscale" (R Core Development Team, 2013) was used to perform the PCO. For the current application, three dimensions were used when available, but in the event of eigenvalues less than zero, two dimensions were used. An important distinction between discriminant function analysis and MDS is that multidimensional scaling focuses on relating the objects to one another in the lowest dimensional space instead of maximizing the variation between objects.

3.4 DATA PROCESSING PROTOCOL SUMMARY

Each of the morphometric and ILD variables for each individual molar were subjected to descriptive statistics to examine central tendencies and variation for each individual. In each of the proceeding biohistory chapters, an independent samples two-tailed t-test was used to test each of the comparison groups to the modern U.S. under review. In the comparison of each of the modern groups, a one-way ANOVA with pairwise comparisons of group means was used to test for significance between biological affinity and individual variables and to test which groups were significantly different from one another. For the shape analyses of each molar, lollipop graphs were generated for the first two principal components to visualize the major shape variation in each molar.

The data for each molar were combined and subjected to a DFA utilizing forward stepwise variable selection. When included, log centroid sizes were used instead of the raw centroid sizes as to not artificially inflate the relative contribution of size in the DFA coefficients because the principal components of shape are all much smaller numbers in comparison. Total correct classifications were reported for each of the four datasets (1. principal components of shape; 2. principal components of shape with centroid size; 3. ILDs; 4. PC of ILDs) along with the corresponding canonical variate plots. Next Mahalanobis D^2 values were calculated from the variance-covariance matrices of each of the datasets. The significance of the D^2 values between groups was tested via permutation tests (Fisher's exact tests). Lastly, each of the D^2 values was subjected to a PCO to examine the relationship of each of the groups in two or three-dimensional space to visualize affinity between groups.

3.5 DISCUSSION

The use of a coordinate digitizer instead of traditional tools reduces the amount of user error by limiting the human error in the process. Coordinate data is collected in an arbitrary coordinate system in reference to the relative position of the specimen to the digitizer. Even though the collected data is continuous in nature, it is not directly relatable and needs to be transformed into a common space in the form of Procrustes coordinates. Even when the data are in a comparable space, they still only represent abstract ideas about spatial relationships as individual coordinates. It is then necessary to subject the coordinate data to a PCA to investigate the shape changes in reference to the entire form.

The principal components based on the Procrustes coordinates represent shapes that show both the magnitude and direction of shape change. The shapes associated with the principal component scores can then be subjected to further statistical analyses to investigate how the shapes vary within and between populations. Using the principal components of shape in a discriminant function is preferable over other analyses, such as a MANOVA, because discriminant function assumes that the variables under analysis are not correlated while a MANOVA optimally performs with moderate correlation between variables (Kachigan, 1991). Further, the interaction of individual variables is observable in a DFA. Given the nature of PCA, each of the components is intrinsically uncorrelated. Further, as Bookstein (1991) has previously shown, centroid size derived in the Generalized Procrustes Analysis is also uncorrelated with the shape variables. Thus, when investigating variation and categorical responses, in this instance, discriminant function is more appropriate.

While discriminant function analysis elucidates group differences, group membership is known a priori, which allows the technique to maximize the differences between groups. Furthermore, PCO examines the most parsimonious relationships between objects or groups by finding the lowest dimensional space between groups, thus elucidating greater relationship patterns. Used in combination with DFA, both differences and similarities can be observed in the data to analyze overall trends and relationships between groups.

3.6 SUMMARY

Landmark data can accurately captured in three dimensions with use of a 3D coordinate digitizer. The raw coordinate data can be subjected to a Generalized Procrustes Analysis to convert data that is in an arbitrary system to a comparable shape space in the form of Procrustes coordinates. The transformed coordinate data can further be refined through a PCA to examine the overall shape variation within the sample. Further, the principal components of shape can be subjected to DFA as a means to examine variation between groups at the individual level and to investigate relative variable importance. Lastly, overall group similarities can be explored through PCO. In sum, the combination of the above mentioned data collection techniques and statistical analyses can be confidently used on molar morphometric data from modern U.S. populations to examine both group differences and similarities, as well as to examine relationships with potential parent populations.

CHAPTER 4: REPEATABILITY, SEXUAL DIMORPHISM, AND ASYMMETRY

4.1 REPEATABILITY

In order to confidently employ the morphometrics of the relative location of cusp apices, it is necessary to demonstrate the repeatability, or intra-observer agreement, of the data collection protocol. To test intra-observer agreement, a randomly selected subset of 18 individuals' maxillary first molar (M^1) was digitized twice, each on separate occasions. The data were submitted to a GPA and PCA to analyze the shape of the entire molar instead of correspondence between mere x or y values. The PC1 scores for each of the separate data collection instances were then subjected to a Pearson's product-moment correlation and Student's two-tailed t-test. Correspondence between the separate data collection instances is good with $r = 0.68$ ($p = 0.02$) (Fig. 4.1). Furthermore, the t-test shows no significant differences between the means ($p = 0.14$) indicating significant consistency in data collection. Additionally, the intraclass coefficient (ICC) was used in accordance with Palmer and Stobeck (2003) and shows an ICC of 0.67, which is significant at $p > 0.05$.

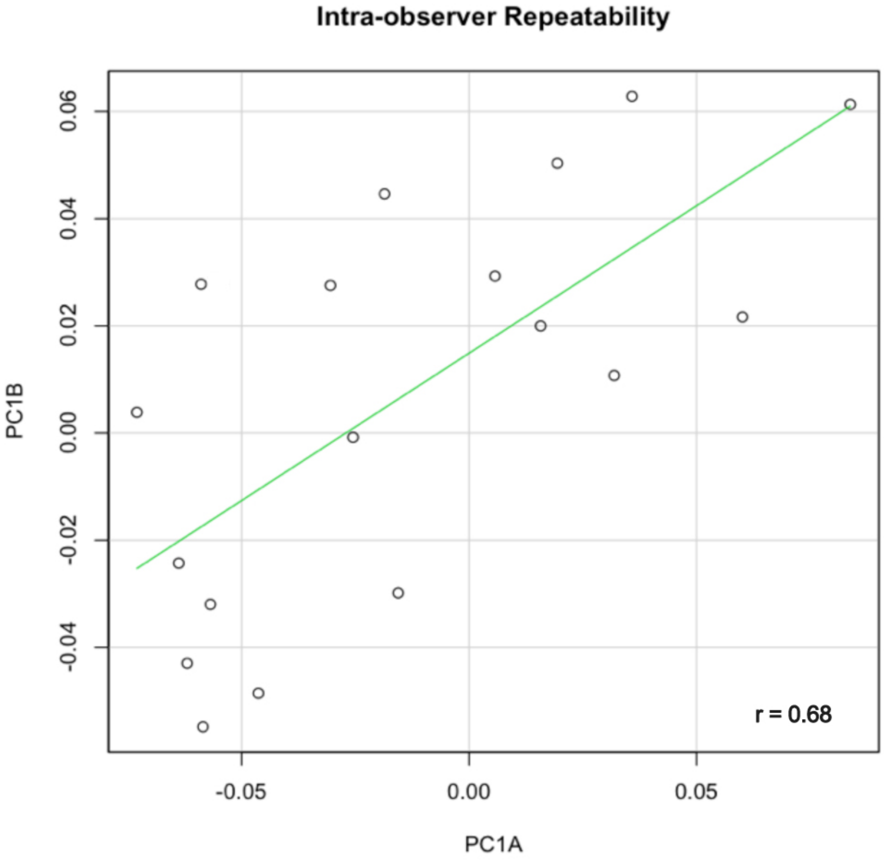


Fig. 4.1. Scatterplot with fitted correlation coefficient for the maxillary first molar repeatability.

4.2 SEXUAL DIMORPHISM

It is standard practice to pool the sexes for dental morphological studies because size is generally the sexually dimorphic factor (Turner et al., 1991). Given the size-negating aspect of a GPA, morphometric shape variables should also demonstrate low sexual dimorphism. The entire modern U.S. datasets for each tooth were used. Females and males were separated by their respective ancestral group and PC1 values for each tooth were subjected to a Student's t-test to examine the significance of sexual dimorphism by each group. The results for M^1 are presented in Table 4.1 and visualized in Figure 4.2-A. Only American black females and males show significant differences in PC1 shape mean scores at $p < 0.05$. However, black females and males demonstrate M^1 PC1 scores that were well below the means of any of the other groups (Fig. 4.2-A). The females and males of the remaining groups show comparable group means. The maxillary second molar (M^2) shows no significant differences between females and males for their respective group mean PC1 scores at $p < 0.05$ (Table 4.2, Fig. 4.2-B). However, white females and males demonstrated consistently higher PC1 scores compared to the other groups. Similarly, the mandibular first molar (M_1) demonstrates no significant differences in PC1 mean scores at $p < 0.05$, but white females and males show the least overlap in scores (Table 4.3, Fig. 4.2-C). Lastly, the mandibular second molar (M_2) does not exhibit any significant sexual dimorphism within the respective groups PC1 mean scores at $p < 0.05$. However, while Hispanic female and male means are strictly speaking non-significant at $p < 0.05$, their means are the most disparate of any of the groups in M_2 scores (Table 4.4, Fig. 4.2-D).

Table 4.1. Means for each group by sex for PC1 values of M^1. Significance determined using a Student's two-tailed t-test. Values significantly different at $p < 0.05$ are in bold.

	Sex		
Group	F	M	*p* =
Asian	0.005502611	0.005831963	0.9666
Black	**-0.04811786**	**-0.03012560**	**0.03627**
Hispanic	0.03364226	0.02205189	0.118
White	-0.002673663	0.008176431	0.1509

Table 4.2. Means for each group by sex for PC1 values of M^2. Significance determined using a Student's two-tailed t-test.

	Sex		
Group	F	M	*p* =
Asian	-0.01232722	-0.01090299	0.9092
Black	-0.0007043068	0.0085445840	0.4179
Hispanic	-0.01101529	-0.01342061	0.8457
White	0.01393896	0.02048523	0.5654

Table 4.3. Means for each group by sex for PC1 values of M_1. Significance determined using a Student's two-tailed t-test.

	Sex		
Group	F	M	*p* =
Asian	-0.01523498	-0.01055445	0.5513
Black	-0.001839787	0.001294793	0.7349
Hispanic	-0.004945216	0.002210448	0.3524
White	0.018903535	0.006006315	0.08479

Table 4.4. Means for each group by sex for PC1 values of M_2. Significance determined using a Student's two-tailed t-test.

	Sex		
Group	F	M	*p* =
Asian	-0.013281056	0.002761068	0.1735
Black	-0.01281585	-0.03101106	0.1069
Hispanic	0.007896046	-0.011657314	0.05061
White	0.02000988	0.02410951	0.6271

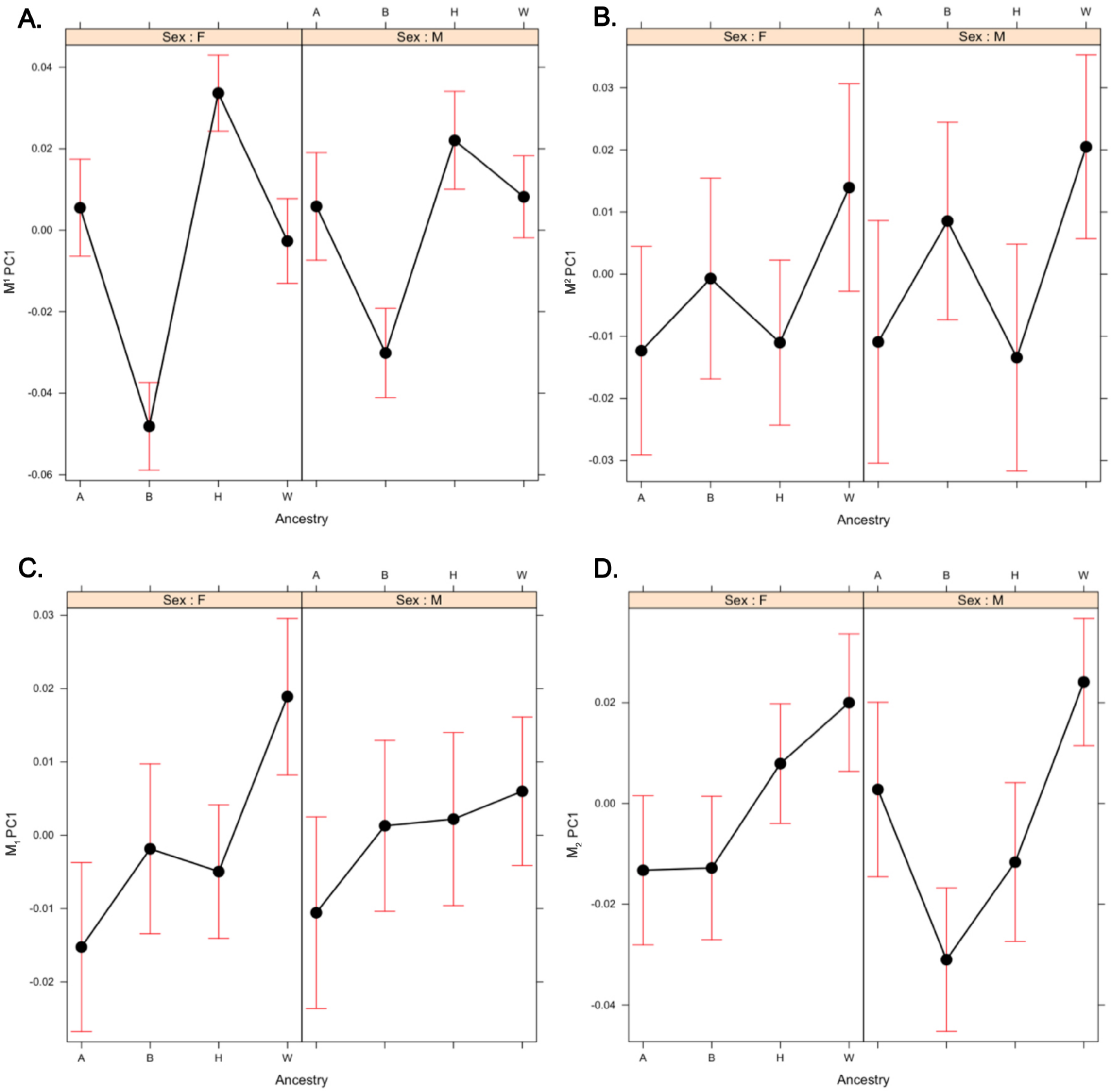


Fig. 4.2. Distributions of PC1 scores for each of the molars with a 95% confidence interval by sex and ancestry. The PC1 scores for M^1 are shown in A, M^2 in B, M_1 in C, and M_2 in D.

4.3 ASYMMETRY

In the current study, left molars were utilized whenever available, however, if the left molar was unsuitable, the right molar was used in its place. The rotation inherent in the GPA should negate the effect of using a different side because each landmark is rotated to a common coordinate system. However, because right molars were sometimes employed in the analysis, it is necessary to test for asymmetry. Morphologically, asymmetry is handled through only using the tooth that has the greatest expression of the particular character state, as this is believed to demonstrate the genetic potential (Turner et al., 1991). Metrically, asymmetry is tested through paired samples t-tests and, in the event of asymmetry, only the left, right, or average is utilized in the analysis (Potter et al*.,* 1981; Lukacs, 1985). Further, tests for antisymmetry, directional asymmetry, and fluctuating asymmetry were performed in accordance with Van Valen (1962). Antisymmetry is examined through a chi-squared test of normality, the degree of directional asymmetry (DA) through subtracting mean scores from each side, and fluctuating asymmetry (FA) through $1\text{-}r^2$. To test for the significance of the asymmetry in the current study, a metrical approach was taken, which utilized the paired samples t-tests. A paired samples t-test makes no presumptions concerning the homogeneity of the variance thus allowing for side differences to be noted more clearly in the event of highly correlated variables (Potter et al., 1981). A subset of 19 left and right antimeres were scored for each of the groups leading to a total sample of 152. Each of the group's shape PC1 was tested against its antimere for each of the aforementioned subjects.

Following Van Valen (1962), antisymmetry is not present in each group's M^1 with each of the chi-squared tests exceeding $p > 0.2$. Directional asymmetry was tested through subtracting the right PC1 scores from the left. Across the board, DA was negligible with American Hispanics showing the greatest amount DA (0.05) and whites showing the least (0.003). American blacks had the second least DA (0.01), while Asians had the second greatest (0.03). The intensity of FA was greatest in American Hispanics (0.99) and lowest in Asians (0.74); blacks had the second lowest FA intensity (0.85) and whites had the second highest (0.95). As in M^1, antisymmetry is not present in M^2 with each of the chi-squared tests again exceeding $p > 0.2$. Following the same trends, DA was nearly identical as in M^1 with American Hispanics showing the greatest amount at 0.05, followed by Asians at 0.04, whites at 0.03, and blacks with 0.01. However, FA in M^2 differed than M^1 with American whites showing the greatest intensity at 0.99, followed by Asians at 0.83, then Hispanics at 0.70, and lastly blacks with 0.64. Just as above, antisymmetry is not present in M_1 with each of the groups chi-squared tests results in p values greater than 0.2. Similarly, DA is negligible among the groups with American Asians, blacks, and Hispanics all showing 0.01 and whites 0.007. Contrary to the maxillary molars, American Asians show the greatest intensity of FA at 0.99, followed by whites at 0.96, blacks at 0.67, and Hispanics at 0.59. Lastly, antisymmetry is also absent in M_2, with each of the group's chi-squared values exceeding 0.2. Directional asymmetry is negligible in M_2 with each of the groups showing values less than or equal to 0.01. Finally, FA shows the greatest intensity in American Asians at 0.97, followed by whites at 0.94, then Hispanics at 0.76, and lastly blacks at 0.73.

The results for M^1 are listed in Table 4.5 and shown in Figure 4.3-A. The only group to express significant asymmetry is American Hispanics with the left side showing much smaller PC1 scores. Next, M^2 does not have any significant asymmetrical differences (Table 4.6, Fig. 4.3-B). Similarly, no significant differences are observed between antimeres of M_1 (Table 4.7, Fig. 4.3-C), or M_2 (Table 4.8, Fig. 4.3-D).

Table 4.5. Group means for PC1 value for comparable left and right maxillary first molars. Significance determined using a paired samples t-test. Values in bold are significantly different at $p < 0.05$.

	Side (means)		
Group	L	R	*p* =
Asian	-0.006057894	0.025042761	0.06696
Black	0.034748639	0.045479396	0.5371
Hispanic	-0.049604826	0.009088576	**<0.001**
White	-0.021134090	-0.032601957	0.6044

Table 4.6. Group means for PC1 of comparable left and right maxillary second molars. Significance determined using paired samples t-test.

	Side (means)		
Group	L	R	*p* =
Asian	-0.03258535	0.00775586	0.09858
Black	-0.013625153	0.003481402	0.5924
Hispanic	-0.001647786	0.049222771	0.09131
White	-0.023425773	0.007833887	0.3591

Table 4.7. Means for each group by sex for PC1 values of the mandibular first molar. Significance determined using a paired samples t-test.

	Side (means)		
Group	L	R	*p* =
Asian	-0.01567612	-0.02756994	0.4251
Black	-0.004678957	-0.020230370	0.3217
Hispanic	0.01697120	0.00568815	0.5098
White	0.02254649	0.02175697	0.9744

Table 4.8. Means for each group by sex for PC1 of the mandibular second molar. Significance determined using a paired samples t-test utilizing.

	Side (means)		
Group	L	R	*p* =
Asian	-0.00681666	-0.01696754	0.6892
Black	-0.02580678	-0.02395525	0.9398
Hispanic	0.008517852	0.016868710	0.7141
White	0.01643930	0.03561665	0.4759

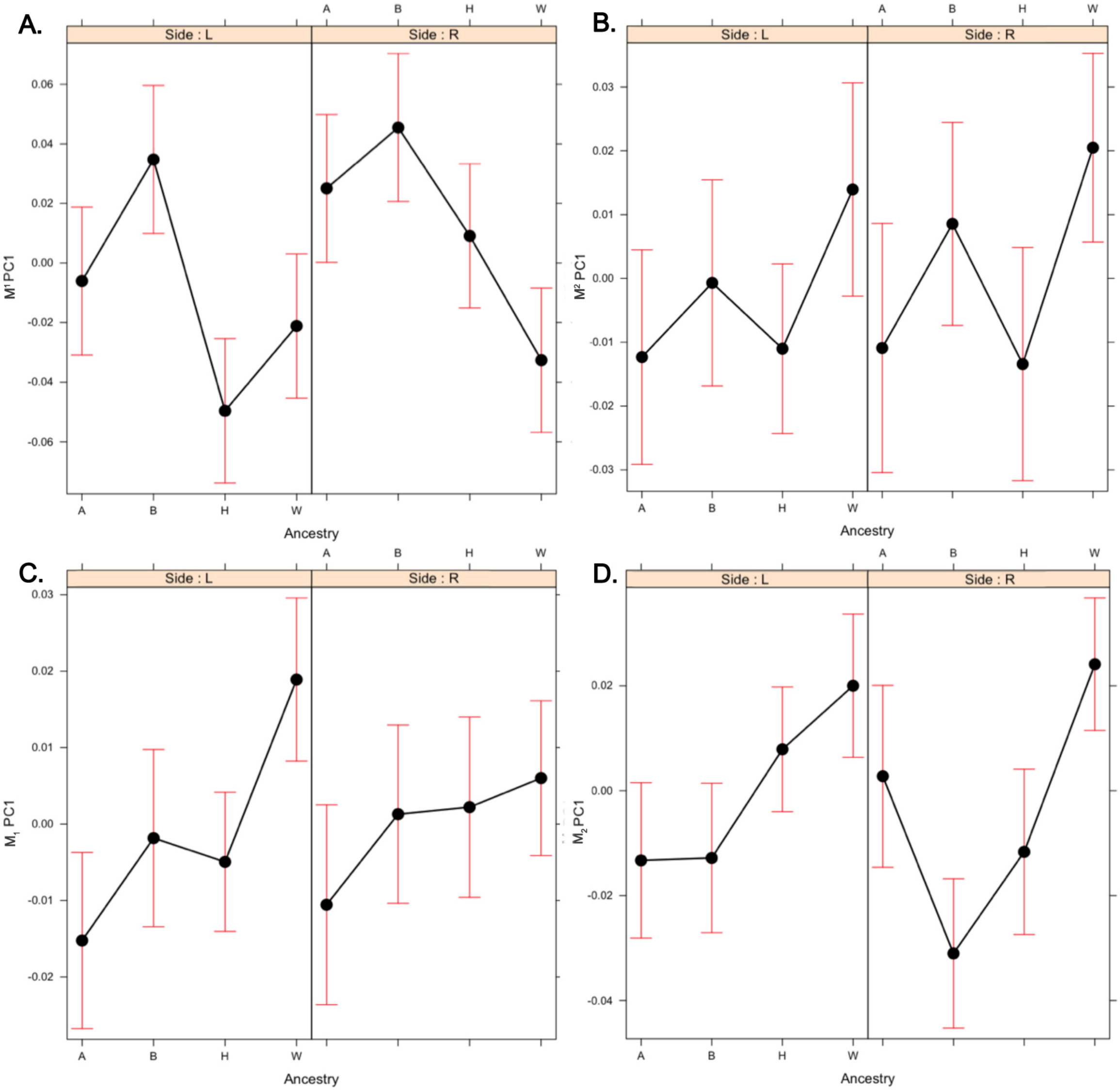


Fig. 4.3. Distributions of each of the molar's PC1 scores with 95% confidence interval by side and ancestry. The PC1 scores for M^1 are shown in A, M^2 in B, M_1 in C, and M_2 in D.

4.4 DISCUSSION

A correlation near 0.7 indicates good replicability and shows that the molar cusp apices can be consistently and confidently recorded. Furthermore, the only detectable sexual dimorphism is between American black females and males in M^1 wherein black males have PC1 scores that were closer to the other groups. The trend for black males to have means closer to the other groups may be a result of the fact that black males are more than two times as likely to intermarry than black females (Taylor et al. 2012a). Antisymmetry is not present in any of the groups molars. Directional asymmetry is negligible in each group for each molar. The intensity of FA is different in each molar, though, American Hispanics consistently show the highest degree. Finally, American Hispanics are the only group to exhibit significant asymmetry in antimeres, and only in M^1, which might reflect the generally lower socioeconomic status of Hispanics (Iceland and Wilkes, 2006).

4.5 SUMMARY

Molar cusp apices can be consistently and reliably digitized to capture two and three-dimensional data. Once size has been removed, the occlusal polygon shapes are not significantly sexually dimorphic in each molar with the exception of American black females and males in M^1. Lastly, asymmetry is only significant in M^1 of American Hispanics. In sum, digitizing molar cusp apices is a viable technique wherein the sexes can be pooled for analyses and lefts and rights can be recorded interchangeably.

CHAPTER 5: MODERN AMERICAN ASIAN COMPARISON

Modern American Asian biohistory was investigated by comparing the modern American Asian (AA) data with those of Asiatic groups from various regions: historic East Asian (EA), historic Southeast Asian (SEA), Native Alaskan (NA), modern Thai (Th), modern American Indian (AI) and modern American white (AW). Given the population history of the United States and known intermarriage rates noted, AA should demonstrate an affinity with EA, and also with AW (Hypothesis 1). Additionally, given the current models on peopling the New World, specifically dental studies (Turner, 1990; Scott and Turner, 2008), Native Alaskan and modern American Indian samples were added for comparative purposes.

5.1 MAXILLARY FIRST MOLAR (M^1)

5.1.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for each of the morphometric variables are listed by group in Table 5.1. The AA's group mean was compared with those of the comparative samples using a two-tailed independent samples t-test. American Asians have significantly different centroid sizes from Th and AW, different PC1 scores from EA, NA, and Th, and different PC2 and PC3 scores from AW. There are no significant differences found in PC4. In size, AA is more similar to EA, but in shape, specifically PC1, AA is most similar to AI and AW.

Table 5.1. Means and standard deviations for PC scores and log centroid size by group for M^1. Cumulative variance explained is listed under each PC. Group means significantly different from American Asians based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M^1 PC1** 33.8%		**M^1 PC2** 62.0%		**M^1 PC3** 82.5%		**M^1 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	2.157	0.065	0.021	0.048	-0.008	0.043	0.010	0.038	-0.004	0.035
AI	2.169	0.067	0.018	0.042	-0.006	0.046	0.019	0.053	-0.012	0.031
EA	2.168	0.068	**-0.015**	0.058	-0.025	0.058	0.009	0.038	0.005	0.034
NA	2.159	0.087	**-0.043**	0.071	-0.001	0.058	0.017	0.048	0.009	0.044
SEA	2.147	0.093	-0.009	0.038	-0.013	0.046	0.013	0.050	-0.003	0.042
Th	**2.199**	0.082	**-0.078**	0.064	-0.031	0.055	0.013	0.048	-0.004	0.040
AW	**2.084**	0.073	0.010	0.058	**0.018**	0.051	**-0.017**	0.041	0.003	0.041

5.1.2 Principal Components of Shape

The first PC accounts for 33.8% of the total shape variation and demonstrates major movement of the protocone (cusp 1) distobucally, the paracone (cusp 2) mesiobuccally, and the hypocone (cusp 4) mesiolingually (Fig. 5.1). As mentioned in Chapter 3, the circle of the "lollipop graph" represents the negative extreme of PC scores, whereas the apex of the stem indicates the positive extreme. Thus, the longer the stem, the greater the magnitude of shape changes. The positive PC1 values, shown by AA, AI, and AW, reflect a rhomboidal molar shape that is exaggerated mesiobuccally. Principal component two accounts for an additional 28.2% of the shape variance and indicates major movement of cusp 1 mesiobuccally, cusp 2 mesiolingually, cusp 3 distolingually, and cusp 4 distobuccally (Fig. 5.1). The negative PC2 scores, (represented by the lollipop circle) demonstrate a comparatively rectangular, mesiodistally-compressed molar and are indicative of each group mean except AW, while the positive PC2 scores represent a more rhomboidal shape.

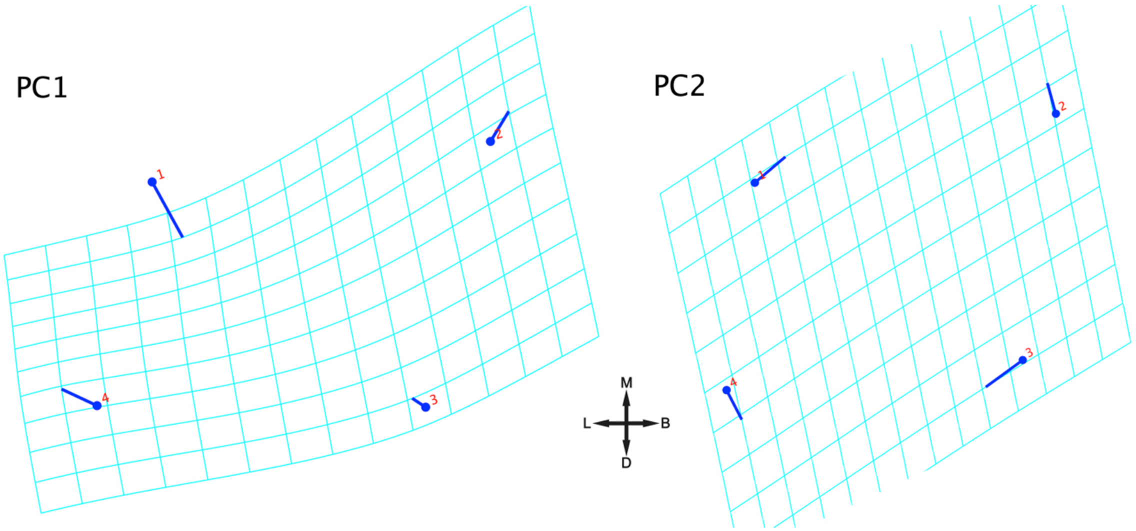


Fig. 5.1. Shape changes associated with PC1 (left) and PC2 (right) of M^1.

5.1.3 Interlandmark Distances (ILDs)

The means and standard deviations for each of the group's ILDs are shown in Table 5.2. Values in bold show the means that are significantly different from the AA sample based on a two-tailed independent samples t-test. American Asians most commonly display significantly different means from either Th, that has larger means, or AW that has smaller means. The diagonal ILD for protocone-to-metacone (cusp 1-3) is unique in AA because they are intermediate to the larger Asian groups and the smaller AW. American Indians and SEA are the only groups to have consistently non-significant means from AA.

Table 5.2. Means and standard deviations for ILDs by group for M^1. Group means significantly different from American Asians based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	7.2	0.6	7.2	0.8	4.7	0.7	5.8	0.7	9.8	0.9	6.9	0.6
AI	7.3	0.8	7.5	0.7	4.5	0.8	5.9	0.7	9.8	0.8	6.9	0.6
EA	7.3	0.8	**7.7**	0.8	4.8	0.8	5.5	0.7	9.8	0.8	7.0	0.7
NA	7.5	1.0	**7.9**	1.1	5.1	1.1	5.9	0.8	9.6	1.4	6.8	1.0
SEA	7.2	0.9	7.5	1.2	4.6	0.6	5.6	0.7	9.8	0.8	7.0	0.9
Th	**7.8**	0.8	**8.6**	1.0	**5.5**	0.8	5.8	0.8	10.0	0.9	**7.2**	0.9
AW	**6.5**	0.6	**6.7**	0.8	4.8	0.7	**5.3**	0.6	**9.3**	0.9	**6.4**	0.7

5.1.4 Principal Components of ILDs

The first PC accounts for 49.0% of the variance and is most heavily loaded by the ILD for cusps 1-3, followed by cusps 1-2, which also happens to be the two ILDs that demonstrate the greatest ranges between group means. The second PC is most heavily loaded by the ILDs for cusp 1-4 and then 2-3. The different loadings for the first two PCs indicate that both lengths and breadths are highly variable.

5.2 MAXILLARY SECOND MOLAR (M^2)

5.2.1 Descriptive Statistics of Principal Components of Shape

Each of the group's means and standard deviations of the morphometric variables have been compiled in Table 5.3. Just as in M^1, centroid size is significantly different between AA and both Th and AW, in which Th has larger second molars and AW has second molars. Modern Thais are consistently distinct from AA, whereas AW is only significantly different from AA in PC2.

Table 5.3. Means and standard deviations for PC scores and log centroid size by group for M^2. Cumulative variance explained is listed under each PC. Group means significantly different from American Asians based on a two-tailed independent samples -test in bold ($p < 0.05$).

	Log Centroid Size		**M^2 PC1** 34.9%		**M^2 PC2** 59.7%		**M^2 PC3** 82.9%		**M^2 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	2.068	0.092	0.005	0.073	-0.027	0.062	-0.001	0.066	0.014	0.053
AI	2.073	0.100	-0.018	0.095	-0.067	0.079	0.002	0.051	0.049	0.072
EA	2.064	0.094	-0.023	0.080	**0.028**	0.047	-0.018	0.069	-0.014	0.065
NA	2.115	0.114	**-0.071**	0.071	**0.047**	0.057	0.011	0.045	-0.007	0.044
SEA	2.029	0.085	-0.021	0.084	0.004	0.071	-0.017	0.053	**-0.043**	0.051
Th	**2.150**	0.100	**-0.035**	0.071	**0.043**	0.055	**-0.037**	0.067	**-0.014**	0.061
AW	**2.016**	0.097	0.020	0.079	**0.007**	0.070	0.013	0.063	-0.001	0.051

5.2.2 Principal Components of Shape

The first principal component accounts for 34.9% of the shape variance and shows major movement of cusp 1 distobuccally, cusp 3 mesiobuccally, and cusp 4 mesiolingually (Fig. 5.2). Positive PC1 scores illustrate a more mesiodistally compressed M^2 that has a more rhomboidal shape due to the distobuccal movement of cusp 1 and mesiolingual movement of cusp 4. American Asians and AW are the only groups to show positive PC1 means. Conversely, the negative PC1 values reflect a more rectangular molar. The second PC accounts for an additional 24.8% of the shape variance and denotes major movement of cusp 1 mesiobuccally, cusp 2 distolingually, cusp 3 mesiobuccally, and cusp 4 distolingually (Fig. 5.2). The positive PC2 scores represent an M^2 that has a more elongated lingual aspect in comparison to the buccal aspect of the molar. Only American Asians and Indians have negative PC2 means.

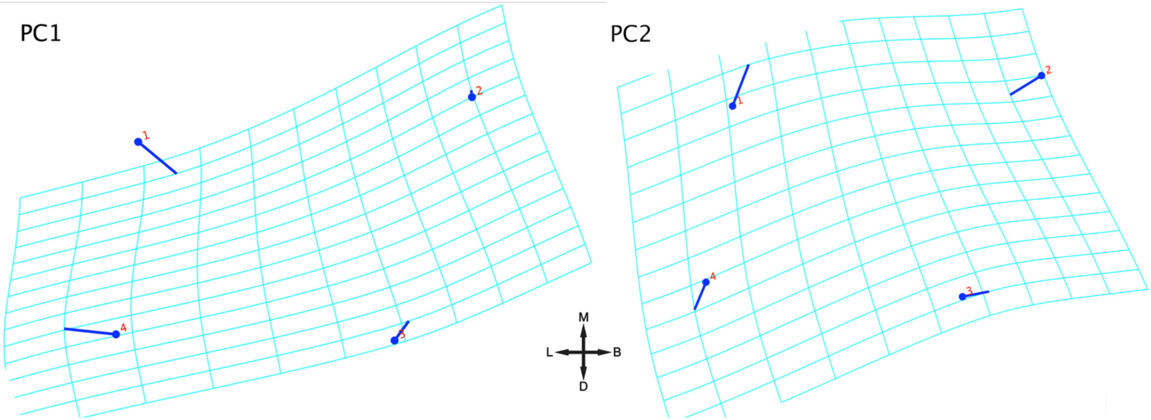


Fig. 5.2. Shape changes associated with PC1 (left) and PC2 (right) of M^2.

5.2.3 Interlandmark Distances (ILDs)

The means and standard deviations for the ILDs of M^2 have been presented in Table 5.4. American Asians are mostly significantly different from either AW, that have smaller means, or Th, that have larger means. There is only one instance in which AA are significantly different from EA. While not significant, AA generally exhibits smaller means than EA.

5.2.4 Principal Components of ILDs

The first principal component accounts for 47.0% of the variance and is most heavily loaded by the ILD for cusps 1-3, followed by 1-2, and then 1-4. The major variations show the increased breadths and lengths emphasized by PC1, though the distal breadth contributes very little to PC1. The second PC accounts for an additional 28.0% of the variance is most heavily loaded by the ILD for cusps 2-4, and then 3-4. The second PC demonstrates more variation in the distal aspects of the molar, especially those not represented in PC1.

Table 5.4. Means and standard deviations for ILDs by group for M^2. Group means significantly different from American Asians based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	7.2	0.7	7.0	0.8	4.2	0.7	5.6	0.7	8.9	1.0	5.8	0.9
AI	7.4	0.8	7.2	0.8	3.8	0.7	6.1	0.8	8.7	1.2	5.7	1.1
EA	7.0	0.7	7.2	0.9	4.6	0.6	**5.1**	0.8	8.8	0.9	5.9	1.1
NA	7.3	1.2	7.6	1.3	**5.6**	1.1	5.7	0.7	8.6	1.7	5.9	1.4
SEA	7.1	0.7	6.7	0.8	4.3	0.7	**4.9**	0.5	8.6	0.9	5.5	1.0
Th	7.7	1.0	**8.0**	1.0	5.1	0.8	5.5	0.8	**9.5**	0.9	**6.5**	1.0
AW	**6.6**	0.7	6.6	0.9	4.5	0.9	**5.3**	0.7	8.6	1.1	5.7	0.9

5.3 MANDIBULAR FIRST MOLAR (M_1)

5.3.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for the M_1 shape variables have been calculated in Table 5.5. American Asians have more significant differences with AW than any other group, followed by Th. Principal component two demonstrates the uniqueness of AA among all of the groups; however, their mean is between the extreme values of EA and AW. Principal components three and six show no differences between AA and other groups. Principal components four and five show significant differences between AA and AW. Consistent with previous analyses, AA has larger centroid sizes than AW. However, the AA M_1 shape variables are more similar to the Asian groups than AW.

Table 5.5. Means and standard deviations for PC scores and log centroid size by group for M_1. Cumulative variance explained is listed under each PC. Group means significantly different from American Asians based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M_1 PC1** 25.7%		**M_1 PC2** 49.7%		**M_1 PC3** 65.1%		**M_1 PC4** 78.6%		**M_1 PC5** 91.0%		**M_1 PC6** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	2.222	0.066	-0.008	0.042	-0.007	0.051	0.001	0.038	-0.012	0.040	-0.006	0.031	0.002	0.030
AI	2.249	0.075	-0.013	0.033	0.020	0.032	0.007	0.037	-0.012	0.032	-0.019	0.027	-0.009	0.031
EA	2.219	0.095	0.011	0.054	**-0.058**	0.051	0.007	0.052	0.010	0.038	-0.003	0.053	0.011	0.025
NA	**2.273**	0.063	0.021	0.079	0.005	0.056	-0.015	0.035	-0.001	0.040	-0.014	0.037	0.013	0.041
SEA	2.209	0.092	0.009	0.036	**-0.048**	0.050	0.011	0.039	0.001	0.040	0.011	0.025	0.004	0.037
Th	**2.271**	0.079	**0.077**	0.069	**-0.066**	0.057	0.001	0.048	-0.008	0.037	-0.015	0.047	-0.010	0.034
AW	**2.168**	0.071	-0.012	0.057	**0.026**	0.053	-0.002	0.042	**0.010**	0.039	**0.010**	0.038	-0.002	0.031

5.3.2 Principal Components of Shape

The first PC accounts for 25.7% of the shape variance and indicates the major movement of cusp 1 mesiobuccally, cusp 2 distolingually, cusp 3 distobuccally, cusp 4 buccally, and cusp 5 mesiolingually (Fig. 5.3). Positive PC1 scores exhibit a shape that is more mesiodistally compressed and elongated buccally with a hypoconulid that is more mesiolingually placed. The second PC accounts for an additional 23.9% of the variance and shows major movement of cusp 1 mesiolingually, cusp 2 mesiobuccally, cusp 3 lingually, cusp 4 distobuccally, and cusp 5 distolingually (Fig. 5.3). Positive PC2 scores indicate an M_1 shape that is elongated mesiodistally and compressed lingobuccally, especially in the distal aspect of M_1.

5.3.3 Interlandmark Distances (ILDs)

The means and standard deviations for the ILDs of M_1 are listed in Table 5.6. American Asians exhibit the most significant differences with Th that has consistently higher ILD means, followed by AW that shows consistently lower ILD means. Consistent with previous findings, AA consistently has mean ILD values that are lower than EA, which indicates intermediacy to the lower means expressed by AW.

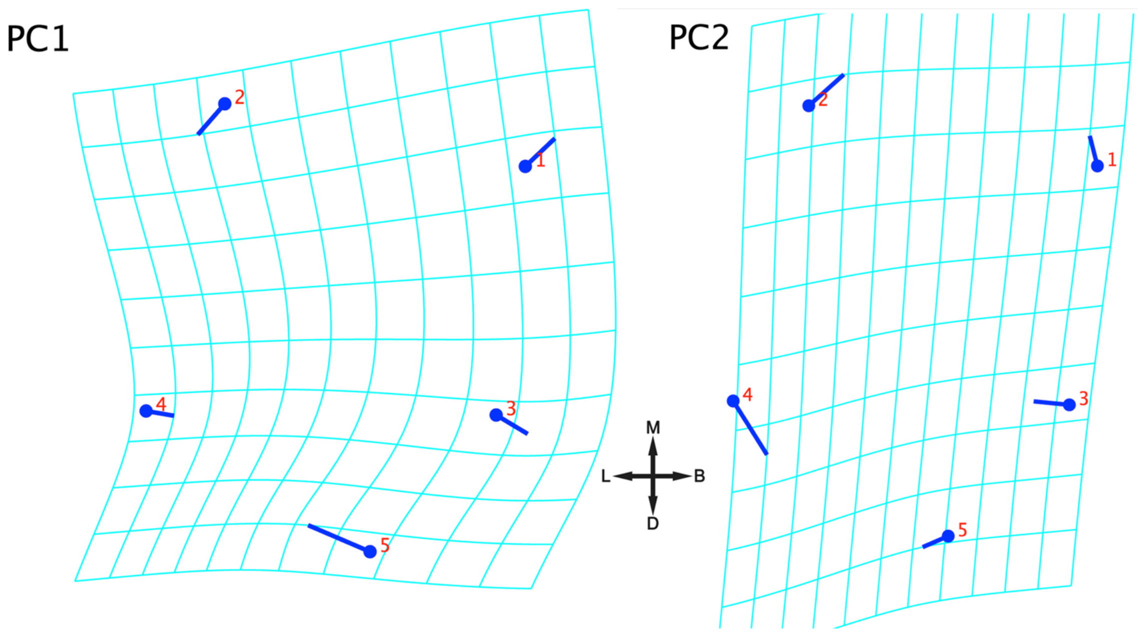


Fig. 5.3. Shape changes associated with PC1 (left) and PC2 (right) of M_1.

Table 5.6. Means and standard deviations for ILDs by group for M_1. Group means significantly different from American Asians based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	AA		**AI**		**EA**		**NA**		**SEA**		**Th**		**AW**	
	Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**
Cusp 1-2	5.7	0.6	5.8	0.6	5.9	0.9	5.9	0.8	6.0	0.8	**6.8**	0.9	**5.4**	0.6
Cusp 1-3	4.5	0.6	4.5	0.4	4.8	0.6	5.0	0.8	**5.0**	0.8	**5.0**	0.7	4.7	0.8
Cusp 1-4	8.4	0.7	8.6	0.7	8.7	0.9	8.8	0.8	8.5	1.0	**8.9**	0.9	**8.0**	0.8
Cusp 1-5	7.6	0.6	7.8	0.6	8.0	0.8	**8.4**	0.9	**8.1**	1.2	**8.4**	0.9	7.6	0.7
Cusp 2-3	7.6	0.6	7.8	0.7	8.0	1.0	7.9	1.0	7.8	1.0	**8.7**	1.1	**7.2**	0.7
Cusp 2-4	5.9	0.7	6.4	0.6	5.8	0.7	6.0	0.8	6.0	1.0	5.5	0.9	5.9	0.8
Cusp 2-5	8.7	0.8	9.1	0.7	8.8	0.8	8.7	1.1	8.9	1.0	8.8	0.9	8.5	0.8
Cusp 3-4	6.7	0.6	6.7	0.7	7.1	1.1	7.0	1.1	6.7	1.1	**7.5**	1.0	**6.0**	0.7
Cusp 3-5	3.6	0.5	3.8	0.6	3.8	0.9	**4.0**	0.7	3.7	0.8	**4.5**	1.0	3.4	0.7
Cusp 4-5	5.0	0.8	5.0	0.6	5.2	0.8	5.0	1.1	5.2	0.8	4.9	0.8	**4.6**	0.8

5.3.4 Principal Components of ILDs

The first PC accounts for 44.7% of the variance and is most heavily loaded by the ILD for cusps 1-4, followed by cusps 3-4, and 2-4. The second PC accounts for an additional 14.1% of the variance and is most heavily loaded by the ILD for cusps 4-5, followed by cusps 1-4. In sum, the distal aspect of M_1 exhibits a high degree of variability in both length and breadth measures.

5.4 MANDIBULAR SECOND MOLAR (M_2)

5.4.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for the shape variables for M_2 are listed in Table 5.7. The only variables that exhibit significant differences between AA and other groups are centroid size and PC1. Centroid sizes are significantly different between AA and SEA, Th and AW. Both SEA and AW have smaller centroid sizes than AA, while modern Th has larger centroid sizes, which is consistent with observations from previously discussed molars. Principal component one is significantly different between AA and EA, Th, and AW, though AA's mean is between EA and AW.

Table 5.7. Means and standard deviations for PC scores and log centroid size by group for M_2. Cumulative variance explained is listed under each PC. Group means significantly different from American Asians based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M_2 PC1** 37.6%		**M_2 PC2** 63.5%		**M_2 PC3** 83.5%		**M_2 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	2.031	0.077	0.001	0.072	0.005	0.059	0.007	0.051	0.005	0.048
AI	2.066	0.081	0.004	0.090	0.020	0.046	-0.012	0.049	0.001	0.034
EA	1.983	0.112	**-0.005**	0.080	-0.001	0.071	-0.001	0.056	-0.008	0.052
NA	2.060	0.088	-0.003	0.078	0.007	0.056	0.012	0.059	0.001	0.047
SEA	**1.961**	0.094	-0.003	0.078	-0.026	0.035	-0.009	0.047	-0.013	0.059
Th	**2.106**	0.107	**-0.006**	0.087	-0.017	0.065	0.010	0.052	0.019	0.043
AW	**2.002**	0.085	**0.002**	0.060	0.001	0.059	-0.006	0.051	-0.004	0.045

5.4.2 Principal Components of Shape

The first PC accounts for 37.6% of the shape variance and is most heavily influenced by the mesiolingual movement of cusp 1, the mesiobuccal movement of cusp 2, the distolingual movement of cups 3, and the distobuccal movement of cusp 4 (Fig 5.4). Comparatively, positive PC1 scores have reduced buccolingual breadths and increased mesiodistal lengths. American Asians, AI, and AW all show positive PC1 means compared to the rest of the Asian groups. Principal component two accounts for an additional 25.9% of the shape variance and indicates movement of cusp 1 distolingually, cusp 2 mesiobuccally, cusp 3 mesiolingually, and cusp 4 distally (Fig. 5.4). Positive PC2 scores reflect a comparably longer lingual aspect of the tooth leading to a trapezoidal shape, whereas negative PC2 scores demonstrate a square shaped M_2. Again, AA, AI, and AW all show positive PC2 scores as compared to the other groups.

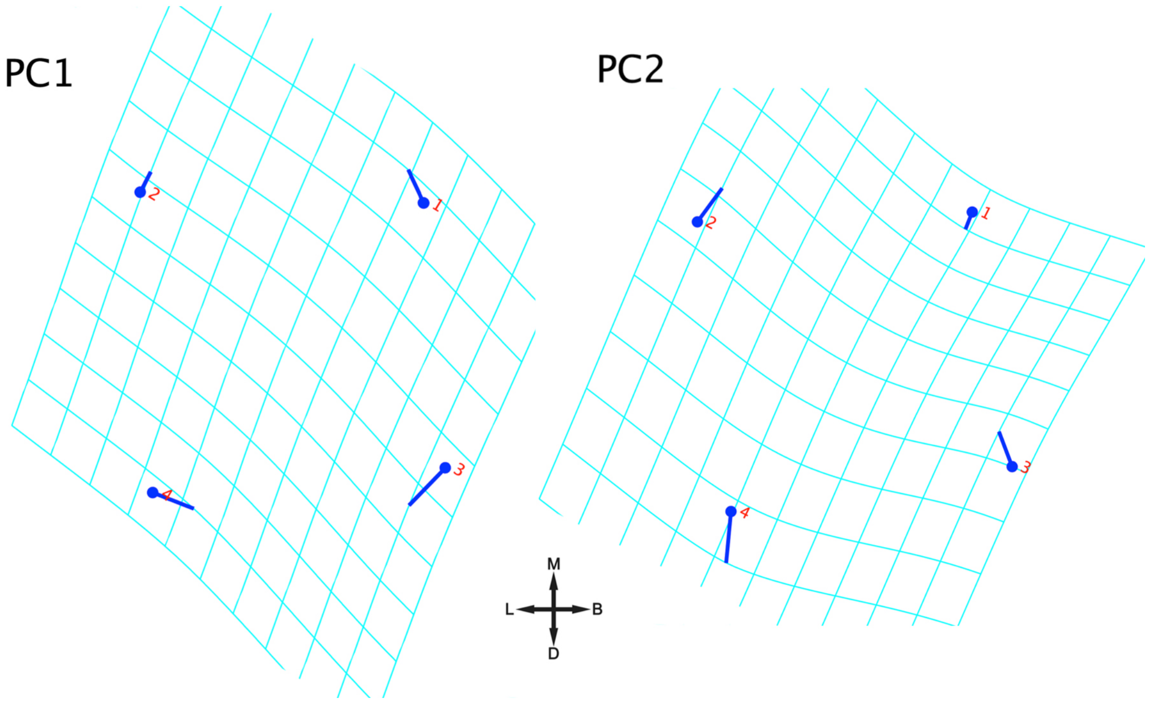


Fig. 5.4. Shape changes associated with PC1 (left) and PC2 (right) of M_2.

5.4.3 Interlandmark Distances (ILDs)

The means and standard deviations for the ILDs of M_2 are presented in Table 5.8. American Asians have the most differences with Th that have greater values and then AW that have smaller ILDs, which is consistent with previous analyses. The ILD for cusp 1-4 demonstrates the most significant differences with SEA, Th, and AW all unique from AA. Unlike previous trends, AA has consistently higher ILDs than EA, though still smaller than Th.

Table 5.8. Means and standard deviations for ILDs by group for M_2. Group means significantly different from American Asians based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	5.6	0.6	5.1	0.7	7.7	0.6	7.9	0.7	5.8	0.7	5.8	0.7
AI	5.8	0.6	5.1	0.8	7.9	0.8	8.3	0.8	6.2	0.6	6.0	0.8
EA	5.3	0.9	**4.6**	0.7	7.5	1.0	7.5	0.9	5.4	0.8	6.0	1.0
NA	5.7	0.7	5.1	0.8	8.1	0.9	8.1	0.8	5.8	0.8	6.2	1.0
SEA	5.2	0.7	4.6	0.6	**7.2**	0.7	**7.4**	0.7	**5.2**	0.6	5.7	0.9
Th	**6.3**	1.0	5.2	0.8	**8.4**	0.9	**8.4**	1.0	5.8	0.8	**6.5**	1.1
AW	**5.3**	0.6	5.1	0.8	**7.4**	0.8	7.8	0.7	5.7	0.7	**5.5**	0.7

5.4.4 Principal Components of ILDs

The first PC accounts for 52.4% of the variance and is most heavily loaded by the ILD for cusps 2-3, followed by cusps 1-4. Both of the most influential ILDs demonstrated diagonal distances, indicating variation in both lengths and breadths. The second PC accounts for an additional 18% of the variance and is most heavily loaded by the ILD for cusps 1-3, followed by cusps 3-4. The second PC illustrates major variation on the buccal aspect of the tooth and also the distal breadth.

5.5 COMBINED MOLARS

Data from each of the molars were combined to examine the influence of each tooth. The shape PCs and ILDs were combined into a comprehensive dataset. The combined molar ILDs were then submitted to a PCA to examine variation across each of the molars. The PCA of the combined molar ILDs resulted in 28 PCs, wherein the first 11 PCs contributed eigenvalues greater than one, which accounts for 79.7% of the total variance and were retained for further analysis. The first PC accounts for 28.2% of the variance and is loaded mainly by the ILD for M_1 1-2, followed by M_2 1-4. The second PC accounts for an additional 12.4% of the variance and is most heavily loaded by the ILD for M_1 3-5, followed by M_1 4-5. Both of the PCs are overwhelmingly loaded by the mandibular molars, and in the case of PC2, the distal aspect of M_1.

5.5.1 Discriminant Function Analysis

The correct classifications for each of the datasets are listed in Table 5.9. The classification matrices from individual analyses are presented in Appendix A. The combined molar ILD PCs has the highest total correct classification followed by the combined molar shape and size variables. The shape variables sans size have the lowest total correct classification. Across each analysis, AA classifies mostly correctly, but misclassifies most commonly as either AI or AW and then EA. American Asians misclassify rarely as NA, SEA, or Th. Consistently, the shape and size variables of M_1 have the greatest contribution to the discriminant function coefficients. Size is especially important as shown through the improved classification rates in each of the size-based analyses. A comparison of the CV plots shows the trend for AA to be intermediate between AW and EA throughout each dataset tested (Fig. 5.5). The modern Thai and NA are the most dissimilar from AA.

Table 5.9. Correct classifications for each of the DFAs ordered by total correct classification. All values are percentages (%).

Dataset	AA	AI	EA	NA	SEA	Th	AW	Total Correct
Combined Molar ILD PC	35.2	63.2	26.1	52.4	17.4	59.1	59.0	48.5
Combined Molar Shape and Size	27.9	47.4	43.5	52.6	36.4	66.7	62.4	47.2
Combined Molar ILD	27.9	68.4	34.8	57.1	34.8	65.9	47.0	44.6
Combined Molar Shape	28.6	47.7	34.8	47.4	9.1	42.9	56.4	42.8

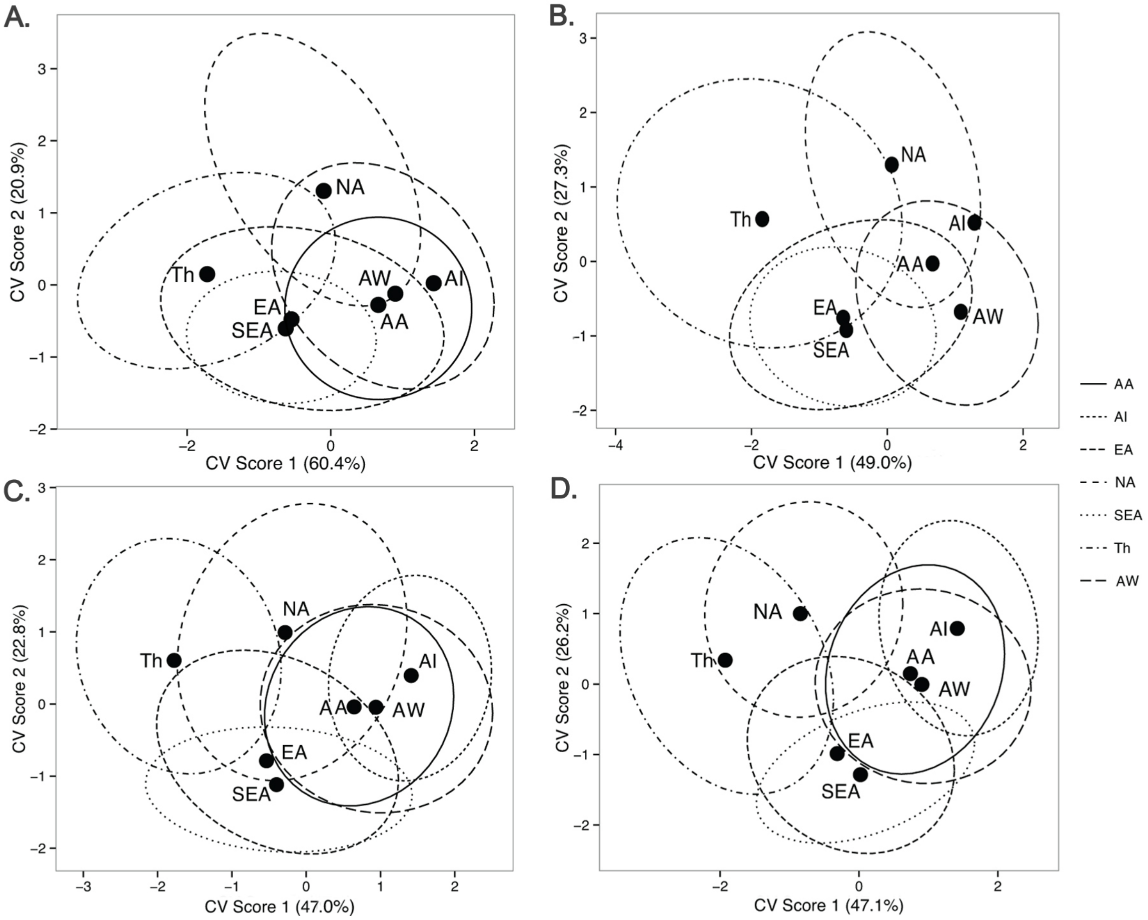


Fig. 5.5. Comparison of canonical variate plots from each of the analyses. The combined molar shape dataset is shown at A, the combined shape and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

The D^2 matrices for each of the analyses are presented in Appendix A. A permutation test on each of the D^2 matrices indicates that each of the groups is significantly different from one another at $p < 0.05$. American Asians consistently share the smallest D^2 values with AW and AI and the largest values with NA and Th. From the potential parental groups, AA shares the smallest D^2 with EA. The shape only analysis resulted in the smallest D^2 between AA and AW, while the inclusion of size caused the two groups to become more dissimilar. In sum, AA is intermediate between AW and EA, though has greater affinity with AW.

5.5.2 Principal Coordinate Analysis

Each of the datasets was subjected to a PCO with D^2 as the distance measure. Eigenvalues for each of the 3D PCOs were greater than zero. The R^2 values for each of the 3D PCOs range from 0.91-0.93, which indicates an excellent goodness-of-fit to the original distances. The 3D PCO plots show AA having greater affinity to the Asian groups, specifically EA, than AW (Fig. 5.6). The shape PC analysis (Fig. 5.6-A) shows AW being the most dissimilar from AA, while the analyses that included size increased the affinity between the two groups. Still, AW consistently shows disparate *z* values from AA, which indicates a greater dissimilarity than demonstrated through the earlier CV plots. Native Alaskans and Th both are the most dissimilar from AA, consistent with earlier analyses.

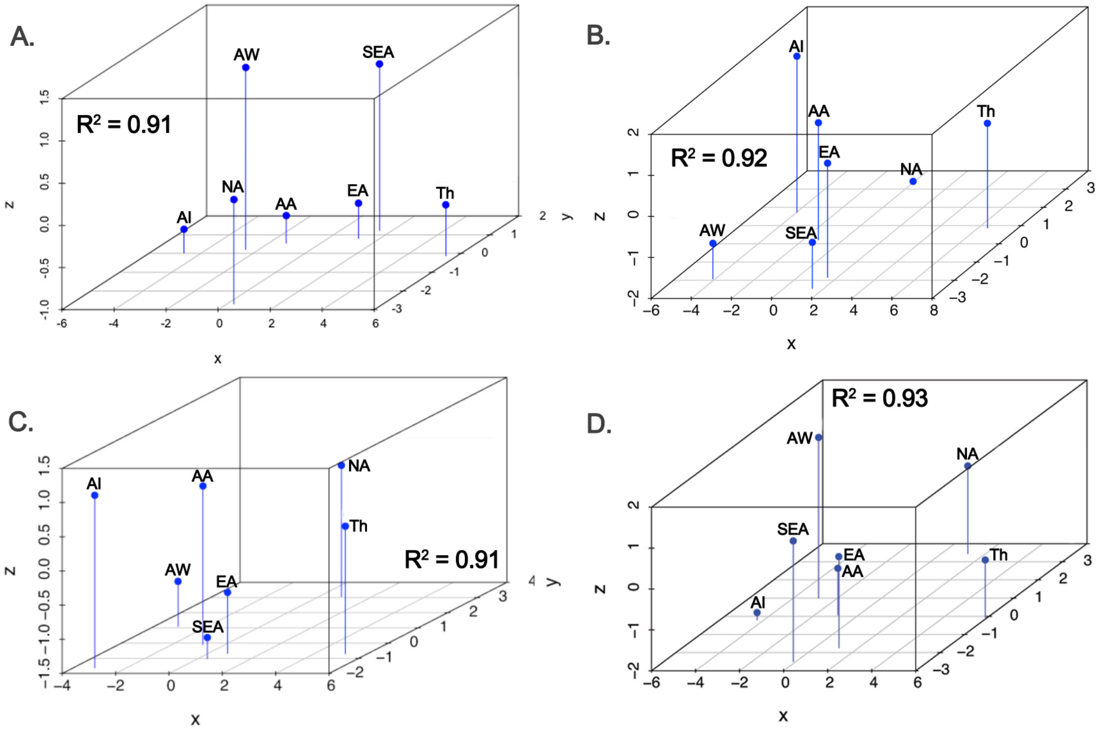


Fig. 5.6. Comparison of three-dimensional PCO perceptual plots for each dataset with individual R^2 values displayed. The PCO of the combined shape PC dataset is shown at A, the combined shape PC and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

5.6 DISCUSSION

The DFA based on the shape PCs achieve the lowest total correct classification out of any of the analyses. The inclusion of centroid size results in better classification, though both ILD analyses have greater correct classifications. The better results achieved by the size-centric analyses indicate that, in Asian populations, size is more diagnostic of population variation than size-free shape. The shape PC analyses show AA as being most similar to AW, though the sized-based analyses demonstrate the increased affinity between AA and EA. In each case, the mandibular first molar displays the most variation by its consistent contribution to each of the models.

American Asians consistently exhibit significantly different D^2 values from each of the groups, though are most constantly clustered near AI or AW first and then EA, thus supporting Hypothesis 1. The significant differences between AA and each of the other groups indicates the uniqueness of this population group within the U.S., but also reveals significant gene flow, especially with AW and AI. Lastly, the affinity observed between AA and AI is consistent with reports on dental morphology, as each group is part of the Sinodont dental complex and thus shares similar ancestral lineages (Turner, 1990).

5.7 SUMMARY

The total correct classifications range from 42.8% (combined molar shape) to 48.5% (combined molar ILD). The Th sample generally has the highest correct classifications and the SEA group has the lowest. American Asians are significantly different from each of their possible parental groups and AW. However, even though AA is significantly different, the affinity between AA and AW has been demonstrated, which is often greater than the affinity between AA and other Asian groups, aside from AI. The affinity of AA and AW demonstrates gene flow between the two groups. Further, assuming that intermarriage is related to intermating, the observed affinity between AA and AW is also reflected in the reported intermarriage rates (Passel et al., 2010; Taylor et al., 2012a). Furthermore, even though each group's mean D^2 is significantly different from one another, overall classification is low. Yet, AA misclassified mostly as either AI or AW, followed by EA, which further shows the overlap between these groups.

CHAPTER 6: MODERN AMERICAN BLACK COMPARISON

Modern American black biohistory was investigated by comparing the modern American black (AB) data with those from historic African groups from varying regions: East African (EA), North African (NA), South African (SA), West African (WA) and also modern American whites (AW). Modern American blacks should demonstrate an affinity with the Western African group and also with modern American whites given that these two population groups have cohabitated the U.S. since the first European colonization (Hypothesis 2).

6.1 MAXILLARY FIRST MOLAR (M^1)

6.1.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviation that were calculated for each of the morphometric variables by group are shown in Table 6.1. Centroid size is significantly different for AB and both NA, that has larger centroid sizes, and AW that has smaller centroid sizes. Additionally, AB is significantly different from NA and AW in PC1. Further, AB has significantly different PC2 scores from SA and AW. Lastly, AB only has significantly different PC3 scores from NA and significantly different PC4 scores from AW.

Table 6.1. Means and standard deviations for PC scores and log centroid size by group for M^1. Cumulative variance explained is listed under each PC. Group means significantly different from American blacks based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M^1 PC1** 35.9%		**M^1 PC2** 65.9%		**M^1 PC3** 84.6%		**M^1 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AB	2.125	0.072	-0.014	0.055	-0.003	0.047	0.004	0.041	0.006	0.032
EA	2.160	0.076	0.007	0.058	-0.006	0.041	0.007	0.027	0.024	0.034
NA	**2.214**	0.097	**-0.04**	0.057	-0.015	0.048	**-0.035**	0.044	0.008	0.045
SA	2.169	0.059	-0.031	0.049	**-0.038**	0.032	-0.013	0.036	0.01	0.042
AW	**2.084**	0.073	**0.023**	0.058	**0.015**	0.052	0.001	0.043	**-0.012**	0.039
WA	2.113	0.089	-0.003	0.058	-0.015	0.046	0.018	0.036	0.009	0.039

6.1.2 Principal Components of Shape

The first PC accounts for 35.9% of the variance and demonstrates major movement of cusp 1 distobuccally, mesiobuccal movement of cusp 2, and mesiolingual movement of cusp 4 (Fig. 6.1). The positive PC1 scores, primarily observed in AW, reflect an M^1 that is comparably compressed mesiodistally on the lingual aspect with a much more distobuccally positioned protocone. Principal component two accounts for an additional 30.0% of the variance. The major shape changes observed in PC2 are the mesiobuccal movement of cusp 1, the mesiolingual movement of cusp 2, the distolingual movement of cusp 3, and the distobuccal movement of cusp 4 (Fig. 6.1). In sum, PC2 demonstrates a rhomboidal shape for positive PC values, which was only observed in AW, and a more rectangular shape for negative PC2 scores.

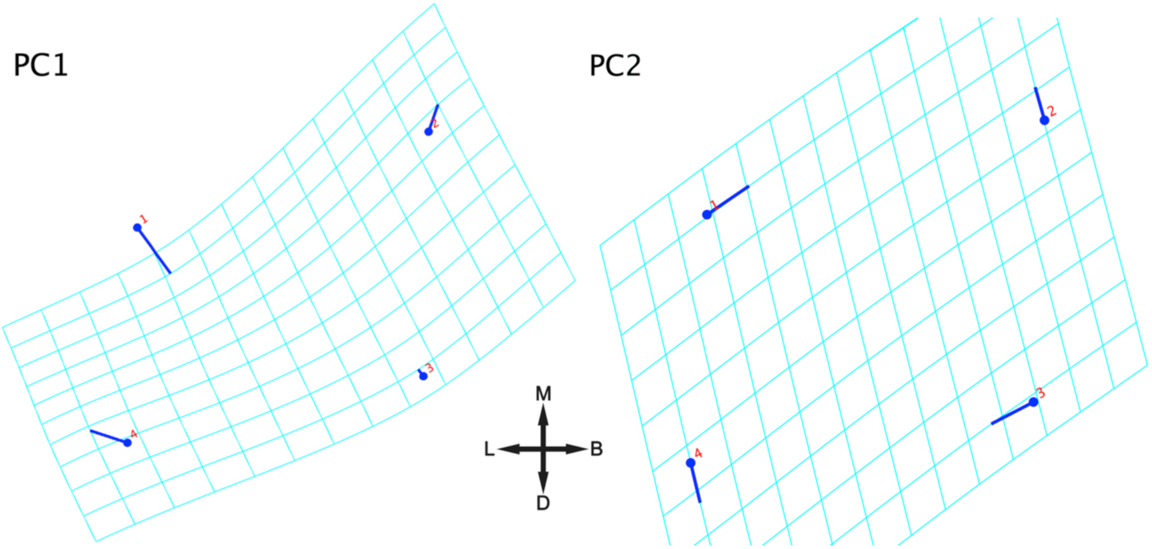


Fig. 6.1. Shape changes of M^1 associated with PC1 (left) and PC2 (right).

6.1.3 Interlandmark Distances (ILDs)

The means and standard deviations for each group's M^1 ILDs were tabulated and presented in Table 6.2. North Africans and AW are most commonly significantly different from AB. Consistently, WA and AB show similar group means. However, when AW is not significantly different from AB, the two groups have comparable means. The ILD for cusp 1-3 demonstrates the greatest range of group means, followed by cusp 1-2, which again highlights the highly variable position of cusp 1. Lastly, the ILD for cusp 3-4 exhibits the smallest group mean ranges, which is consistent with the comparably less variably positioned cusps on the distal aspect of M^1 noted above.

Table 6.2. Means and standard deviations for ILDs by group for M^1. Group means significantly different from American blacks based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AB	6.5	0.8	7.2	0.8	5.0	0.8	5.3	0.8	9.3	0.9	6.6	0.8
EA	6.9	0.7	7.6	0.9	4.8	0.7	**5.9**	0.6	9.8	0.8	7.0	0.8
NA	**7.8**	1.0	**8.5**	1.1	**5.3**	0.8	**6.0**	0.9	**10.1**	0.9	**7.1**	0.9
SA	**7.2**	0.6	**8.1**	0.8	4.9	0.7	5.6	0.5	9.7	0.5	7.0	0.6
AW	6.4	0.7	**6.7**	0.8	**4.8**	0.7	5.3	0.6	9.3	0.9	**6.4**	0.7
WA	6.5	0.8	7.2	0.9	4.9	0.8	5.3	1.0	9.1	1.1	6.8	0.8

6.1.4 Principal Components of ILDs

The first PC accounts for 52.4% of the variation and is most heavily loaded by the ILD for cusps 1-3, which is also the ILD that has the greatest range between group means. The ILD that contributes the least to PC1 was for cusps 1-4, which has the smallest range of the ILDs. Principal component two accounted for 14.5% of the variation and is most heavily loaded by the ILD for cusps 1-4, contrary to PC1. The loadings of the PCs indicate that lengths of M^1 are more variable than breadths.

6.2 MAXILLARY SECOND MOLAR (M^2)

6.2.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for each of the group's M^2 morphometric variables have been presented in Table 6.3. The M^2 shape PCs are more variable across the board than for those of M^1. American blacks have significantly different centroid sizes from each group except for WA and AW. Though not significant, AB has a smaller centroid size than WA, and a larger centroid size than AW. Principal component one varies significantly between AB and both NA and AW, but is comparable to WA. Principal component two only differs significantly between AB and AW. Lastly, AB only has significantly different PC3 means from NA, and PC4 means from EA.

Table 6.3. Means and standard deviations for PC scores and log centroid size by group for M^2. Cumulative variance explained is listed under each PC. Group means significantly different from American blacks based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M^2 PC1** 37.0%		**M^2 PC2** 62.4%		**M^2 PC3** 84.6%		**M^2 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AB	2.091	0.092	-0.008	0.066	-0.013	0.065	0.005	0.049	0.001	0.036
EA	**2.160**	0.076	0.004	0.058	-0.001	0.041	-0.001	0.028	**0.026**	0.031
NA	**2.213**	0.097	**-0.043**	0.056	-0.010	0.046	**-0.032**	0.044	-0.006	0.045
SA	**2.169**	0.059	-0.036	0.048	-0.031	0.032	-0.009	0.038	0.002	0.039
AW	2.084	0.732	**0.024**	0.057	**0.019**	0.051	-0.001	0.042	-0.008	0.039
WA	2.113	0.089	-0.005	0.058	-0.007	0.047	0.014	0.034	0.015	0.040

6.2.2 Principal Components of Shape

Principal component one accounts for 37.0% of the variance and shows movement of cusp 1 distobuccally, cusp 3 mesiobuccally, and of cusp 4 mesiolingually (Fig. 6.2). American whites have the greatest PC1 mean, which indicates an exaggerated rhomboidal M^2 shape with the comparatively distobuccally placed protocone and lingually placed hypocone. Negative PC1 scores reflect a more rectangular molar. Principal component two accounts for an additional 25.4% of the shape variance. Principal component two demonstrates major movement of cusps 1 and 2 distolingually, cusp 3 buccally, and cusp 4 mesiobuccally (Fig. 6.2). Positive PC2 scores, shown only by AW, have mesiodistally-compressed molars.

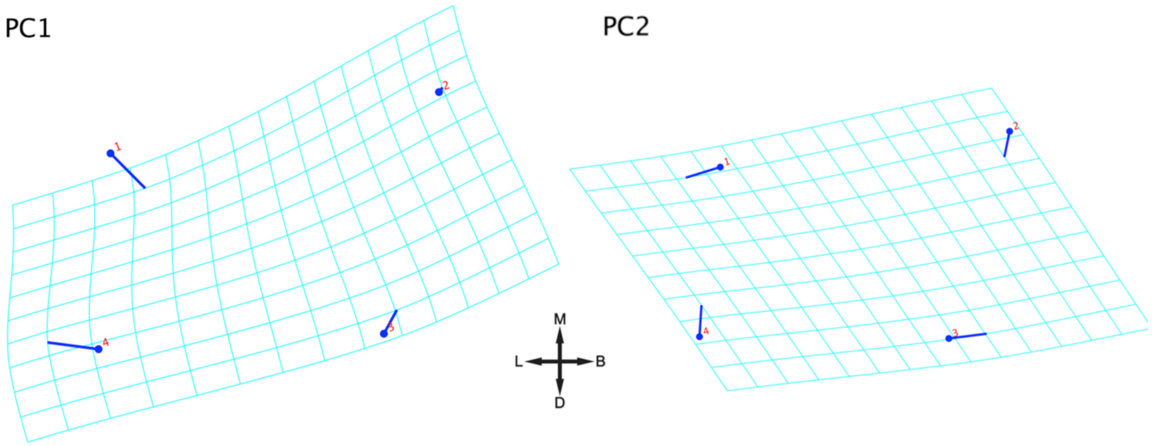


Fig. 6.2. Shape changes of M^2 associated with PC1 (left) and PC2 (right).

6.2.3 Interlandmark Distances (ILDs)

American blacks share similar means with every African group for each of the ILDs (Table 6.4). The only group to significantly differ from AB is AW in the ILDs for cusps 1-2, 1-3, and 3-4. American whites have consistently smaller M^2 ILDs compared to the African groups and AB. Overall, the ILDs for M^2 are less variable than those of M^1, contrary to the shape PCs.

6.2.4 Principal Components of the ILDs

The first PC accounts for 44.0% of the variance and is most heavily loaded by the ILD for cusps 1-3, followed by cusps 2-4. The second PC contributes another 19.7% of the variance and is mostly loaded by the ILD for cusps 1-4, followed by cusps 2-3, and then relatively equally between the remaining ILDs. The first PC indicates that the diagonal measures of M^2 are more variable, while PC2 focuses on the variability of mesiodistal lengths.

Table 6.4. Means and standard deviations for ILDs by group for M^2. Group means significantly different from American blacks based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AB	6.8	0.9	7.1	1.0	4.7	1.2	5.5	0.8	8.9	1.2	6.0	1.1
EA	6.8	0.5	7.1	1.0	4.8	0.7	5.2	0.8	8.9	0.9	6.0	1.5
NA	7.2	0.9	7.1	1.0	4.3	0.7	5.1	0.7	8.7	1.1	5.9	0.9
SA	7.4	0.6	7.3	0.8	4.5	0.6	5.3	0.6	9.0	0.8	6.0	0.9
AW	**6.6**	0.7	**6.6**	0.8	4.5	0.9	5.3	0.7	8.6	1.1	**5.7**	0.9
WA	6.6	0.8	6.8	1.4	4.8	1.6	5.3	1.3	8.5	1.5	5.9	1.0

6.3 MANDIBULAR FIRST MOLAR (M_1)

6.3.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations by group for the shape PCs and centroid sizes for M_1 are shown in Table 6.5. Both NA and AW have significantly different centroid sizes from AB; NA has larger centroid sizes and AW has smaller centroid sizes. None of the groups are significantly different from AB in PC1 and PC6. American blacks have significantly different PC2 scores from NA, SA, and AW; significantly different PC3 scores from NA, WA, and AW; PC4 scores from NA; and PC5 scores from NA and AW.

6.3.2 Principal Components of Shape

Principal component one accounts for 26.2% of the variance and reflects the movement of cusps 1 and 2 mesiobuccally, cusp 3 distolingually, cusp 4 distobuccally, and cusp 5 mesiolingually (Fig. 6.3). In sum, positive PC1 scores are indicative of an M_1 shape that is distally constricted and mesially elongated. Principal component two accounts for an additional 24.1% of the variance. The major shape changes associated with PC2 are: the mesiobuccal movement of cusp 1, the distolingual movement of cusp 2, the distobuccal movement of cusp 3, the mesial movement of cusp 4, and the mesiolingual movement of cusp 5 (Fig. 6.3). Positive PC2 scores represent an M_1 shape that is elongated buccally, constricted lingually, and compressed distally.

Table 6.5. Means and standard deviations for PC scores and log centroid size by group for M_1. Cumulative variance explained is listed under each PC. Group means significantly different from American blacks based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	AB		EA		NA		SA		AW		WA	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
Log Centroid Size	2.197	0.082	2.232	0.07	**2.267**	0.084	2.252	0.06	**2.168**	0.071	2.175	0.083
PC1	0.004	0.061	-0.001	0.039	0.015	0.047	-0.01	0.041	-0.001	0.058	-0.018	0.05
PC2	0.002	0.049	0.033	0.059	**0.072**	0.053	**0.071**	0.059	**-0.037**	0.053	0.009	0.056
PC3	-0.011	0.045	-0.019	0.036	**0.012**	0.041	-0.003	0.043	**0.003**	0.039	**0.012**	0.04
PC4	-0.003	0.038	-0.001	0.037	**0.029**	0.035	0.017	0.032	-0.006	0.04	-0.002	0.045
PC5	-0.013	0.036	0.008	0.038	**0.002**	0.029	-0.007	0.034	**0.011**	0.038	-0.004	0.034
PC6	0.004	0.035	-0.012	0.035	-0.001	0.03	-0.019	0.029	0.001	0.031	-0.005	0.036

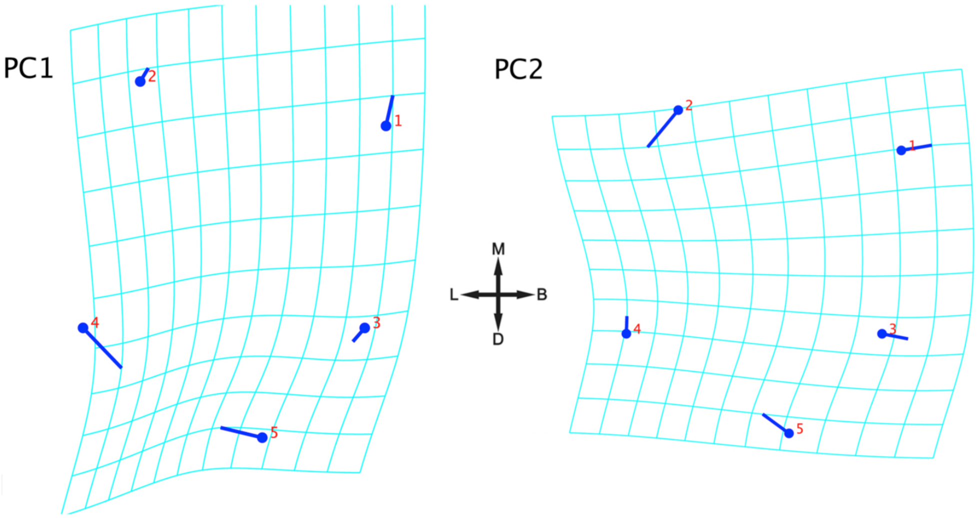


Fig. 6.3. Shape changes associated with PC1 (left) and PC2 (right) of M_1.

6.3.3 Interlandmark Distances

Table 6.6 shows the means and standard deviations for each of the M_1 ILDs, as well as the significance of the group means between AB and all other groups. North Africans most frequently have significantly different means from AB, followed by AW. West Africans have only one instance in which their mean is significantly different from AB (cusp 1-4). Further, the ILD for cusp 1-4 is the most unique in AB, wherein each of the African groups, sans WA, have larger means and AW and WA have smaller means. In general, AB has smaller ILDs than the African groups, with the exception of WA.

Table 6.6. Means and standard deviations for ILDs by group for M_1. Group means significantly different from American blacks based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	AB		**EA**		**NA**		**SA**		**AW**		**WA**	
	Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**
Cusp 1-2	5.6	0.6	5.9	0.6	**6.7**	0.8	**6.2**	0.9	**5.4**	0.6	5.5	0.7
Cusp 1-3	4.5	0.6	**4.9**	0.6	**5.1**	0.6	4.9	0.4	4.7	0.8	4.7	0.7
Cusp 1-4	8.4	0.8	**9.0**	0.7	**9.2**	0.8	**9.1**	0.6	**8.0**	0.8	**8.0**	1.1
Cusp 1-5	7.8	0.8	**8.3**	0.6	**8.2**	0.7	8.0	0.5	7.6	0.7	7.6	0.7
Cusp 2-3	7.5	0.7	7.7	0.7	**8.4**	0.9	**8.1**	0.8	**7.2**	0.7	7.4	1.2
Cusp 2-4	5.9	0.7	5.9	0.7	5.9	0.6	5.7	0.4	5.9	0.8	5.9	0.8
Cusp 2-5	8.5	0.9	8.8	0.6	8.7	0.8	8.6	0.6	8.5	0.8	8.6	0.8
Cusp 3-4	6.5	0.8	6.8	0.7	**7.2**	0.9	**7.4**	0.8	**6.0**	0.7	6.4	1.1
Cusp 3-5	3.9	0.6	3.9	0.4	3.8	0.6	3.8	0.6	**3.4**	0.7	3.6	0.8
Cusp 4-5	4.7	0.8	5.0	0.5	5.0	0.7	5.2	0.7	4.6	0.8	4.9	0.9

6.3.4 Principal Components of the ILDs

The first PC accounts for 46.1% of the variance and was most heavily loaded by the ILD for cusp 1-4, followed by 1-5, and then 2-5. The second PC accounts for an additional 12.6% of the variation and was most heavily loaded by the ILD for cusp 1-3, followed by 2-3, and then 3-5. The ILDs loading both PC1 and PC2 are mostly focusing on the mesiodistal elongation of the tooth, which was also noted in the PC1 shape changes associated with M_1.

6.4 MANDIBULAR SECOND MOLAR (M_2)

6.4.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations by group for the shape PCs and centroid size for M_1 are shown in Table 6.7. American whites and WA both have centroid sizes of M_2 that are significantly smaller than those of AB, which has the second largest centroid size. American blacks have significantly different PC1 scores from SA, WA, and AW; significantly different PC3 scores from AW; and significantly different PC4 scores from EA.

6.4.2 Principal Components of Shape

Principal component one accounts for 38.2% of the variance and shows the movement of cusp 1 distobuccally, cusp 2 distolingually, cusp 3 mesiobuccally, and cusp 4 mesiolingually (Fig. 6.4). Each group except AW has a positive PC1 mean score. In total, the shape changes for positive PC1 scores represent an M_2 shape that is compressed mesiodistally and broadened buccolingually. Principal component two accounts for an additional 24.9% of the variance and indicates movement of cusp 1 distally, cusp 2 mesiobuccally, cusp 3 mesiolingually, and cusp 4 distobuccally (Fig. 6.4). The overall shape represented by positive PC2 scores is rhomboidal compared to the negative PC2 scores, which are more squared.

Table 6.7. Means and standard deviations for shape PCs and centroid size by group for M_2. Cumulative variance explained is listed under each PC. Group means significantly different from American blacks based on a two-tailed Student's t-test in bold ($p < 0.05$).

	Log Centroid Size		**PC1** 38.2%		**PC2** 63.0%		**PC3** 83.6%		**PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AB	2.036	0.091	0.007	0.077	0.006	0.055	-0.009	0.053	0.002	0.046
EA	2.007	0.114	0.018	0.077	0.005	0.055	-0.004	0.046	**-0.034**	0.035
NA	2.014	0.114	0.023	0.075	-0.014	0.048	-0.001	0.047	-0.006	0.047
SA	2.046	0.087	**0.083**	0.074	-0.019	0.048	-0.017	0.054	-0.010	0.040
AW	**2.001**	0.085	**-0.038**	0.059	0.001	0.060	**0.013**	0.051	0.006	0.044
WA	**2.000**	0.096	**0.051**	0.067	-0.002	0.053	-0.008	0.047	-0.006	0.050

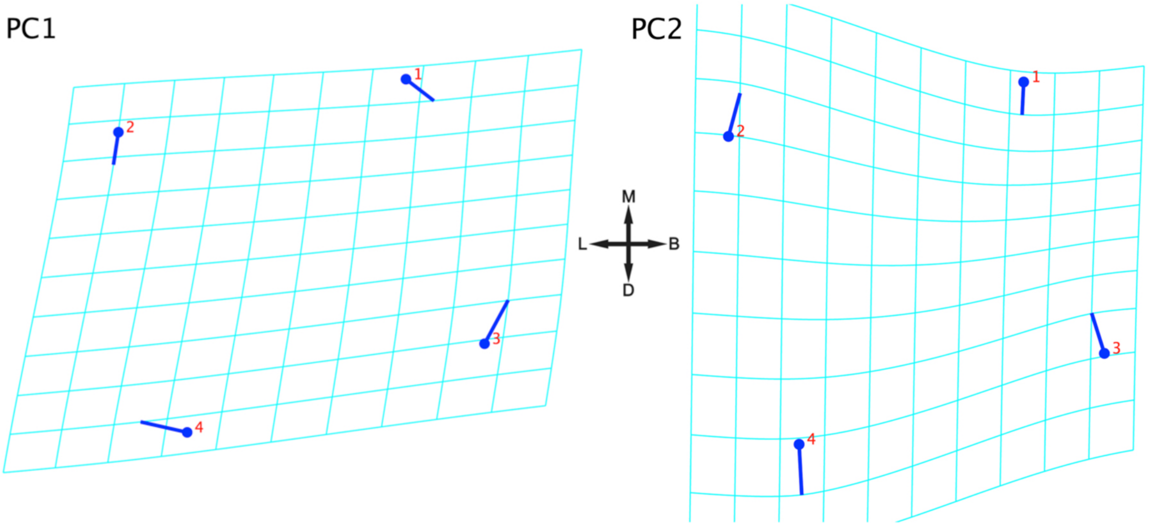


Fig. 6.4. Shape changes associated with PC1 (left) and PC2 (right) of M_2.

6.4.3 Interlandmark Distances (ILDs)

The means and standard deviations for the ILDs of M_2 are presented in Table 6.8. The mandibular second molar shows the least variation and thus has the least number of significant ILDs between AB and the rest of the groups. The greatest range between ILDs is within cusp 1-2, which shows the greater variation in the mesial breadth of M_2 compared to the rest of the molar. American blacks have larger ILDs for cusp 1-2 comparable to the majority of the African groups, while AW has lower values.

Table 6.8. Means and standard deviations for ILDs by group for M_2. Group means significantly different from American blacks based on a two-tailed Student’s t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AB	5.5	0.7	5.1	0.8	7.9	0.8	7.8	0.8	5.7	0.8	6.0	0.8
EA	**4.8**	1.2	5.0	0.5	7.7	0.8	7.4	1.0	5.7	0.9	6.0	0.9
NA	5.4	0.8	5.0	0.7	7.7	1.0	7.6	0.9	5.4	0.7	5.9	1.0
SA	5.6	0.7	4.8	0.6	8.0	1.0	7.7	0.7	5.4	0.7	6.4	0.9
AW	**5.3**	0.6	5.1	0.8	**7.4**	0.7	7.8	0.7	5.7	0.7	**5.5**	0.7
WA	5.3	0.7	**4.7**	0.6	7.7	0.9	**7.3**	0.8	**5.4**	0.7	6.1	0.9

6.4.4 Principal Components of ILDs

The first PC accounts for 50.6% of the variance and is most heavily loaded by the ILD for cusp 1-4, followed by cusp 2-3. The first PC demonstrates variation in both diagonal aspects of the molar showing both length and breadth variation. The addition of PC2 accounts for an additional 18.0% of the variance and is most heavily loaded by the ILD for cusp 1-3, followed by cusp 3-4, which indicates more of a distal breadth component in comparison to PC1.

6.5 COMBINED MOLARS

As before, the morphometric variables and ILDs were each combined into respective datasets representing each molar. The ILDs were submitted to a PCA and yielded 28 PCs. The first 8 PCs contributed eigenvalues greater than 1.0 and accounted for a combined 71.2% of the variance. The first principal component accounts for 27.0% of the variance and is most heavily loaded by ILDs from M_1 and then M^1. The second PC accounts for an additional 14.4% of the variance and is most heavily loaded by ILDs from M_1.

6.5.1 Discriminant Function Analysis

The total correct classifications for each dataset are presented in Table 6.9. The classification matrices from each of the individual analyses are shown in Appendix B. The combined molar shape and size dataset has the highest correct classification. Thus, both shape and size are important in discriminating AB from the rest of the groups. In each analysis, AB classifies mostly correctly. In the analyses that included a size aspect, AB misclassifies most frequently as AW; conversely in the, size-free shape analysis, AB misclassifies mostly as WA. Similarly, while AW has the highest correct classifications, the group misclassifies most commonly as AB and rarely as the other groups. In each of the datasets, the variables of M_1 contribute the most to each of the discriminant function coefficients. A comparison of the individual analyses' CV plots is shown in Figure 6.5. In the morphometric analyses (Fig. 6.5-A, Fig. 6.5-B) AB is closest to WA, though in the ILD analyses, AB is intermediate to WA and AW. Generally, NA and SA are the most different from AB.

Table 6.9. Correct classifications for each of the DFAs ordered by total correct classification. All values are percentages (%).

Dataset	**AB**	**EA**	**NA**	**SA**	**AW**	**WA**	**Total Correct**
Combined Molar Shape and Size	56.8	38.1	57.1	42.9	62.9	47.8	56.4
Combined Molar Shape	49.5	38.1	50.8	42.9	67.7	43.3	55.0
Combined Molar ILD	39.5	39.1	58.7	40.0	61.1	41.1	50.1
Combined Molar ILD PC	43.5	47.8	58.7	40.0	53.9	32.9	47.7

Each of the individual analyses' D^2 matrices is available in Appendix B. The D^2 were subjected to a permutation test. All of the group's D^2 values are significantly different from one another at $p < 0.05$ with the exception of D^2 between EA and SA. American blacks are most similar to WA in the shape analysis. In the size analyses, AB is most similar to AM, followed by WA. In each instance, AB is mostly different from NA, followed by SA. Altogether, AB is intermediate between WA and AW, though more similar to WA in shape and more similar to AW in size.

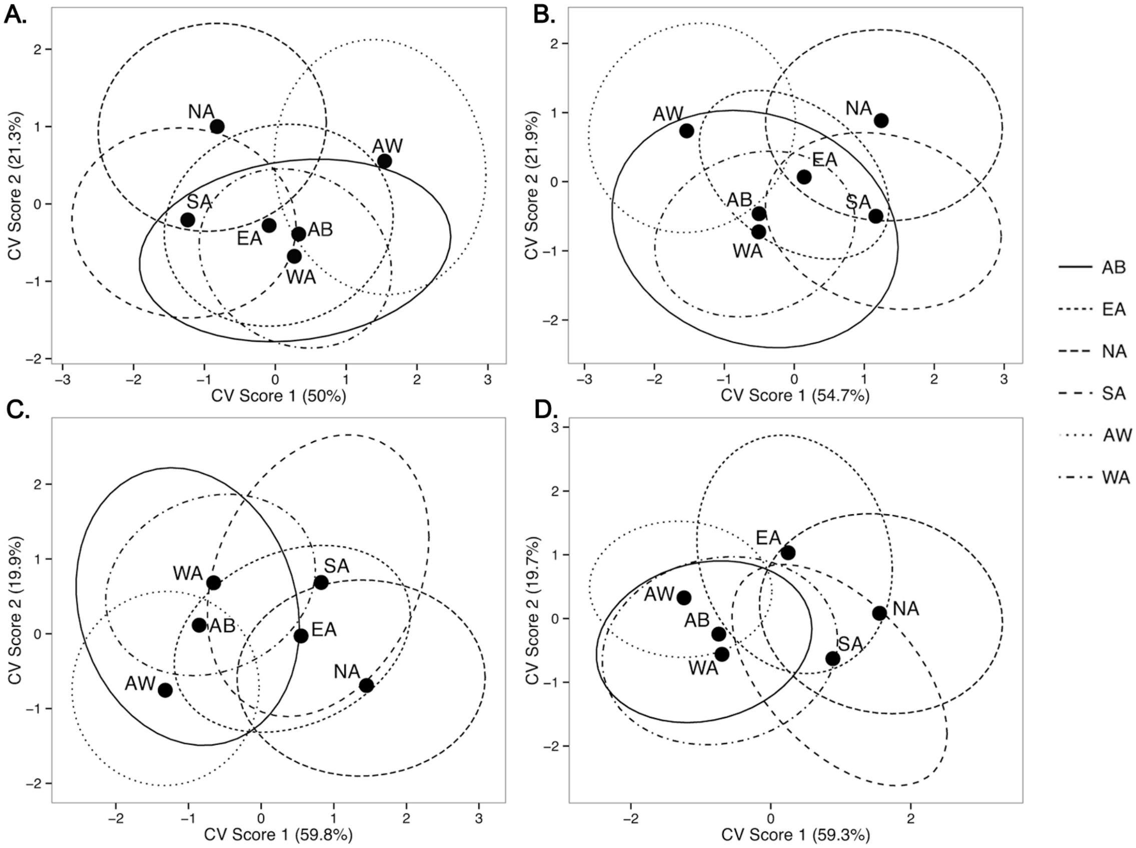


Fig. 6.5. Comparison of canonical variate plots from each of the analyses. The combined molar shape dataset is shown at A, the combined shape and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

6.5.2 Principal Coordinate Analysis

Each of the dataset's D^2 matrices were subjected to a PCO that resulted in three dimensions with eigenvalues greater than zero. The R^2 for the 3D PCOs ranged from 0.91-0.94, which shows that each plot has an acceptable goodness-of-fit to the original distances. The comparison of the 3D PCO perceptual plots is shown in Figure 6.6. While the CV plots showed AB and WA having the greatest affinity, the 3D PCO plots show the uniqueness of AB, specifically in *z* values. The *z* value of AW is more consistent with AB than WA, though the intermediacy of AB between WA and AW is clearly shown. Both of the morphometric-based analyses (Fig. 6.6-A, Fig. 6.6-B) demonstrate a greater affinity of AB to AW, while the ILD analyses (Fig. 6.6-C, Fig. 6.6-D) show a greater affinity of AB to WA. Consistently, NA and SA are the most dissimilar from AB.

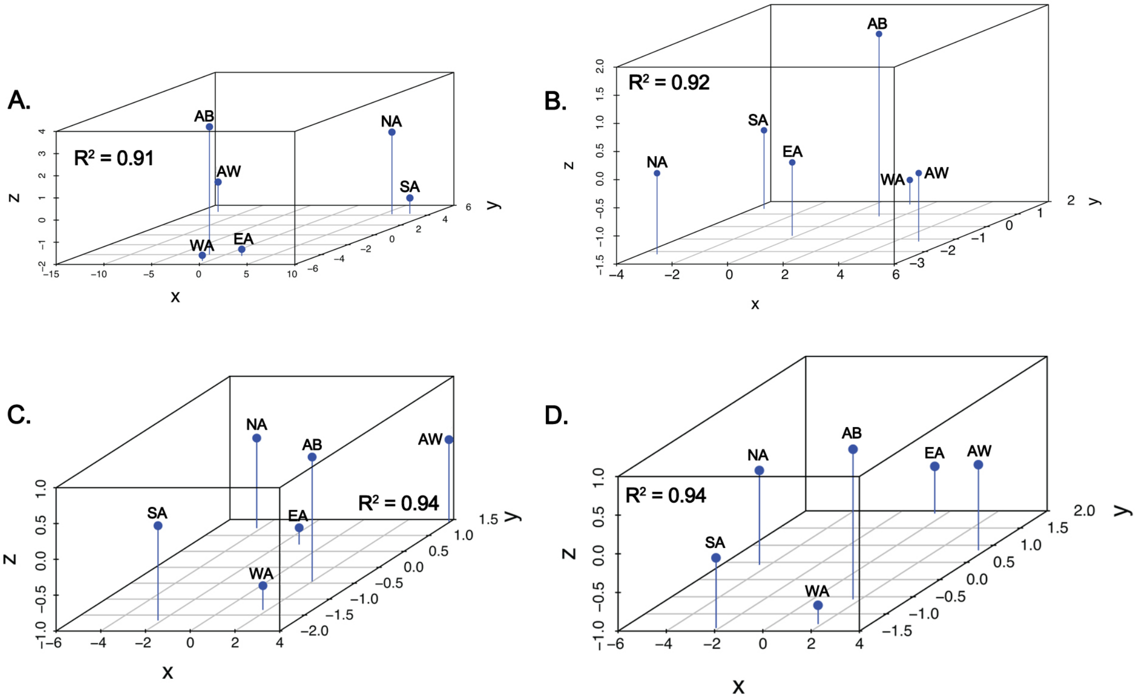


Fig. 6.6. Comparison of three-dimensional PCO perceptual plots for each dataset with individual R^2 values displayed. The PCO of the combined shape PC dataset is shown at A, the combined shape PC and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

6.6 DISCUSSION

American blacks are significantly different from each of the groups based on permutation tests on the Mahalanobis distances. Further, AB consistently clusters with WA and shows intermediacy between WA and AW, thus substantiating Hypothesis 2. The remaining African groups form clusters with one another. The different analyses of shape and size express different trends in affinity. For example, the analyses of the shape PCs demonstrate that AB is most similar to WA, however, when size is added, the distance to WA increased, while the distance to AW decreased. Further, in the ILD analysis, AB and AW share the smallest D^2 value.

The shape analyses have greater total correct classifications than both the ILD and ILD analyses. However, the inclusion of size in the shape analyses boosted model performance even further indicating that both shape and size are important variables. The raw ILDs outperformed the ILD PCs, which may be due to the redundant information present in the PCs of the ILDs as compared to individual linear measures. The PCA of the ILDs could not describe the shape of the molars as well as the Procrustes based analyses. The mandibular first molar demonstrates the greatest discriminating power and variability. Specifically, the distal aspects of M_1 show the greatest variation out of any of the molars (Fig. 6.3). Similarly, M_1 contributed the most variables to the ILD discriminant function and most heavily loaded the first two PCs of the ILD PCA.

6.7 SUMMARY

The total correct classifications range from 47.7% (combined molar ILD PC) to 56.4% (combined molar shape and size). American blacks are a unique group both morphometrically and odontometrically. American blacks show the greatest affinity with WA in the morphometric analyses, but with AW in the ILD analyses. The intermediacy of AB to WA and AW demonstrates the gene flow expressed by the intermarriage rates (Passel et al., 2010; Taylor et al., 2012a), thus supporting Hypothesis 2. The size and shape variables show different trends. For instance, based on shape alone, AB is more similar to WA groups, but with the inclusion of size, and especially in the case of the ILDs, AB shows an increased affinity to AW. Size, then, might be more sensitive to environmental conditions as opposed to shape as the modern AB and WA are from vastly different environments.

CHAPTER 7: MODERN AMERICAN HISPANIC COMPARISON

Modern American Hispanic biohistory was investigated by comparing the modern American Hispanic (AH) data with those from historic Spain (Sp), historic Mexican (Mex), modern American white (AW), and modern American Indian (AI). Some researchers have included African groups when investigating Hispanic populations (Ross et al., 2002); though, their Hispanic sample was primarily derived from Caribbean populations that had contact with peoples of African descent through the slave trade. As discussed in Chapter 3, the American Hispanic sample in the present study is from the American Southwest, and primarily of Mexican descent. Given the population history, American Hispanics should demonstrate intermediacy to historic Spanish and Mexican groups, as well as American whites (Hypothesis 3). Additionally, American Hispanics have the highest intermarriage rates with American whites (Passel et al., 2010; Taylor et al., 2012b). Finally, because the American Hispanic and Indian samples are from the same geographic location (American Southwest), it is likely that these two groups will also demonstrate biological affinity with one another.

7.1 MAXILLARY FIRST MOLAR (M^1)

7.1.1 Descriptive Statistics of Principal Components of Shape

Table 7.1 shows the means and standard deviation for each of the morphometric variables by group. Each group mean was tested against the American Hispanic mean via an independent samples two-tailed t-test. American Hispanics significantly differ from Mex in log centroid size and PC1, from Sp and AW in PC3, and only AW in PC4. American Hispanics have centroid sizes intermediate to Sp and AW that have smaller sizes and Mex that have larger sizes.

Table 7.1. Means and standard deviations for PC scores and log centroid size by group for M^1. Cumulative variance explained is listed under each PC. Group means significantly different from American Hispanics based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M^1 PC1** 35.3%		**M^1 PC2** 61.3%		**M^1 PC3** 82.8%		**M^1 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AI	2.170	0.068	0.001	0.037	0.021	0.049	0.008	0.051	0.004	0.037
AH	2.123	0.078	-0.028	0.053	0.006	0.046	0.014	0.044	0.016	0.037
Sp	2.091	0.053	0.027	0.061	-0.001	0.057	**-0.009**	0.036	-0.013	0.049
Mex	**2.186**	0.061	**0.084**	0.065	0.017	0.048	0.037	0.042	0.001	0.029
AW	2.106	0.073	-0.017	0.062	-0.006	0.051	**-0.010**	0.044	**-0.017**	0.039

7.1.2 Principal Components of Shape

The first principal component accounts for 35.3% of the variance and shows the major movement of the cusp 1 mesiolingually, cusp 2 distolingually, cusp 3 buccally, and cusp 4 distobuccally. Put another way, the negative PC1 values reflect a trapezoidal shape, while the positive PC1 scores show a more rhomboidal shape (Fig. 7.1). Principal component two accounts for an additional 26% of the variance and indicates movement of cusp 1 distolingually, cusp 2 distally, cusp 3 buccally, and cusp 4 mesiolingually. In sum, PC2 shows that negative scores represent longer molars mesiodistally and are compressed buccolingually, while positive PC2 scores show molars compressed mesiodistally and elongated buccolingually (Fig. 7.1).

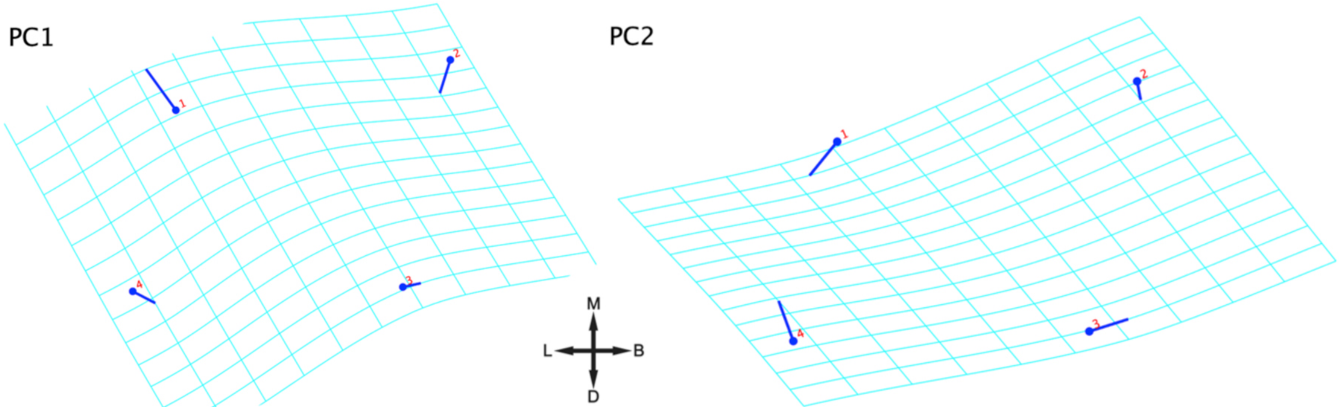


Fig. 7.1. Shape changes associated with PC1 (left) and PC2 (right) of M^1.

7.1.3 Interlandmark Distances (ILDs)

The means and standard deviations for each of the groups ILDs are shown in Table 7.2. American Hispanics demonstrate significantly different means from AW and Mex in the ILDs for cusp 1-2, 1-3, and 1-4. Additionally, AH has significantly different means from Sp and AW for the ILD for cusp 2-3. American Hispanics have ILDs that are larger than AW that consistently has the smallest ILDs, but are not as large as AI or Mex.

Table 7.2. Means and standard deviations for ILDs by group for M^1. Group means significantly different from American Hispanics based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AI	7.3	0.8	7.4	0.7	4.5	0.8	5.8	0.7	9.8	0.8	6.9	0.6
AH	6.8	0.7	7.0	0.8	4.4	0.7	5.9	0.7	9.6	0.9	6.5	0.8
Sp	6.5	0.5	6.8	0.8	4.5	0.8	**5.2**	0.4	9.1	0.7	6.3	0.8
Mex	**7.7**	0.8	**8.3**	0.9	**5.1**	0.8	5.7	0.6	9.6	0.6	6.8	0.8
AW	**6.5**	0.7	**6.7**	0.9	**4.8**	0.8	**5.4**	0.7	9.4	0.9	6.4	0.7

7.1.4 Principal Components of ILDs

The first PC accounts for 47.4% of the variance and is most heavily loaded by the ILD for cusp 2-4, followed by cusp 1-2, then cusp 1-3. The ILD for cusp 2-4 shows the greatest distances while the ILDs for cusp 1-2, and 1-3 has the greatest ranges. The second PC accounts for an additional 16.2% of the variance and is most heavily loaded by the ILD for cusp 1-4, 2-3, and then relatively equally among the remaining ILDs. Thus, both lengths and widths of M^1 contribute to the variance equally.

7.2 MAXILLARY SECOND MOLAR (M^2)

7.2.1 Descriptive Statistics of Principal Components of Shape

Table 7.3 shows the means and standard deviations for each of group's M^2 morphometric variables. Just as with M^1, AH has a significantly smaller centroid size than Mex. Moreover, Mex differs significantly from AH in each of the shape variables. Further, AW significantly differs from AH in PC2 and PC4, which Sp also differs. American Hispanics are again intermediate between the much larger Mex and smaller AW and Sp. Though not significantly different, AH has intermediate PC1 means between Sp and AW.

Table 7.3. Means and standard deviations for PC scores and log centroid size by group for M^2. Cumulative variance explained is listed under each PC. Group means significantly different from American Hispanics based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M^2 PC1** 40.4%		**M^2 PC2** 66.3%		**M^2 PC3** 85.0%		**M^2 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AI	2.073	0.100	-0.026	0.097	0.058	0.076	0.001	0.054	0.034	0.071
AH	2.041	0.102	0.001	0.087	0.019	0.069	-0.008	0.059	0.012	0.055
Sp	1.950	0.131	-0.011	0.125	-0.004	0.103	0.016	0.055	**-0.041**	0.046
Mex	**2.061**	0.079	**-0.084**	0.104	**-0.045**	0.057	**0.056**	0.046	**-0.024**	0.047
AW	2.017	0.097	0.018	0.082	**-0.016**	0.071	-0.003	0.063	**-0.009**	0.051

7.2.2 Principal Components of Shape

The first PC accounts for 40.4% of the variance and is most heavily influenced by the distobuccal movement of cusp 1, slight mesiolingual movement of cusp 2, the mesiobuccal movement of cusp 3, and the lingual movement of cusp 4 (Fig. 7.2). Negative PC1 scores reflect a mesiodistally-compressed rectangle, while positive PC1 scores show more of a buccally oriented trapezoid. Principal component two accounts for an additional 25.9% of the variance and indicates movement of cusp 1 distolingually, cusp 2 mesiobuccally, cusp 3 mesiodistally, and cusp 4 mesiobuccally (Fig. 7.2). Negative PC2 scores show a trapezoid with a comparably longer mesiodistal dimension buccally and positive PC2 scores demonstrate a trapezoidal shape with comparably compressed mesiodistal dimensions lingually.

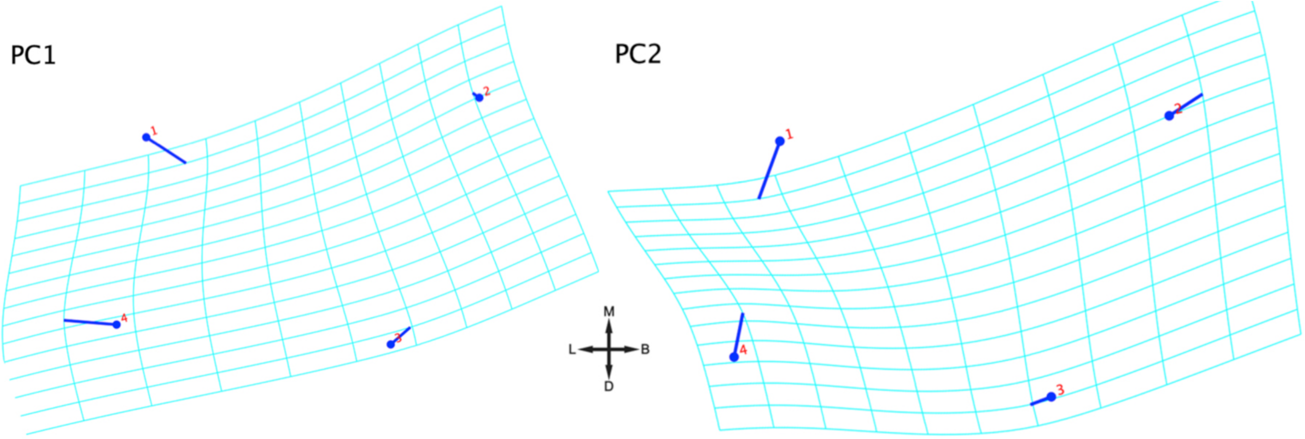


Fig. 7.2. Shape changes associated with PC1 (left) and PC2 (right) of M^2.

7.2.3 Interlandmark Distances (ILDs)

The means and standard deviations for each group's M^2 ILDs are listed in Table 7.4. American Hispanics are significantly different from AW and Mex in the ILDs for cusp 1-2 and 1-4. Historic Mexicans also differ from AH in the ILD for cusp 1-3. Lastly, each of the other groups is significantly different from AH in the ILD for cusp 2-3, wherein AH demonstrate an intermediate mean between AW and AI. The ILDs for M^2 are more variable than those of M^1, especially the lingual aspect, which corroborates the shape change noted for cusps 1 and 4 previously.

Table 7.4. Means and standard deviations for ILDs by group for M^2. Group means significantly different from American Hispanics based on a two-independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AI	7.4	0.8	7.2	0.8	3.8	0.7	**6.1**	0.8	8.7	1.1	5.7	1.0
AH	6.9	0.8	6.8	0.9	4.2	0.8	5.6	0.7	8.7	1.0	5.6	1.0
Sp	6.5	0.8	6.2	0.8	3.9	1.2	**4.7**	0.8	8.1	1.3	5.2	1.2
Mex	**7.3**	0.8	**7.5**	0.7	**4.9**	0.7	**5.0**	0.5	8.3	0.8	5.5	1.1
AW	**6.6**	0.7	6.6	0.9	**4.5**	0.9	**5.3**	0.7	8.6	1.1	5.7	0.9

7.2.4 Principal Components of the ILDs

The first PC accounts for 45.2% of the variance and is most heavily loaded by the ILD for cusp 2-4, followed by 2-3. Similar to the ILDs for M^1, the ILD for cusp 2-4 carry the most weight and is the largest ILD, though is not significantly different between groups. The ILD for cusp 2-3 is the most distinct between groups. The second PC accounts for an additional 17.3% of the variance and is most heavily loaded by the ILD for cusp 3-4, followed by cusps 2-3. Both lengths and breadths of M^2 influence the first two PCs relatively equally.

7.3 MANDIBULAR FIRST MOLAR (M_1)

7.3.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations of the morphometric variables are listed in Table 7.5 for each group. Following previous analyses, AH demonstrates significantly different mean centroid sizes from Mex and AW. American Hispanics differ from AW in PC1 and PC4, and from Mex in PC2 and PC3. Principal components five and six show no significant differences between group means. Just as before, AW has smaller centroid sizes than AH and Mex has larger centroid sizes.

7.3.2 Principal Components of Shape

Principal component one accounts for 27.1% of the variance and demonstrates major movement of cusp 1 distolingually, mesiobuccal movement of cusp 3, mesiolingual movement of cusp 4, and distobuccal movement of cusp 5 (Fig. 7.3). Negative PC1 scores represent molars that are comparably longer mesiodistally and narrower buccolingually. Principal component two contributes an additional 22.9% of the variance and shows the movement of cusp 1 distolingually, cusp 2 mesiobuccally, cusp 3 lingually, cusp 4 distally, and cusp 5 buccally (Fig. 7.3). Negative PC2 scores reflect an M_1 that is more constricted mesiodistally, but broader buccolingually, while positive PC2 scores indicate an elongated mesiodistal dimension lingually and a comparably constricted mesiodistal dimension buccally.

Table 7.5. Means and standard deviations for PC scores and log centroid size by group for M_1. Cumulative variance explained is listed under each PC. Group means significantly different from American Hispanics based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	AI		**AH**		**Sp**		**Mex**		**AW**	
	Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**
Log Centroid Size	2.249	0.075	2.202	0.085	2.149	0.101	**2.257**	0.069	**2.169**	0.07
PC1 27.1%	0.001	0.033	0.007	0.053	-0.003	0.05	0.002	0.051	**-0.007**	0.056
PC2 50.0%	0.002	0.029	0.001	0.047	-0.034	0.056	**-0.045**	0.041	0.006	0.051
PC3 65.6%	0.015	0.035	0.003	0.039	-0.019	0.045	**-0.04**	0.033	0.001	0.043
PC4 79.4%	0.018	0.036	0.01	0.038	-0.005	0.022	0.007	0.032	**-0.012**	0.039
PC5 90.5%	0.016	0.025	0.001	0.03	-0.003	0.027	0.005	0.034	-0.003	0.039
PC6 100%	0.006	0.032	-0.003	0.032	0.002	0.032	-0.01	0.023	0.004	0.03

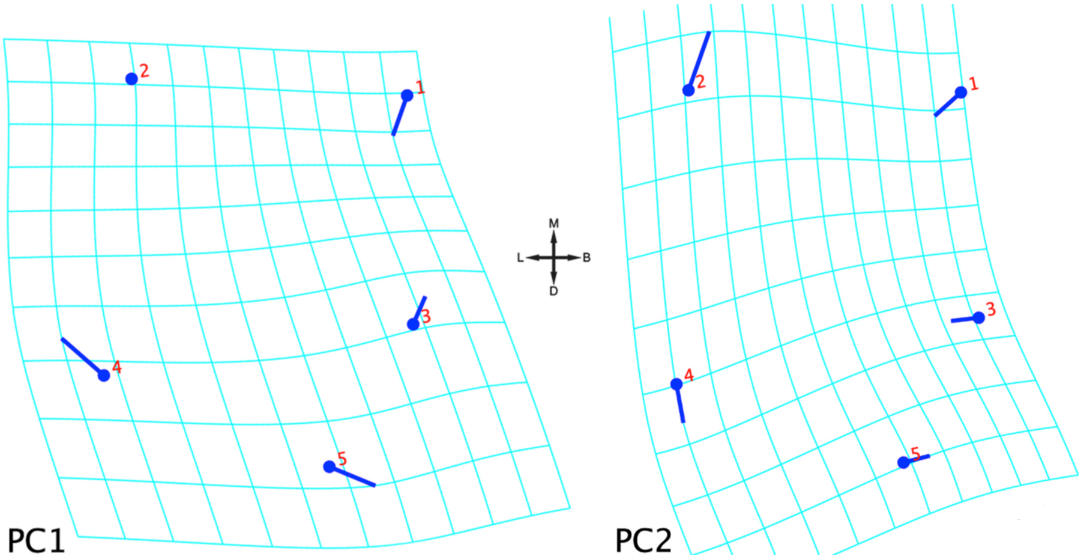


Fig. 7.3. Shape changes associated with PC1 (left) and PC2 (right) of M_1.

7.3.3 Interlandmark Distances (ILDs)

Table 7.6 shows the means and standard deviations for each of the M_1 ILDs, as well as the significance of the group means between AH and all other groups. American Hispanics most commonly differ significantly from Mex, followed by AW. Generally, AW has smaller dimensions than AH and Mex has larger dimensions. Moreover, AH do not significantly differ from AI or Sp in any of the dimensions. Generally speaking, AH has M_1 ILDs that are intermediate to each of the groups.

7.3.4 Principal Components of the Interlandmark Distances

The first PC accounts for 47.9% of the variance and is most heavily loaded by the ILD for cusp 2-5, followed by cusp 3-4, then cusp 1-4. The second PC accounts for an additional 13.6% of the variance and is most heavily loaded by the ILD for cusp 1-3, then cusp 4-5. Both lengths and breadths heavily load the first two PCs. However, breadths, especially diagonal breadths show the most variation in M_1.

Table 7.6. Means and standard deviations for ILDs by group for M_1. Group means significantly different from American Hispanics based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	AI		**AH**		**Sp**		**Mex**		**AW**	
	Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**
Cusp 1-2	5.8	0.6	5.5	0.7	5.5	0.8	**6.1**	0.6	**5.4**	0.6
Cusp 1-3	4.5	0.4	4.5	0.7	4.6	0.6	**5.2**	0.8	**4.7**	0.8
Cusp 1-4	8.6	0.7	8.3	0.8	8.1	1.0	**8.8**	1.1	**8.0**	0.8
Cusp 1-5	7.8	0.6	7.5	0.7	7.7	0.8	**8.3**	0.9	7.6	0.7
Cusp 2-3	7.8	0.7	7.4	0.7	7.2	0.7	**8.0**	1.1	**7.2**	0.7
Cusp 2-4	6.4	0.6	6.0	0.7	5.6	0.7	6.2	0.8	5.9	0.8
Cusp 2-5	9.0	0.7	8.6	0.8	8.4	0.8	**9.1**	0.9	8.5	0.8
Cusp 3-4	6.8	0.7	6.4	0.7	6.1	0.6	**7.0**	0.7	**6.0**	0.7
Cusp 3-5	3.8	0.6	3.4	0.6	3.5	0.7	**3.8**	1.0	3.4	0.7
Cusp 4-5	5.0	0.6	4.9	0.8	4.7	0.6	5.2	0.8	**4.6**	0.8

7.4 MANDIBULAR SECOND MOLAR (M_2)

7.4.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for each of the group's morphometric variables are available in Table 7.7. American Hispanics are significantly different from both AW and Mex in PC1, different from AW in PC3, and from Mex in PC4. Again, AH shows intermediacy in most of the variables between AW and the other groups. Notably, the centroid sizes and PCs were much more variable than previously discussed molars as shown through the greater standard deviations. Even though AH are not significantly different from any group in centroid size, they are smaller than Mex and larger than AW, following suit of previous molar trends.

Table 7.7. Means and standard deviations for shape PCs and centroid size by group for M_2. Cumulative variance explained is listed under each PC. Group means significantly different from American Hispanics based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**PC1** 37.4%		**PC2** 63.6%		**PC3** 83.3%		**PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AI	2.066	0.081	-0.012	0.089	-0.014	0.046	-0.010	0.049	0.007	0.035
AH	2.014	0.099	-0.005	0.069	-0.001	0.056	0.014	0.049	0.001	0.045
Sp	1.995	0.109	0.002	0.038	-0.014	0.044	-0.002	0.044	0.005	0.037
Mex	2.030	0.091	**-0.064**	0.068	0.012	0.043	-0.006	0.043	**-0.029**	0.046
AW	2.001	0.085	**0.015**	0.061	0.001	0.058	**-0.012**	0.051	0.003	0.044

7.4.2 Principal Components of Shape

The first PC accounts for 37.5% of the variance and reflects the movement of cusp 1 mesiolingually, cusp 2 mesiobuccally, cusp 3 distolingually, and cusp 4 distobuccally (Fig. 7.4). The negative PCs show an M_2 shape that is comparably compressed mesiodistally, but elongated buccolingually, as compared to positive PC1 scores. The second PC accounts for an additional 26.2% and shows the major movement of cusp 1 mesiobuccally, cusp 2 distolingually, cusp 3 distobuccally, and cusp 4 mesiolingually (Fig. 7.4). Negative PC2 scores represent a more squared shape, while positive PC2 scores indicate a trapezoidal shape wherein the buccal side is comparatively longer mesiodistally than the lingual side.

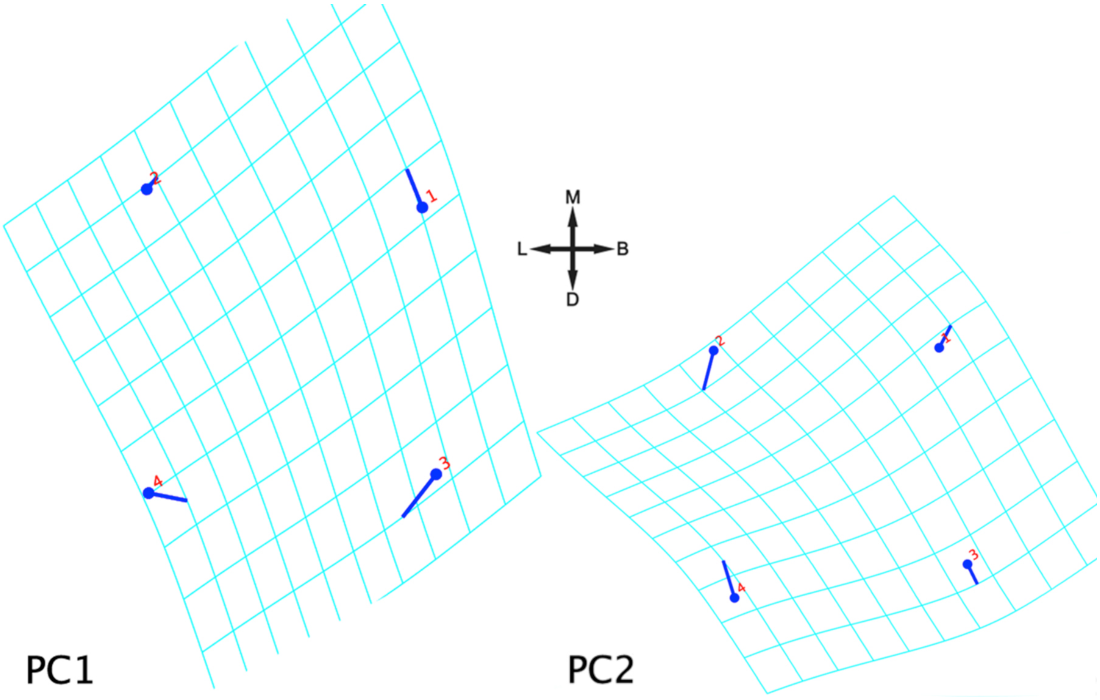


Fig. 7.4. Shape changes associated with PC1 (left) and PC2 (right) of M_2.

7.4.3 Interlandmark Distances (ILDs)

The means and standard deviations for the M_2 ILDs are presented in Table 7.8. American Hispanics only differ from AI in the ILD for cusps 1-4. Further, AH is significantly different from both Mex and AW in the ILD for cusp 3-4. The overwhelming majority of the ILDs demonstrate no significant differences. Notably, the distal aspect of the tooth is more variable than the mesial aspect. However, M_2 shows the least variation out of any of the previously discussed molars.

Table 7.8. Means and standard deviations for ILDs by group for M_2. Group means significantly different from American Hispanics based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AI	5.8	0.6	5.1	0.8	7.9	0.8	**8.3**	0.8	6.2	0.6	6.0	0.8
H	5.4	0.7	5.1	0.8	7.6	0.9	7.7	0.9	5.8	0.8	5.7	0.8
Sp	5.1	0.7	5.0	0.7	7.3	1.5	7.2	1.2	5.9	0.5	5.4	0.8
Mex	5.4	0.7	4.9	0.9	7.6	0.9	7.8	0.8	5.7	0.7	**6.3**	0.7
W	5.3	0.6	5.1	0.8	7.4	0.8	7.8	0.7	5.7	0.7	**5.5**	0.7

7.4.4 Principal Components of ILDs

The first PC accounts for 50.4% of the variance and is most heavily loaded by the ILD for cusp 1-2, followed by 2-3. The second PC accounts for an additional 16.8% of the variance and is most heavily loaded by the ILD for cusp 1-3, followed by cusp 2-4. Contrary to the findings in the raw ILDs for M_2, the mesial aspect of the tooth seemingly demonstrates more variability. However, the increased variability of the mesial aspect of the tooth is likely due to the high standard deviations of each of the ILDs leading to greater variability.

7.5 COMBINED MOLARS

Following previous analyses, each of the morphometric and ILD datasets for each molar was combined. Again, the combined molar ILD dataset was subjected to a PCA to examine the variation across each of the molars, while only the shape PCs and centroid sizes were combined for the morphometric datasets. The combined ILDs yielded 28 principal components. Of the 28 PCs, the first 12 contribute eigenvalues greater than 1 and account for 82.4% of the variance. The first PC accounts for 27.8% of the variance and is most heavily loaded by the ILDs from M_1, specifically, cusp 1-4. The second PC accounts for an additional 14.4% of the variance and is again most heavily loaded by ILDs from M_1, specifically mesiodistal length measures.

7.5.1 Discriminant Function Analysis

Table 7.9 shows the total correct classifications for each of the datasets. Each of the individual analyses' classification matrices is available in Appendix C. The combined molar ILD has the highest correct classification, followed by the combined molar shape PC and size dataset. Each of the discriminant function coefficients is heavily influenced by both shape and size variables of M^1. In fact, in the combined molar shape and size DFA, the only size variable stepwise selected was M^1 centroid size. In each of the analyses, AH classifies mostly correctly, but consistently misclassifies most commonly as AI, followed by AW, then Sp, but rarely as Mex. A comparison of each of the DFA's CV plots is shown in Figure 7.5. In shape only (Fig. 7.5-A), AH is intermediate to AW, AI, and Sp. However, with size included, AH is more dissimilar to Sp and more similar to AI. Across the board, AH is intermediate to AI and AW.

Table 7.9. Correct classifications for each of the DFAs ordered by total correct classification. All values are percentages (%).

Dataset	AI	AH	Sp	Mex	AW	Total Correct
Combined Molar ILD	57.9	43.0	27.3	81.5	55.7	50.7
Combined Molar Shape and Size	63.2	45.8	30.0	84.0	47.6	49.3
Combined Molar ILD PC	57.9	32.0	27.3	77.8	54.5	44.8
Combined Molar Shape	52.6	37.0	30.0	72.0	39.0	40.5

The D^{2-} matrices for each of the analyses are available in Appendix C. As in previous chapters, the D^2 values were subjected to a permutation test. The majority of the distances are significant at $p < 0.05$. Notably, AH and AI have non-significant means in both the combined shape PC and ILD PC analyses. In each instance, AH are most similar to AI, followed by AW, and then Sp, and are most dissimilar to Mex. In sum, AH is most similar to AI, especially in regards to shape, though the inclusion of size makes AH unique to AI.

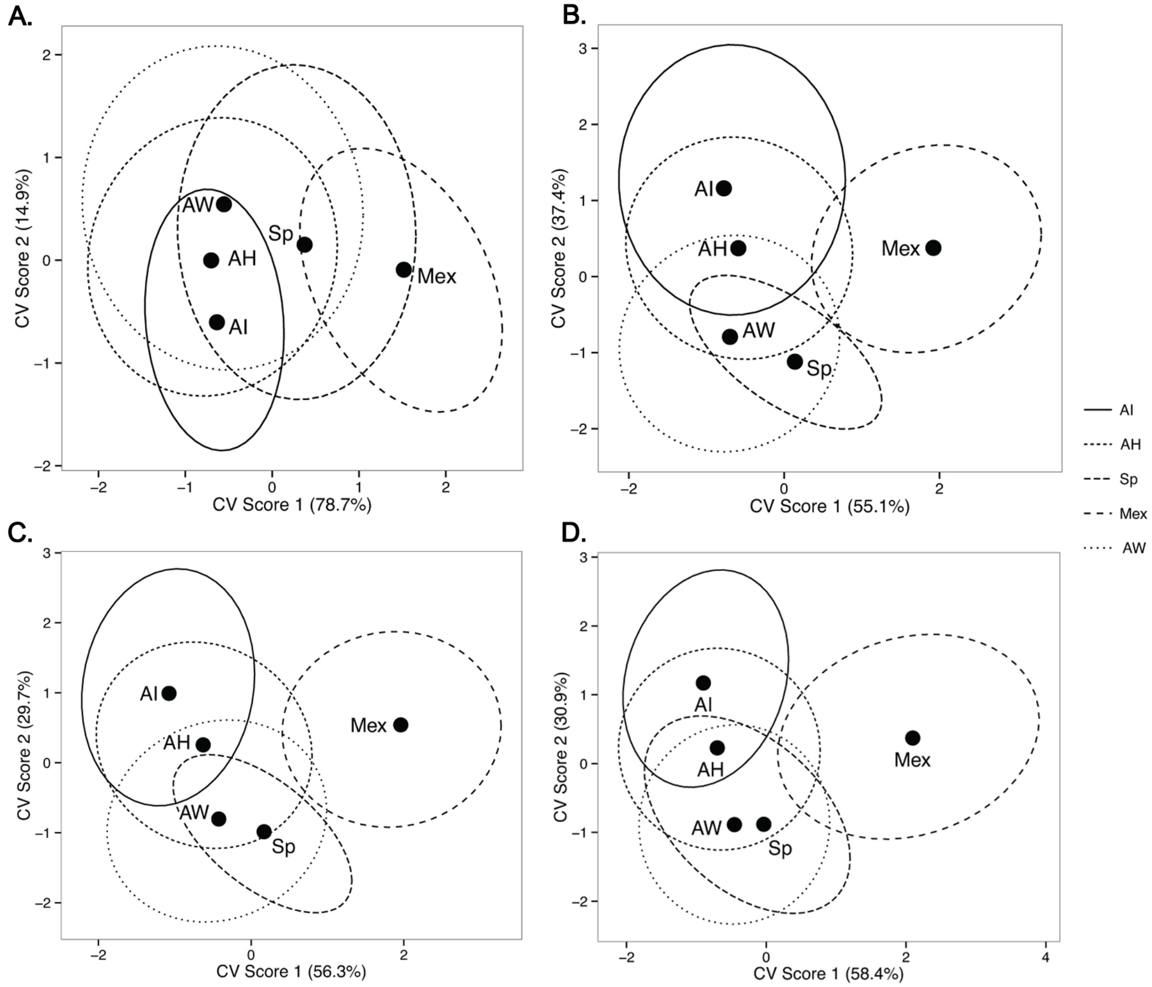


Fig. 7.5. Comparison of canonical variate plots from each of the analyses. The combined molar shape dataset is shown at A, the combined shape and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

7.5.2 Principal Coordinate Analysis

Each dataset's D^2 matrix was subjected to a PCO. Both morphometric-based analyses resulted in only two dimensions with eigenvalues greater than zero. A comparison of the 2D PCO perceptual plot is shown in Figure 7.6. The R^2 values are 0.94 for the combined shape PC dataset and 0.95 for the combined shape PC and size dataset, indicating a great goodness-of-fit to the original distances. In the shape PC PCO, AH is intermediate to AW, Sp, and AI, showing affinity with each of the groups (Fig. 7.6-A). Though, when size was included, Sp shows greater affinity to AW as opposed to AH. The PCO of each of the ILD datasets resulted in three dimensions with eigenvalues greater than zero and are shown in Figure 7.7. The R^2 values are 0.98 for the ILD dataset, and 0.95 for the ILD PC dataset, indicating excellent goodness-of-fit. The 3D PCO plot of the ILD dataset show AH being intermediate to AW and AI in each dimension, thus showing the affinity to both groups (Fig. 7.7-A). The ILD PC dataset shows the uniqueness of AH compared to AI and AW with a much lower *z* value. Just as in the 2D MDS, Mex are most dissimilar from each of the groups. In total, AH has the greatest affinity with AI and AW.

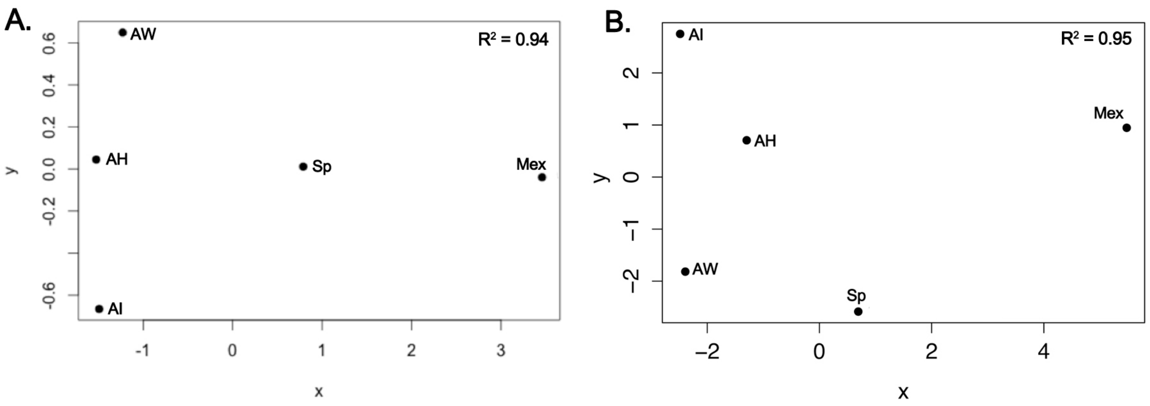


Fig. 7.6. Comparison of two-dimensional PCO perceptual plots for each morphometric dataset with individual R^2 values displayed. The PCO of the combined shape PC dataset is shown at A and the combined shape PC and size dataset at B.

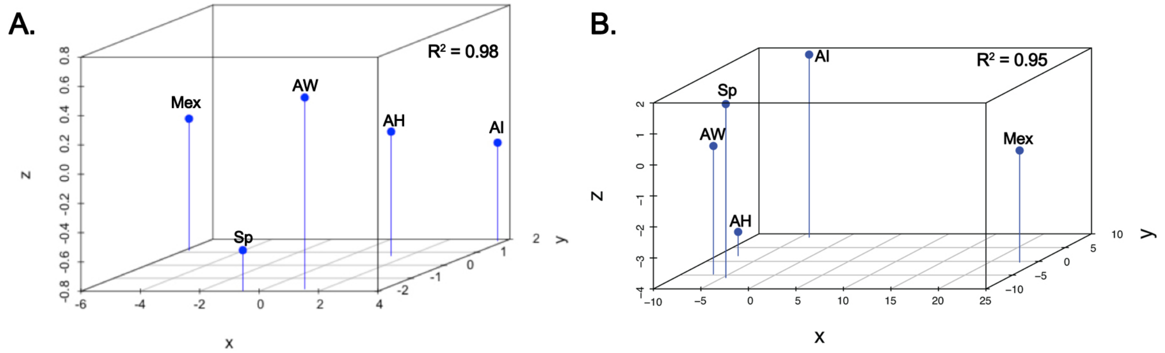


Fig. 7.7. Comparison of three-dimensional PCO perceptual plots for each ILD dataset with individual R^2 values displayed. The PCO of the combined ILD dataset is shown at A and the combined ILD PC and size dataset at B.

7.6 DISCUSSION

The analyses with size demonstrated higher total correct classifications than the shape analyses, which may describe different patterns of inheritance of size and shape. The shape analyses show the intermediacy of AH to AI, AW, and Sp, while the inclusion of size indicates a greater dissimilarity between Sp and AH. The historic Mexican group is consistently the most dissimilar group in both size and shape, which indicates a greater divergence from this population and more gene flow with modern groups, specifically AI and AW. American Hispanics are not significantly different from AI in the shape analyses (shape PCs and ILD PCs), but are significantly different from AI in both of the size analyses (shape PCs with centroid size and ILDs), thus showing the importance of size variation when examining highly admixed population groups. The influence of size on discriminating between highly admixed populations was also noted in previous chapters, but was notably present in the American Asian analyses in Chapter 5.

The similarity between American Hispanics and Indians could be due to proximity as the specimens for both of these groups came from the same collection (ASU Economides collection). In addition to proximity, the ancestries prescribed at the Economides collection were done post-hoc by two independent observers based on skin color, name, and location (Edgar et al., 2011). The ambiguous way in which ancestry was assigned likely caused noise in the data and thus higher misclassification rates, particularly between American Hispanics and Indians.

7.7 SUMMARY

The correct classifications for the AH population history range from 40.5% (combined molar shape) to 50.7% (combined molar ILD). In each analysis, Mex has the highest correct classifications and Sp has the lowest. The size centric analyses achieve higher total correct classifications than the shape centric analyses, which suggest size is more informative than shape in highly admixed populations. Further, even due to the high levels of admixture and nebulous group definition, American Hispanics are significantly different from potential parent populations and AW, thus demonstrating their relative distinctiveness as a group. However, AH did show intermediacy between AI and AW, though only showed affinity with Sp in one analysis, and was consistently the most dissimilar from Mex, thus not supporting Hypothesis 3. Instead, the proximity of the samples (AI and AH), as well as the nebulous way in which ancestry was assigned at the Economides collection, explains the similarity between AH and AI. Further, affinity of AH and AW confirms the known intermarriage rates between the two groups (Passel et al., 2010; Taylor et al., 2012b).

CHAPTER 8: MODERN AMERICAN WHITE COMPARISON

Modern American white biohistory was examined by comparing data from modern American whites (AW) with American Asians (AA), American Indians (AI), American Blacks (AB), historic Europeans (EU), and American Hispanics (AH). Given the homogeneity of dental morphology found within Europe, in conjunction with the admixture of European groups in the United States historically, American whites should be the most similar to the European group (Hypothesis 4). Additionally, given the intermarriage rates in the U.S., American whites should be the most similar to American Hispanics, and least similar to American blacks.

8.1 MAXILLARY FIRST MOLAR (M^1)

8.1.1 Descriptive Statistics of Principal Components of Shape

Table 8.1 lists the means and standard deviations for each of the morphometric variables by group. Each group mean was tested against the AW mean with a two-tailed independent samples t-test. American whites have significantly different centroid sizes from AA, AI, and AH; different PC1 scores from AB, AH, and EU; PC2 scores from AA, AI, and AB; PC3 scores from AA, AI, AH, and EU; and PC4 from AB and AH. American whites have the smallest centroid sizes. Across the board, AW has the least amount of significant differences with EU.

Table 8.1. Means and standard deviations for PC scores and log centroid size by group for M^1. Cumulative variance explained is listed under each PC. Group means significantly different from American whites based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M^1 PC1** 34.2%		**M^1 PC2** 62.4%		**M^1 PC3** 84.0%		**M^1 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	**2.157**	0.065	0.013	0.046	**-0.013**	0.041	**-0.007**	0.038	-0.006	0.035
AI	**2.169**	0.066	0.009	0.039	**-0.013**	0.046	**0.017**	0.052	0.002	0.032
AB	2.092	0.091	**-0.031**	0.064	**-0.013**	0.064	0.016	0.050	**0.004**	0.037
EU	2.096	0.076	**-0.041**	0.069	0.005	0.046	**-0.004**	0.041	-0.015	0.042
AH	**2.121**	0.078	**0.026**	0.052	0.005	0.047	**-0.023**	0.045	**0.013**	0.037
AW	2.084	0.073	0.002	0.058	0.016	0.051	0.017	0.040	-0.008	0.041

8.1.2 Principal Components of Shape

Principal component one accounts for 34.2% of the variance and indicates the major movement of the cusp 1 distobuccally, cusp 2 mesiobuccally, cusp 3 lingually, and cusp 4 mesiolingually (Fig. 8.1). In sum, negative PC1 scores represent a rhomboidal shape (EU), while positive PC1 scores reflect a more trapezoidal shape (AH). The second PC accounts for an additional 28.2% of the variance and shows the mesiobuccal movement of cusp 1, mesiolingual movement of cusp 2, lingual movement of cusp 3 and the distobuccal movement of cusp 4 (Fig. 8.1). Overall, negative PC2 scores demonstrate a mesiodistally compressed rectangular molar (AA, AI, AB), while positive PC2 scores show a more rhomboidal molar (AW).

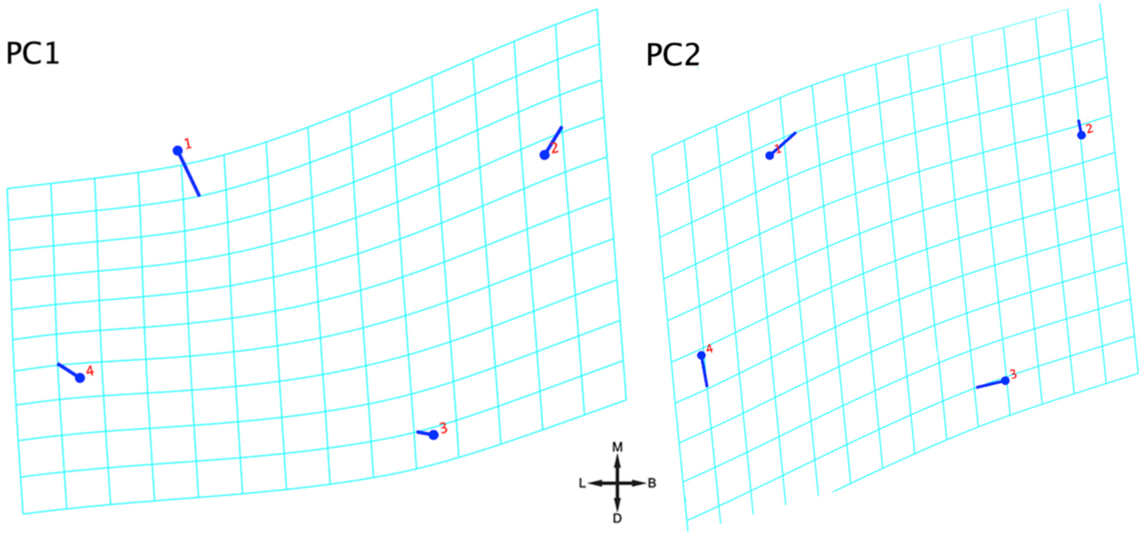


Fig. 8.1. Shape changes associated with P1 (left) and PC2 (right) of M^1.

8.1.3 Interlandmark Distances (ILDs)

Group means and standard deviations for the ILDs of M^1 are compiled in Table 8.2. American whites are most commonly significantly different from AA, wherein only one ILD (cusp 1-4) was comparable. American whites have the least significant differences with the EU group, where both groups consistently have the smallest dimensions. The ILD for cusps 1-3 is the most distinct in AW and is consistent with the distobuccal movement of cusp 1 noted earlier.

8.1.4 Principal Components of ILDs

The first PC accounts for 45.5% of the variance and is most heavily loaded by the ILD for cusps 2-4, followed by cusps 1-3, which are the largest two ILDs. The second principal component accounts for an additional 17.5% of the variance and is mostly loaded by the ILD for cusp 1-4. Overall, PC1 accounts for the diagonal distances indicating the importance of both lengths and breadths, while PC2 focused on mesiodistal length measures.

Table 8.2. Means and standard deviations for ILDs by group for M^1. Group means significantly different from American whites based on a two-tailed Student's t-test in bold (p < 0.05). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	**7.2**	0.6	**7.2**	0.8	4.7	0.7	**5.8**	0.7	**9.8**	0.9	**6.9**	0.6
AI	**7.3**	0.8	**7.5**	0.7	4.5	0.8	**5.9**	0.7	9.8	0.8	**6.9**	0.6
AB	6.5	0.8	**7.2**	0.8	**5.0**	0.8	5.3	0.8	9.3	0.9	**6.6**	0.8
EU	6.7	1.0	**7.1**	0.9	4.9	0.9	5.3	1.0	9.1	1.0	6.3	0.8
AH	**6.8**	0.7	**7.0**	0.8	**4.5**	0.8	**5.9**	0.7	9.5	0.9	6.5	0.8
AW	6.5	0.7	6.7	0.8	4.8	0.7	5.3	0.6	9.3	0.9	6.4	0.7

8.2 MAXILLARY SECOND MOLAR (M^2)

8.2.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for each of the group's M^2 morphometric variables are tabulated in Table 8.3. American whites are significantly different from AA in centroid size, wherein AA has much larger M^2 centroids compared to AW. American whites only differ from EU in PC1; differ from AA, AI, and AH in PC2; from AA and AB in PC3 scores; and AI, AH and EU in PC4 scores. American whites have smaller centroid sizes compared to the rest of the groups, with the exception of EU that showed the smallest centroids.

Table 8.3. Means and standard deviations for PC scores and log centroid size by group for M^2. Cumulative variance explained is listed under each PC. Group means significantly different from American whites based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M^2 PC1** 34.3%		**M^2 PC2** 59.3%		**M^2 PC3** 83.4%		**M^2 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	**2.067**	0.093	-0.003	0.073	**0.015**	0.064	**-0.008**	0.066	0.005	0.056
AI	2.073	0.100	-0.034	0.010	**0.047**	0.072	-0.020	0.056	**0.041**	0.070
AB	2.042	0.110	0.008	0.087	-0.025	0.076	**-0.018**	0.082	-0.005	0.062
EU	2.000	0.237	**-0.029**	0.119	-0.017	0.073	0.001	0.070	**-0.040**	0.061
AH	2.040	0.010	-0.005	0.086	**0.021**	0.068	0.005	0.063	**0.016**	0.057
AW	2.016	0.097	0.013	0.086	-0.008	0.069	0.020	0.066	-0.008	0.052

8.2.2 Principal Components of Shape

Principal component one accounts for 34.3% of the variance and details the movement of cusp 1 distobuccally, no movement of cusp 2, mesiobuccal movement of cusp 3, and the lingual movement of cusp 4 (Fig. 8.2). Overall, negative PC1 scores represent a more trapezoidal molar with an elongated mesiodistal aspect buccally (AI, EU), whereas positive PC1 scores reflect a more rhomboidal shape, again with a comparatively longer buccal aspect (AW). The second PC accounts for an additional 25.0% of the variance and shows the movement of cusp 1 mesiobuccally, cusp 2 distolingually, cusp 3 buccally, and cusp 4 distolingually (Fig. 8.2). More generally, negative PC2 scores display a much more compressed lingual aspect mesiodistally (AB, EU, AW), while positive PC2 scores again show a less compressed rhomboidal shape (AA, AI, AH).

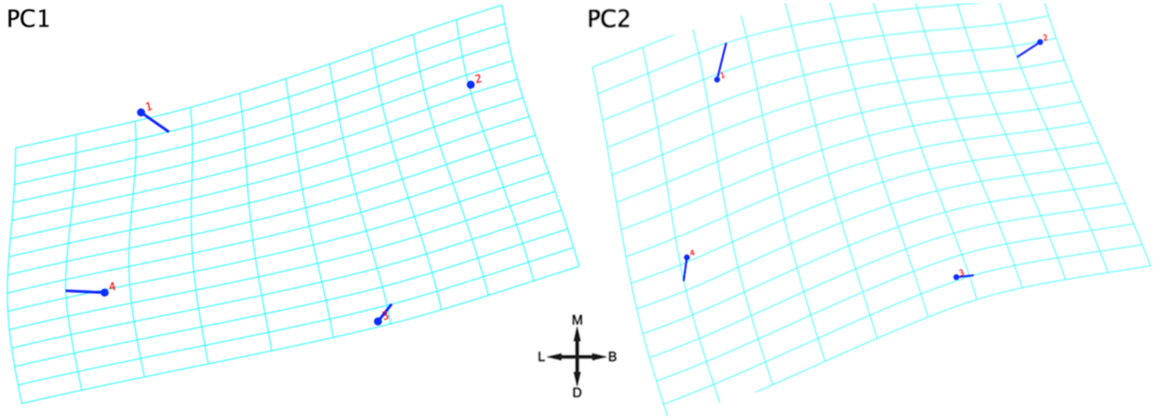


Fig. 8.2. Shape changes associated with P1 (left) and PC2 (right) of M^2.

8.2.3 Interlandmark Distances (ILDs)

Table 8.4 lists the means and standard deviations for M^2 by group. American whites have significantly different ILDs for cusp 1-2 from each of the groups except EU; both AW and EU have smaller cusp 1-2 ILDs than each of the other groups. Next, AA and AB have significantly greater ILDs for cusp 1-3 from AW. The ILD for cusp 1-4 is significantly different between AW and AA, AI, and AH, in which AW has larger ILDs. The ILD for cusp 2-3 is significantly larger in each of the groups as compared to AW except for AB. The ILD for cusp 2-4 is only significantly different between AW and EU that has smallest values. Lastly, the ILD for cusp 3-4 is significantly different in AB that has larger values, and EU that has smaller values. American whites typically demonstrate ILDs intermediate between historic Europeans and the other American groups.

Table 8.4. Means and standard deviations for ILDs by group for M^2. Group means significantly different from American whites based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	**7.2**	0.7	**7.0**	0.8	**4.2**	0.7	**5.6**	0.7	8.9	1.0	5.8	0.9
AI	**7.4**	0.8	7.2	0.8	**3.8**	0.7	**6.1**	0.8	8.8	1.2	5.7	1.0
AB	**6.9**	0.9	**7.1**	1.9	4.7	1.1	5.5	0.8	8.9	1.2	**6.0**	1.1
EU	6.5	0.7	6.3	0.8	4.3	1.4	**4.9**	0.8	**8.2**	1.0	**5.2**	1.0
AH	**6.9**	0.8	6.8	0.9	**4.2**	0.7	**5.6**	0.7	8.7	1.0	5.6	1.0
AW	6.6	0.7	6.6	0.9	4.5	0.9	5.3	0.7	8.6	1.1	5.7	0.9

8.2.4 Principal Components of ILDs

Principal component one accounts for 45.4% of the variance and is most heavily loaded by the ILD for cusp 2-4, followed by 1-3, just as with the ILDs of M^1. The second PC accounts for an additional 16.7% of the variance and is most heavily loaded by the ILD for cusp 1-4, followed by 2-3, again, similar to PC2 of M^1. The length measures contribute more than breadth measures showing the variability in the mesiodistal dimension of M^2.

8.3 MANDIBULAR FIRST MOLAR (M_1)

8.3.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for the morphometric variables of M_1 are listed in Table 8.5. American whites differ significantly from each of the groups sans EU in centroid size. Just as in previously discussed molars, AW and EU have smaller centroids than other groups. Principal component one only differs between AW and AA. Next, PC2 differs between AW and AA, AB, and EU. The third PC is significantly different between AW and both AB and EU. The only group not significantly different from AW in PC4 is AI. Similarly, only EU is significantly different from AW in PC5. There are no significant differences between group means in PC6. Like in the previously discussed morphometric analyses, AW most frequently has significant differences with AA.

Table 8.5. Means and standard deviations for PC scores and log centroid size by group for M_1. Cumulative variance explained is listed under each PC. Group means significantly different from American whites based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	AA		AI		AB		EU		AH		AW	
	Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**
LCS	**2.222**	0.066	**2.249**	0.075	**2.197**	0.081	2.181	0.088	**2.202**	0.085	2.168	0.071
PC1	**-0.01**	0.045	0.002	0.034	0.007	0.060	0.009	0.045	-0.007	0.053	0.006	0.055
PC2	**0.008**	0.048	-0.016	0.029	**0.019**	0.049	**0.042**	0.05	-0.013	0.046	-0.016	0.053
PC3	-0.004	0.039	-0.012	0.034	**-0.008**	0.043	**0.03**	0.049	-0.002	0.039	0.007	0.04
PC4	**0.011**	0.038	0.007	0.037	**-0.001**	0.039	**0.009**	0.042	**0.005**	0.038	-0.015	0.04
PC5	**-0.005**	0.030	**-0.012**	0.028	**-0.011**	0.036	0.003	0.034	**0.001**	0.03	0.012	0.039
PC6	-0.002	0.030	0.011	0.03	0.006	0.034	-0.007	0.037	-0.003	0.033	0.001	0.031

8.3.2 Principal Components of Shape

The first PC of M_1 accounts for 26.8% of the variance and demonstrates the movement of cusp 1 mesiobuccally, no significant movement of cusp 2, distolingual movement of cusp 3, distobuccal movement of cusp 4, and mesiolingual movement of cusp 4 (Fig. 8.3). In total, negative PC1 scores represent an M_1 that is more elongated mesiodistally and has a more buccally oriented hypoconulid (AA), while positive PC1 scores represent longer molars mesiodistally with compressed distal breadths and a more mesiolingually-situated hypoconulid (AW). Principal component two accounts for an additional 22.1% of the variance. The shape changes associated with PC2 show the mesiobuccal movement of cusp 1, the distolingual movement of cusp 2, the buccal movement of cusp 3, mesiolingual movement of cusp 4, and the lingual movement of cusp 4

(Fig. 8.3). Negative PC2 scores show comparably narrower molars buccolingually (AH, AW), while positive PC2 scores are compressed distolingually on the lingual aspect of the tooth (AB, EU).

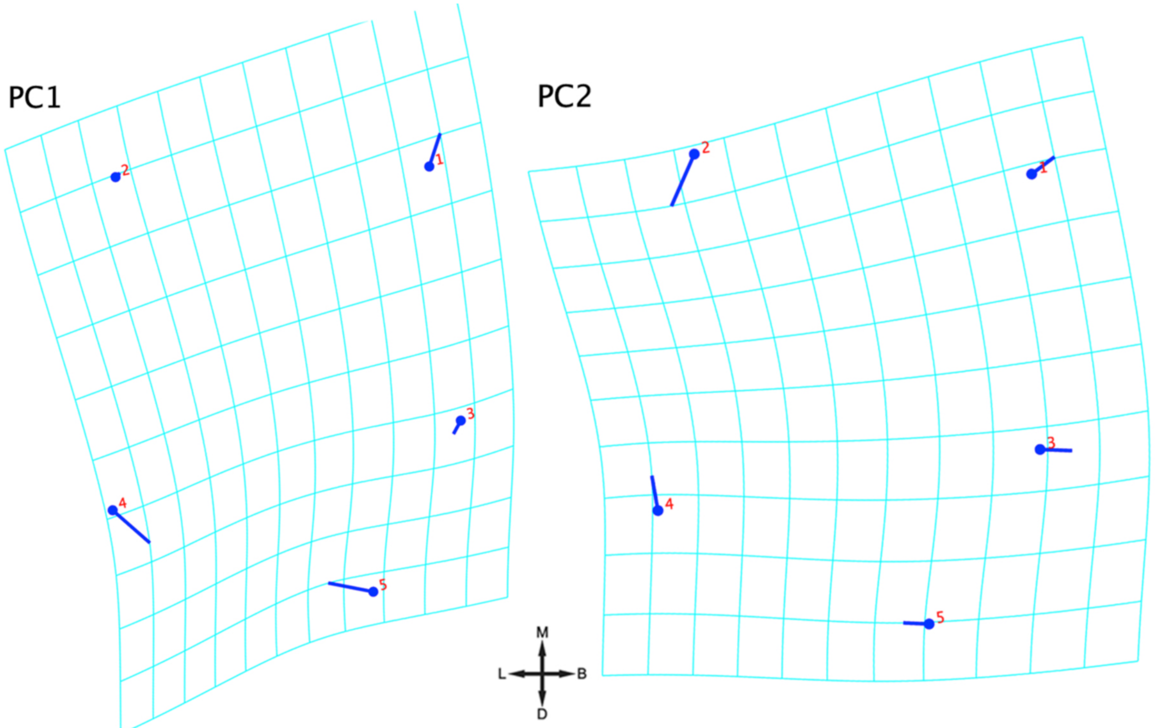


Fig. 8.3. Shape changes associated with P1 (left) and PC2 (right) of M_1.

8.3.3 Interlandmark Distances (ILDs)

The means and standard deviations for the ILDs of M_1 are listed in Table 8.6. American whites have the most significantly different mean ILDs from AH, followed by AA, and then AB. The most unique ILDs to AW are from cusps 1-4, 2-3, and 3-4, in which all of the groups are significantly different from AW. In each of the aforementioned ILDs, AW has consistently smaller ILDs than the rest of the groups.

Table 8.6. Means and standard deviations for ILDs by group for M_1. Group means significantly different from American whites based on a two-tailed Student's t-test in bold ($p < 0.05$). All measurements in mm.

	AA		**AI**		**AB**		**EU**		**AH**		**AW**	
	Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**
Cusp 1-2	**5.7**	0.6	5.8	0.6	**5.6**	0.6	**5.8**	0.9	**5.5**	0.7	5.4	0.6
Cusp 1-3	4.5	0.6	4.5	0.4	4.5	0.6	4.9	0.6	**4.5**	0.7	4.7	0.8
Cusp 1-4	**8.4**	0.8	**8.6**	0.7	**8.4**	0.8	**8.4**	0.9	**8.3**	0.8	8.0	0.8
Cusp 1-5	7.6	0.6	7.8	0.6	7.8	0.8	7.8	0.7	7.5	0.7	7.6	0.7
Cusp 2-3	**7.6**	0.6	**7.8**	0.7	**7.5**	0.7	**7.7**	0.9	**7.4**	0.7	7.2	0.7
Cusp 2-4	5.9	0.7	6.4	0.6	5.9	0.7	5.7	0.6	6.0	0.7	5.9	0.8
Cusp 2-5	8.7	0.8	**9.1**	0.7	8.5	0.9	8.5	0.8	8.6	0.8	8.5	0.8
Cusp 3-4	**6.7**	0.6	**6.8**	0.7	**6.5**	0.8	**6.4**	0.7	**6.4**	0.7	6.0	0.7
Cusp 3-5	3.6	0.5	3.8	0.6	**3.9**	0.6	3.4	0.5	3.4	0.6	3.4	0.7
Cusp 4-5	**5.0**	0.8	4.9	0.6	4.7	0.8	4.7	0.6	**4.9**	0.8	4.6	0.8

8.3.4 Principal Components of ILDs

The first PC accounts for 47.0% of the variance and is most heavily loaded by the ILDs for cusp 1-4, followed by 2-5. An additional 13.6% of the variance is accounted by PC2, which is most heavily loaded by the ILDs for cusps 1-3, followed by cusp 3-5. Again, both lengths and breadths, focusing on diagonals, represent in the majority of the variation of M_1.

8.4 MANDIBULAR SECOND MOLAR (M_2)

8.4.1 Descriptive Statistics of Principal Components of Shape

The individual group means and standard deviations of M_2 are listed in Table 8.7. American whites have the most significantly different means from both AA and AB. American whites differ significantly in centroid size from AA, AI, and AB, all of which have larger centroid sizes than AW. Lastly, AW significantly differs in PC1 and PC3 from AA, AB, and AH. Again, AW has the smallest teeth of any of the American groups with only EU demonstrating smaller molars.

Table 8.7. Means and standard deviations for PC scores and log centroid size by group for M_2. Cumulative variance explained is listed under each PC. Group means significantly different from American whites based on a two-tailed independent samples t-test in bold ($p < 0.05$).

	Log Centroid Size		**M_2 PC1** 38.8%		**M_2 PC2** 63.9%		**M_2 PC3** 83.4%		**M_2 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	**2.031**	0.077	**-0.005**	0.072	-0.001	0.058	**0.001**	0.050	0.005	0.049
AI	**2.066**	0.081	-0.001	0.090	0.017	0.045	-0.017	0.049	0.005	0.034
AB	**2.036**	0.091	**-0.021**	0.077	-0.001	0.055	**0.011**	0.052	0.001	0.048
EU	1.967	0.121	-0.008	0.073	-0.019	0.053	-0.010	0.050	-0.014	0.052
AH	2.014	0.099	**0.002**	0.070	0.007	0.056	**0.009**	0.049	-0.001	0.045
AW	2.001	0.085	0.021	0.060	-0.002	0.059	-0.016	0.051	0.001	0.044

8.4.2 Principal Components of Shape

The first principal component accounts for 38.8% of the variance and indicates movement of cusp 1 mesiolingually, cusp 2 mesiobuccally, cusp 3 distolingually, and cusp 4 distobuccally (Fig. 8.4). In sum, negative PC1 scores show molars that are comparably compressed mesiodistally and elongated buccolingually (AA, AB) as opposed to positive PC1 scores (AH, AW). Principal component two accounts for an additional 25.0% of the variance and demonstrates movement of cusp 1 distolingually, cusp 2 mesiobuccally, cusp 3 mesially, and cusp 4 distally (Fig. 8.4). Negative PC2 scores are show comparably longer mesiodistal dimensions buccally and compressed mesiodistal dimensions lingually (EU, AW, AA, AB) as compared to positive PC2 scores (AH).

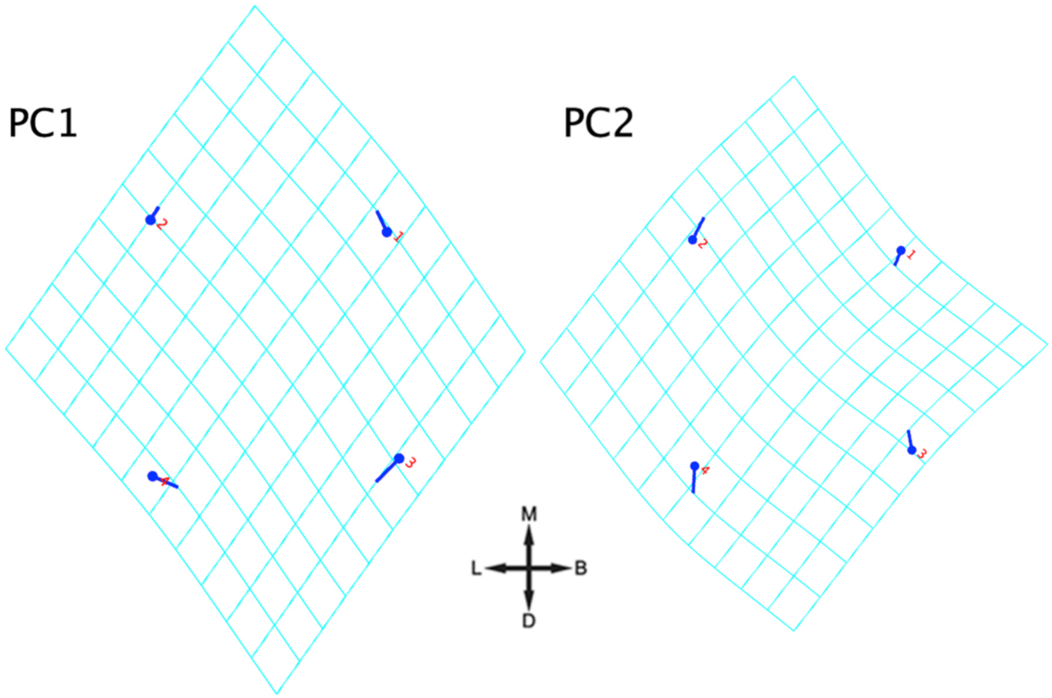


Fig. 8.4. Shape changes associated with P1 (left) and PC2 (right) of M_2.

8.4.3 Interlandmark Distances (ILDs)

The group means and standard deviations for the ILDs of M_2 are presented in Table 8.8. American whites have the most significant differences with AA. In the majority of the ILDs, AW has smaller ILDs than the other American groups, but larger ILDs than EU. Each of the ILDs has significant differences between American whites and at least one group with the exception for the ILD for cusp 1-3, which has little variation among groups. The ILD for cusp 1-2 is the most variable, with AA, AI, and AB all showing significant differences with AW.

Table 8.8. Means and standard deviations for ILDs by group for M_2. Group means significantly different from American whites based on a two-tailed independent samples t-test in bold ($p < 0.05$). All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	**5.6**	0.6	5.1	0.7	**7.7**	0.7	7.9	0.7	5.8	0.7	**5.8**	0.7
AI	**5.8**	0.6	5.1	0.8	7.9	0.8	**8.3**	0.8	6.2	0.6	6.0	0.8
AB	**5.5**	0.7	5.1	0.8	**7.9**	0.8	7.8	0.8	5.7	0.8	**6.0**	0.8
EU	5.1	0.8	4.9	0.7	7.2	1.0	**7.4**	1.0	**5.4**	0.8	5.6	1.0
AH	5.4	0.7	5.1	0.8	7.6	0.9	7.7	0.9	5.8	0.8	**5.7**	0.8
AW	5.3	0.6	5.1	0.8	7.4	0.8	7.8	0.7	5.7	0.7	5.5	0.7

8.4.4 Principal Components of ILDs

The first PC accounts for 51.7% of the variance and is most heavily loaded by the ILD for cusp 1-4, followed by cusp 2-3, both of which are the largest ILDs in M_2. An additional 17.1% of the variance is accounted for by PC2 that is most heavily loaded by cusp 1-3. Both of the first two PCs indicate that length contributes most to the variation in M_2, but the diagonal measures in PC1 do show that breadth is also important.

8.5 COMBINED MOLARS

The PCA of the combined molar ILDs resulted in 28 PCs. The first 12 PCs contribute eigenvalues greater than one and account for 83.5% of the variance. The first PC accounts for 24.1% of the variance and is most heavily loaded by the ILD for M_1 1-4, followed by an even distribution of the other remaining M_1 variables. The second PC accounts for an additional 14.3% of the variance and is most heavily loaded again by ILDs from M_1, with the ILD for cusp 3-5 having the greatest loading. The variables of M_2 consistently contribute the least to the PCs, which shows the lack of variability in this tooth as compared to other molars.

8.5.1 Discriminant Function Analysis

Each of the dataset's total correct classifications are listed in Table 8.9. The individual classification matrices for each analysis are available in Appendix D. The combined molar shape and size dataset has the highest correct classification, followed by the combined molar shape PC dataset. The combined molar ILD dataset has the lowest total correct classification. Across the board, AW classified correctly more often than not. When AW misclassifies, it is generally into either AH, EU, or AB. In the shape PC analysis, AW misclassifies mostly as AH, but in the analyses were size was added, AW misclassifies mostly as either EU or AB. The discriminant function coefficients in the morphometric analyses are mostly influenced by the shape variables of M^2 followed by M^1. The DFA coefficients in the ILD analyses are mostly influenced by M^1 followed by M_1. The mandibular second molar contributed very little to each discriminant function. A comparison of each DFA's CV plot is shown in Figure 8.5. In both of the morphometric-based DFAs (Fig. 8.5-A, Fig. 8.5-B), AW is unique on CV2, but intermediate to each group on CV1. In each CV plot, AA, AI, and AH form clusters and in the ILD-based analyses, AW, AB, and EU tend to cluster with one another.

Table 8.9. Correct classifications for each of the DFAs ordered by total correct classification. All values are percentages (%).

Dataset	AA	AI	AB	EU	AH	AW	Total Correct
Combined Molar Shape and Size	28.6	52.6	47.1	58.5	42.5	57.5	45.6
Combined Molar Shape	23.6	52.6	42.0	51.2	46.1	53.3	43.3
Combined Molar ILD PC	31.7	26.3	45.2	50.0	35.3	40.7	38.3
Combined Molar ILD	36.6	36.8	35.5	47.7	34.3	42.5	37.9

Each dataset's D^2 matrix is available in Appendix D. In both morphometric based analyses, each of the groups is significantly different from one another at $p < 0.05$. In shape only, AW shares the closest distance with AA, then AH, followed by AB. The inclusion of size causes AW to be most similar to AH, followed by AB, and then AA. Both of the ILD analyses resulted in smaller distanced between each of the groups. In terms of raw ILDs, AW is most similar to AB, followed by AH and then nearly equally similar to EU and AA, and least similar to AI. In each instance, AW is most dissimilar to AI. The addition of size changes which groups AW shares the greatest affinity, which is due to AW showing consistently smaller molars than the rest of the comparison groups.

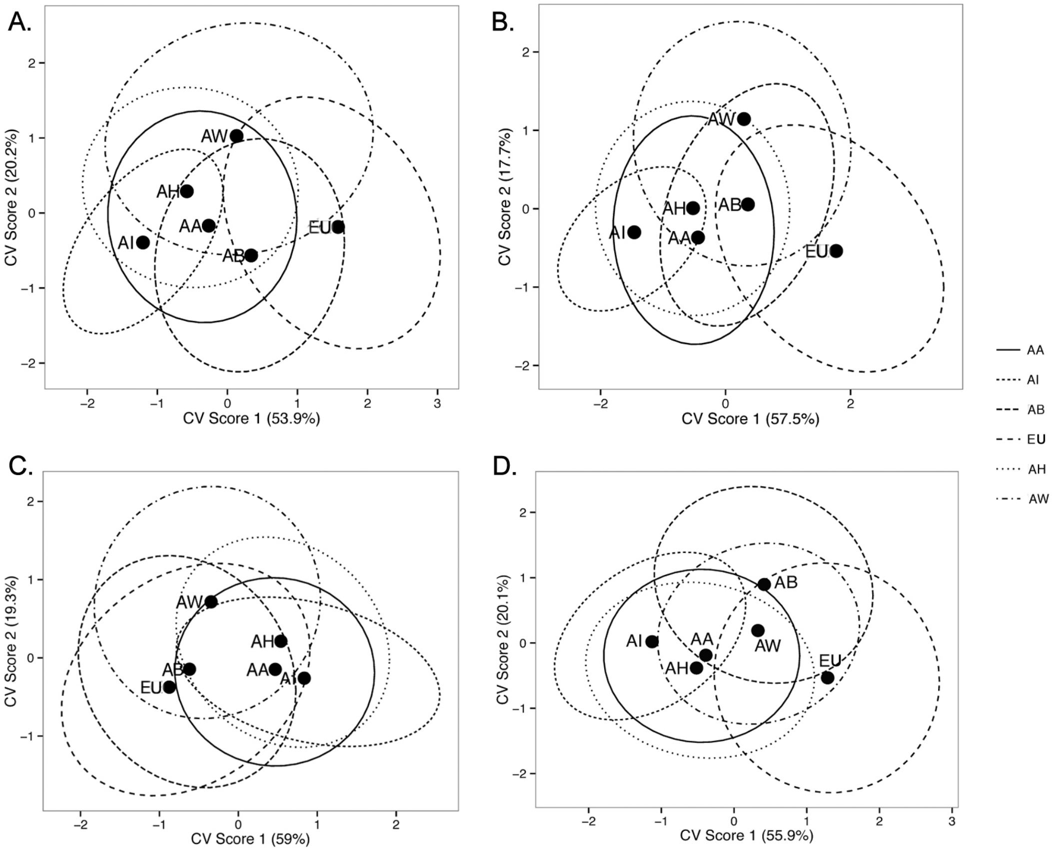


Fig. 8.5. Comparison of canonical variate plots from each of the analyses. The combined molar shape dataset is shown at A, the combined shape and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

8.5.2 Principal Coordinate Analysis

Each D^2 matrix was submitted to a PCO wherein three dimensions contributed eigenvalues greater than zero for each dataset. A comparison of the 3D PCO perceptual plots is available in Figure 8.6. The R^2 values range from 0.91-0.96, indicating a good goodness-of-fit to the original distances. American whites generally cluster with AH on the *x* and *y*-axis, though are unique in the *z*-axis, which is comparable to the *z* values shown by AB. The morphometric-based analyses (Fig. 8.6-A, Fig. 8.6-B) show AW clustering with AH and AI, though, in each case, AW still shows unique *z* values, more on par with AB. The ILD-based perceptual plots (Fig. 8.6-C, Fig. 8.6-D) show American whites clustering more with AB and EU, but, again, the *z* values of AW are unique across each group. In sum, American whites share affinity with each group while remaining unique.

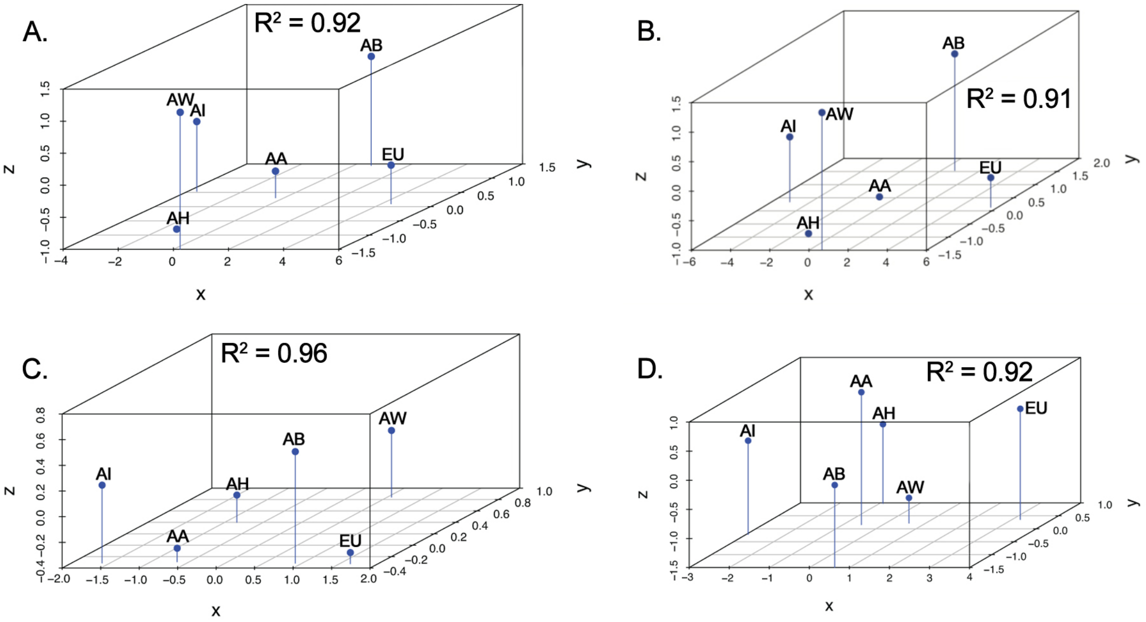


Fig. 8.6. Comparison of three-dimensional PCO perceptual plots for each dataset with individual R^2 values displayed. The PCO of the combined shape PC dataset is shown at A, the combined shape PC and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

8.6 DISCUSSION

American whites demonstrate significant differences in molar morphometrics and ILDs from each of the groups. Additionally, out of all of the groups, AW is consistently the most similar to EU. However, even though AW is the closest group to EU, AW shares greater affinity with modern American groups, thus discrediting Hypothesis 4. Still, of the American groups, AW has the smallest molars, which was more consistent with EU. Further, the reported intermarriage rates are consistent with the affinities of AW shown above, wherein AH has the highest rate of intermarriage with AW, followed by AA, and lastly AB.

Notably, AW is most commonly similar to AA and AH in shape variables, but demonstrate greater affinities with AB in the size analyses. Just as with the American black biohistory analyses, the combined molar shape and size analysis resulted in the greatest total correct classification. Both American blacks and whites are the least of the admixed groups as shown by their lowest level of intermarriage (Taylor et al., 2012a). Thus, in populations that are not as highly admixed, shape and size are both more variable between groups than within groups.

8.7 SUMMARY

The total correct classifications range from 37.9 (combined molar ILD) to 45.6% (combined molar shape and size). The size and shape analyses elucidate different trends in affinity. American whites show the greatest affinities with AA and AH through the shape variables, while the size analyses increased the affinity of AW with AB and EU. Yet, even though AW is the most similar group to EU in the analysis, they are not the two most similar groups, thus not supporting Hypothesis 4. The continued gene flow and admixture of AW with other European descendants, as well as other U.S. groups has caused AW to be a unique group. Overall, AW is significantly different from each of the groups, but demonstrates affinities with each of the groups in the analyses, which varies by shape and size.

CHAPTER 9: COMPARISON OF MODERN AMERICAN GROUPS

It has been demonstrated in the previous chapters that each of the four modern American groups is significantly unique from the potential parental group, though still shows biological affinity with the parental groups, which mimicked population histories. To further investigate similarities and differences among the four modern U.S. groups, descriptive and classification statistics were used on each molar separately for each of the shape and ILD variables, as well as on the combined molar datasets. Given the known intermarriage rates (Passel et al., 2010; Taylor et al., 2012a), it is hypothesized that groups with lower intermarriage rates will demonstrate less within group variation, i.e. lower misclassification rates, than groups with higher intermarriage rates (Hypothesis 5). Thus, American Asians and Hispanics will be the most variable groups; this variability should reflect in lower correct classifications and greater misclassifications and similarities with American whites. Further, American blacks and whites should be the most homogenous of the groups due to the comparatively low intermarriage rates shown by each group.

9.1 MAXILLARY FIRST MOLAR (M^1)

9.1.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for each of the morphometric variables of M^1 are listed in Table 9.1. Each of the groups' variable means was tested via a one-way ANOVA. Log centroid size is significantly different for ancestry among all groups ($F = 32.2$; $p < 0.001$); however, a pairwise comparison reveals that the log centroid size between AB and AW is not significant. American Asians demonstrate the largest centroid sizes, followed by AH; AW has the smallest centroid sizes. Ancestry is also significantly different in PC1 ($F = 38.9$; $p < 0.001$), though PC1 is not significantly different between AA and AW.

Ancestry is significantly different in PC2 (F = 15.0; $p < 0.001$); however, AB share non-significant PC2 shapes with AA and AH. Ancestry is significantly different in PC3 (F = 44.6; $p < 0.001$), but AB and AW are not significantly different from one another. Lastly, ancestry is significantly different in PC4 (F = 14.7; $p < 0.001$); however, AA shows non-significant differences from AB and AW.

Table 9.1. Means and standard deviations for PC scores and log centroid size by group for M^1. Cumulative variance explained is listed under each PC.

	Log Centroid Size		**M^1 PC1** 34.5%		**M^1 PC2** 62.9%		**M^1 PC3** 84.1%		**M^1 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	2.157	0.065	0.007	0.049	-0.015	0.043	-0.008	0.038	-0.007	0.035
AB	2.092	0.090	-0.034	0.064	-0.009	0.064	0.016	0.049	0.003	0.037
AH	2.121	0.078	0.024	0.052	0.001	0.046	-0.025	0.045	0.012	0.037
AW	2.084	0.073	0.002	0.058	0.017	0.050	0.015	0.041	-0.009	0.041

9.1.2 Principal Components of Shape

Principal component one accounts for 34.5% of the variance and indicates the movement of the cusp 1 distobuccally, cusp 2 mesiobuccally, cusp 3 lingually, and cusp 4 mesiolingually (Fig. 9.1). Negative PC1 scores show a rhomboidal shape, while positive PC1 scores reflect a trapezoidal shape that is emphasized by the distobuccal movement of cusp 1 and the lingual movement of cusp 3. American Hispanics have the greatest positive PC1 scores, while AB has the greatest negative scores. The shape changes associated with PC2 are the mesiobuccal movement of cusp 1, mesiolingual movement of cusp 2, distolingual movement of cusp 3, and the distobuccal movement of cusp 4 (Fig 9.1). The negative PC2 scores show a broader and squatter M^1 in comparison to positive PC2 scores, which reflect a more elongated molar mesiodistally. American Asians and AB have the lowest negative PC2 scores, leading to broader molars buccolingually, while AW has the greatest positive PC2 scores, leading to elongated molars mesiodistally.

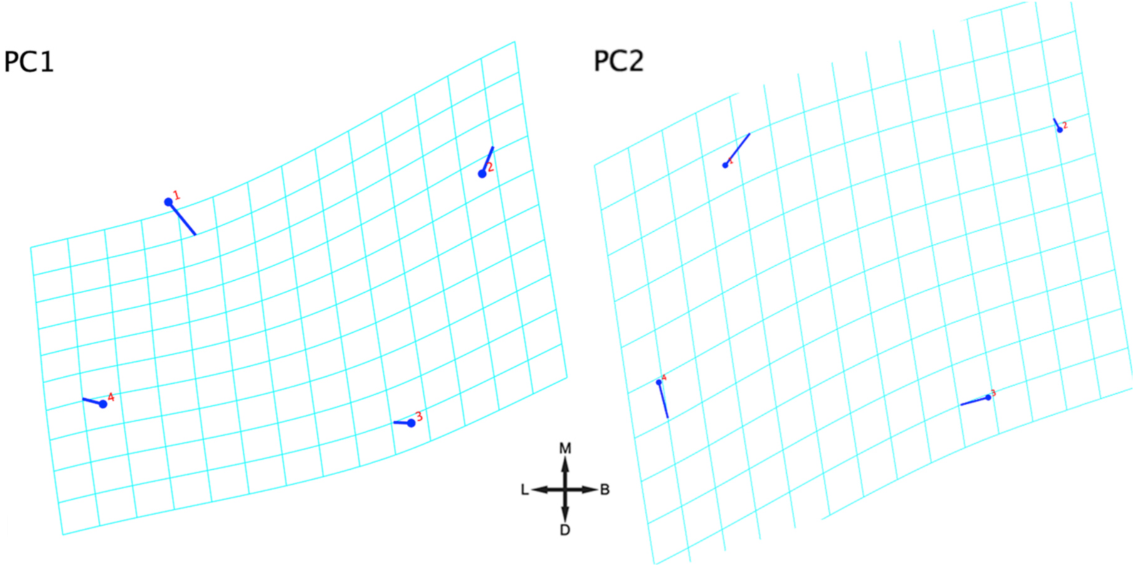


Fig. 9.1. Shape changes associated with PC1 (left) and PC2 (right) of M^1.

9.1.3 Interlandmark Distances (ILDs)

The means and standard deviations for each groups' ILDs are tabulated in Table 9.8. Ancestry was tested for each ILD through a one-way ANOVA. Further, pairwise comparisons of groups were conducted to test individual significances between group means. Ancestry is significantly different in the ILD for cusp 1-2 (F = 39.3; $p < 0.001$); however, this ILD is not significantly different between AB and AW. Ancestry is also significant in the ILD for cusp 1-3 (F = 20.0; $p < 0.001$); though AB has non-significantly different means from AA and AH. The ILD for cusp 1-4 demonstrates that ancestry is significantly different (F = 22.5; $p < 0.001$); however, AA is not significantly different from AW. Ancestry is also significantly different in the ILD for cusp 2-3 (F = 43.9; $p < 0.001$); yet, AA and AA show no significant differences, nor did AB and AW. Again, ancestry is significantly different in the ILD for cusp 2-4 (F = 13.6; $p < 0.001$); still, AB is not significantly different from AW. Lastly, ancestry is significant for the ILD for cusp 3-4 (F = 13.8; $p < 0.001$), although, AH is not significantly different from AB or AW. In sum, AW generally has the smallest values. However, AH has smaller ILDs for cusps 1-3 and 1-4, which reflects the distally oriented protocone of AH in comparison to other groups. Generally AA has the greatest ILDs, followed by AH.

Table 9.2. Means and standard deviations for ILDs by group for M^1. All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	7.2	0.6	7.2	0.8	4.7	0.7	5.8	0.7	9.8	0.9	6.9	0.6
AB	6.5	0.8	7.2	0.8	5.0	0.8	5.3	0.8	9.3	0.9	6.6	0.8
AH	6.8	0.7	7.0	0.8	4.4	0.8	5.9	0.7	9.5	0.9	6.5	0.8
AW	6.5	0.7	6.7	0.8	4.8	0.7	5.3	0.6	9.3	0.9	6.4	0.7

9.1.4 Principal Components of ILDs

The ILDs were submitted to a PCA and yielded six principal components. The first four PCs contributed eigenvalues greater than one, which accounts for 87.2% of the variance and were retained for analysis. The first PC accounts for 45.6% of the variance and is most heavily loaded by the ILD for cusp 2-4, which is the largest overall ILD in the analysis. The second PC accounts for an additional 17.0% of the variance and was most heavily loaded by the ILD for cusp 1-4.

9.2 MAXILLARY SECOND MOLAR (M^2)

9.2.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for the M^2 morphometric variables are shown in Table 9.3. A one-way ANOVA shows that ancestry is significantly different in centroid size ($F = 6.8$; $p < 0.001$). A pairwise comparison of means indicates that AW has significantly smaller mean centroid sizes than both AA and AB. Principal component one means shows a significant difference in ancestry ($F = 4.5$; $p = 0.004$); AW has significantly different PC1 means from AA and AH. Ancestry is significantly different in PC2 ($F = 24.1$; $p < 0.001$); each group mean is significantly different except between AH and AW. Principal component three is also significantly different in ancestry ($F = 6.8$; $p < 0.001$); AW has significantly different means from AA and AB. Lastly, PC4 is significantly different in ancestry ($F = 5.2$; $p = 0.002$); though a pairwise comparison of means demonstrates that only AH has significantly different means from AB and AW.

Table 9.3. Means and standard deviations for PC scores and log centroid size by group for M^2. Cumulative variance explained is listed under each PC.

	Log Centroid Size		**M^2 PC1** 32.7%		**M^2 PC2** 58.7%		**M^2 PC3** 83.6%		**M^2 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	2.066	0.093	-0.009	0.076	0.014	0.069	-0.009	0.060	0.002	0.052
AB	2.043	0.109	0.001	0.077	-0.032	0.077	-0.012	0.079	-0.004	0.061
AH	2.041	0.101	-0.009	0.083	0.024	0.067	0.002	0.064	0.011	0.057
AW	2.017	0.097	0.016	0.077	-0.005	0.067	0.016	0.068	-0.009	0.050

9.2.2 Principal Components of Shape

The first PC accounts for 32.7% of the variance and shows the movement of cusp 1 distobuccally, no movement of cusp 2, mesiobuccal movement of cusp 3, and lingual movement of cusp 4 (Fig. 9.2). Overall, negative PC1 scores reflect a rectangular shape (AA, AH); whereas positive PC2 scores show a more rhomboidal molar that has an elongated distal aspect buccolingually (primarily AW). Principal component two accounts for an additional 26.0% of the variance and shows the movement of cusp 1 distobuccally, cusp 2 mesiobuccally, cusp 3 lingually, and little movement of cusp 4 (Fig. 9.2). In sum, negative PC2 scores show a molar shape that is rectangular and positive PC2 scores reflect a trapezoidal shape with the paracone being exaggerated mesiobuccally in comparison to the lingually compressed metacone. American blacks show the greatest negative PC2 mean, while AH has the greatest positive PC2 mean.

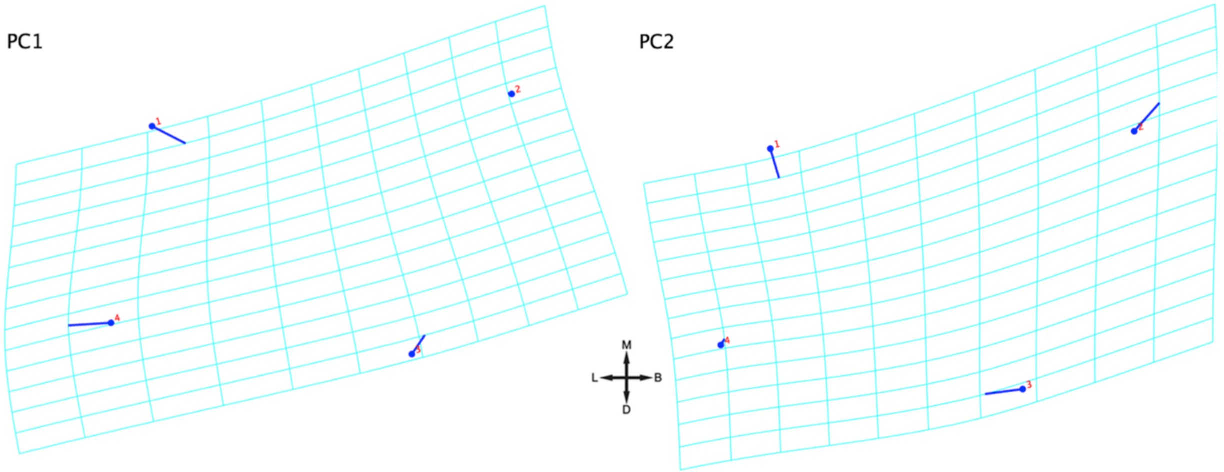


Fig. 9.2. Shape changes associated with PC1 (left) and PC2 (right) of M^2.

9.2.3 Interlandmark Distances (ILDs)

The means and standard deviations for the M^2 ILDs are listed in Table 9.22. The ILD for cusp 1-2 has significant differences in ancestry (F = 19.7; $p < 0.001$); the only groups to not have significantly different means in a pairwise comparison are AB and AH. The ILD for cusp 1-3 is significantly different in ancestry (F = 10.1; $p < 0.001$); however, AA is not significantly different from AB or AH, while AW is not significantly different from AH. The ILD for cusp 1-4 has significant differences for ancestry (F = 15.4; $p < 0.001$); the only groups to not show significant mean differences are AA and AH and also AB and AW. The ILD for cusp 2-3 is significantly different for ancestry (F = 10.0; $p < 0.001$); AA, AB, and AH are not significantly different from one another. The ILD for cusp 2-4 is not significantly different for ancestry (F = 2.3; $p = 0.07$) with each group showing similar means and large standard deviations. Lastly, the ILD for cusp 3-4 is significantly different for ancestry (F = 6.1; $p < 0.001$); though the only significant differences among group means is between AB with AH and AW.

Table 9.4. Means and standard deviations for ILDs by group for M^2. All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	7.2	0.7	7.0	0.8	4.2	0.7	5.6	0.7	8.9	1.0	5.8	0.9
AB	6.9	0.8	7.1	1.0	4.7	1.1	5.5	0.8	8.9	1.2	6.0	1.1
AH	6.9	0.8	6.8	0.9	4.2	0.8	5.6	0.7	8.7	1.0	5.6	1.0
AW	6.6	0.7	6.6	0.9	4.5	0.9	5.3	0.7	8.6	1.1	5.7	0.9

9.2.4 Principal Components of ILDs

The M^2 ILDs were submitted to a PCA and yielded six PCs. Of the six PCs, the first four contributed eigenvalues greater than 1.0 and account for 88.9% of the variance. The first PC accounts for 45.1% of the variance and is heavily loaded by the ILD for cusp 2-4, followed by cusp 1-3, which are the largest ILDs in the analysis. The second PC accounts for an additional 17.1% of the variance and is most heavily loaded by the ILD for cusp 2-3, followed by 1-4, indicating the importance of lengths in the total variation.

9.3 MANDIBULAR FIRST MOLAR (M_1)

9.3.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for the shape variables of M_1 are listed in Table 9.5. Log centroid size is significantly different in ancestry (F = 15.1; $p < 0.001$); through a pairwise comparison of means, however, AH is not significantly different from AA or AB. Principal component one is significantly different in ancestry (F = 5.2; $p = 0.002$), though, only AW shows significant differences from AA and AH. Principal component two is significantly different in ancestry (F = 21.1; $p < 0.001$); AH and AW are the only groups not significantly different. Principal component three is significantly different in ancestry (F = 8.2; $p < 0.001$); however, AA, AB, and AH are not significantly different from one another. The fourth PC is significantly different in ancestry (F = 18.0; $p < 0.001$), but AH is not significantly different from AA or AB. Principal component five is significantly different in ancestry (F = 14.9; $p < 0.001$); AA is not significantly different from AB and AH, nor is AW different from AH. Principal component six is not significantly different in ancestry (F = 1.5; $p = 0.209$).

9.3.2 Principal Components of Shape

The first PC accounts for 26.8% of the variance and indicates the movement of cusp 1 and 2 mesiobuccally, cusp 3 distolingually, cusp 4 distobuccally, and cusp 5 mesiolingually (Fig. 9.3). The most variation is in cusps 4 and 5, which show the greatest magnitude of shape change. Negative PC1 scores reflect molars that have closer relative positions of cusps 1 and 3, but are relatively longer because of the more distobuccally positioned cusp 5 (shown by AA and AH), while positive PC1 scores represent molars that have increased relative lengths between cusp 1 and 4, but have a much more mesiolingually positioned cusp 5 (as seen in AB and AW). The second PC accounts for another 22.0% of the variance and demonstrates the movement of cusp 1 mesiobuccally, cusp 2 distolingually, cusp 3 buccally, cusp 4 mesially, and cusp 5 lingually (Fig. 9.3). Negative PC2 scores show molars that are elongated mesiodistally on the lingual aspect of the tooth and have comparatively shorter buccolingual breadths (AH and AW) as opposed to positive PC2 scores (AA and AB). Again, negative PC2 scores show the more buccal placement of cusp 5 in comparison to positive PC2 scores.

Table 9.5. Means and standard deviations for PC scores and log centroid size by group for M_1. Cumulative variance explained is listed under each PC.

	AA		**AB**		**AH**		**AW**	
	Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**
Log Centroid Size	2.222	0.066	2.197	0.083	2.202	0.085	2.168	0.071
PC1 27.7%	-0.011	0.048	0.002	0.06	-0.003	0.053	0.009	0.054
PC2 49.7%	0.007	0.047	0.022	0.047	-0.012	0.047	-0.01	0.051
PC3 65.3%	-0.004	0.04	-0.008	0.043	-0.001	0.039	0.011	0.039
PC4 79.3%	0.013	0.038	0.001	0.037	0.005	0.037	-0.015	0.041
PC5 90.2%	-0.003	0.031	-0.012	0.034	0.002	0.031	0.009	0.038
PC6 100%	0.002	0.03	-0.001	0.035	0.002	0.032	-0.003	0.03

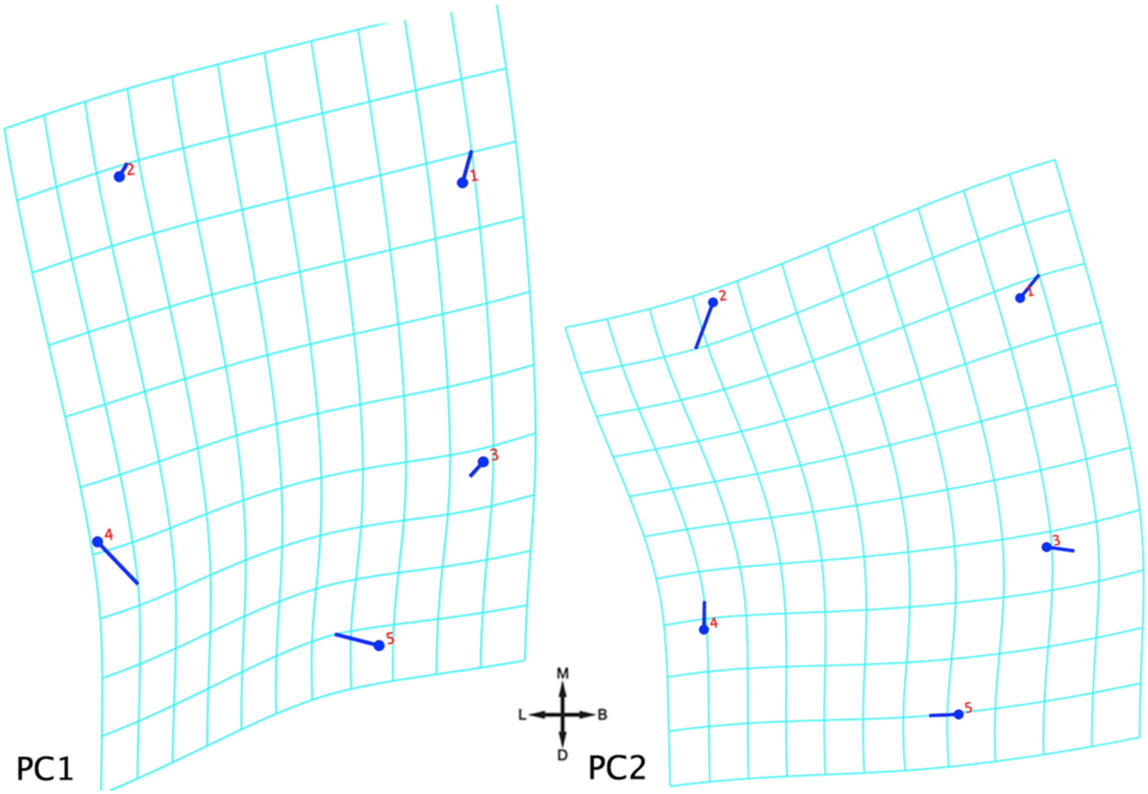


Fig. 9.3. Shape changes associated with PC1 (left) and PC2 (right) of M_1.

9.3.3 Interlandmark Distances (ILDs)

The means and standard deviations for the M_1 ILDs are presented in Table 9.6. Once submitted to a one-way ANOVA, ancestry is significantly different in the ILD for cusp 1-2 (F = 10.7; $p < 0.001$); however, in a pairwise comparison of means, AB is not significantly different AA or AH. The ILD for cusp 1-3 is significantly different in ancestry (F = 3.9; $p = 0.009$), though only AW has significantly different means from AB and AH. The ILD for cusp 1-4 is significantly different in ancestry (F = 10.8; $p < 0.001$) with AA showing significantly different means from each of the groups. The ILD for cusp 1-5 is significantly different in ancestry (F = 5.4; $p = 0.001$), though only AB has significantly different means from AH and AW. The ILD for cusp 2-3 is significantly different in ancestry (F = 9.2; $p < 0.001$) wherein

AW is significantly different from each of the groups. The ILD for cusp 2-4 is not significantly different in ancestry (F = 1.2; *p* = 0.317). Likewise, the ILD for cusp 2-5 is also not significantly different in ancestry (F = 1.5; *p* = 0.213). The ILD for cusp 3-4 is significantly different in ancestry (F = 30.6; *p* < 0.001), though AB is not significantly different from AA and AH. The ILD for cusp 3-5 is significantly different in ancestry (F = 20.3; *p* < 0.001), with AB having significantly different means from each of the groups. Lastly, the ILD for cusp 4-5 is significantly different in ancestry (F = 10.5; *p* < 0.001), wherein AA and AH are not significantly different, nor are AB and AW.

Table 9.6. Means and standard deviations for ILDs by group for M_1. All measurements in mm.

	AA		**AB**		**AH**		**AW**	
	Mean	**sd**	**Mean**	**sd**	**Mean**	**sd**	**Mean**	**sd**
Cusp 1-2	5.7	0.6	5.6	0.6	5.5	0.7	5.4	0.6
Cusp 1-3	4.5	0.6	4.5	0.6	4.5	0.7	4.7	0.8
Cusp 1-4	8.4	0.8	8.4	0.8	8.3	0.8	8.0	0.8
Cusp 1-5	7.6	0.6	7.8	0.8	7.5	0.7	7.6	0.7
Cusp 2-3	7.6	0.6	7.5	0.7	7.4	0.7	7.2	0.7
Cusp 2-4	5.9	0.7	5.9	0.7	6.0	0.7	5.9	0.8
Cusp 2-5	8.7	0.8	8.5	0.9	8.6	0.8	8.5	0.8
Cusp 3-4	6.7	0.6	6.5	0.8	6.4	0.7	6.0	0.7
Cusp 3-5	3.6	0.5	3.9	0.6	3.4	0.6	3.4	0.7
Cusp 4-5	5.0	0.8	4.7	0.8	4.9	0.8	4.6	0.8

9.3.4 Principal Components of ILDs

The ILDs were subjected to a PCA and yielded ten PCs. Of the ten PCs, the first five contributed eigenvalues greater than one, which account for 87.2% of the variance and were retained for further analyses. The first PC accounts for 46.5% of the variance and is most heavily loaded by the ILD for cusp 1-4. The second PC accounts for an additional

18.8% of the variance and is mostly loaded by the ILD for cusp 1-3. In sum, the lengths of M_1 account for the majority of the variation in the sample.

9.4 MANDIBULAR SECOND MOLAR (M_2)

9.4.1 Descriptive Statistics of Principal Components of Shape

The means and standard deviations for the M_2 shape variables are listed in Table 9.7. Centroid size is significantly different in ancestry (F = 6.2; $p < 0.001$), though only AW has significantly different means from AA and AB. Principal component one is significantly different in ancestry (F = 12.7; $p < 0.001$) and only AA is not significantly different from AB or AH. Ancestry is not significantly different in PC2 (F = 1.6; $p = 0.19$). Principal component three is significantly different in ancestry (F = 13.5; $p < 0.001$); however, AB is not significantly different from either AA or AH and AA is not significantly different from AH. Lastly, ancestry is not significantly different in PC4 (F = 0.6; $p = 0.6$).

9.4.2 Principal Components of Shape

The first PC accounts for 37.9% of the variance and shows the movement of cusp 1 mesiolingually, cusp 2 mesiobuccally, cusp 3 distolingually, and cusp 4 distobuccally (Fig. 9.4). Overall, negative PC1 scores represent a molar that is compressed mesiodistally, and slightly broader buccolingually (AA, AB) than positive PC1 scores (AH, AW). An additional 25.5% of the variance is explained by PC2, which shows the movement of cusp 1 distolingually, cusp 2 mesiobuccally, cusp 3 mesiolingually, and cusp 4 distolingually (Fig 9.4). Negative PC2 scores reflect a square molar (AA, AB, AW), while positive PC2 scores demonstrate molars that are constricted mesiodistally on the buccal aspect, but are elongated mesiodistally on the lingual aspect (AH).

Table 9.7. Means and standard deviations for PC scores and log centroid size by group for M_2. Cumulative variance explained is listed under each PC.

	Log Centroid Size		**M_2 PC1** 37.9%		**M_2 PC2** 63.4%		**M_2 PC3** 83.5%		**M_2 PC4** 100%	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	2.031	0.077	-0.006	0.072	-0.001	0.059	0.001	0.050	-0.004	0.049
AB	2.036	0.091	-0.021	0.076	-0.001	0.055	-0.011	0.053	-0.001	0.045
AH	2.014	0.099	0.001	0.070	0.007	0.056	-0.008	0.049	0.001	0.045
AW	2.001	0.085	0.020	0.060	-0.004	0.059	0.017	0.051	0.001	0.044

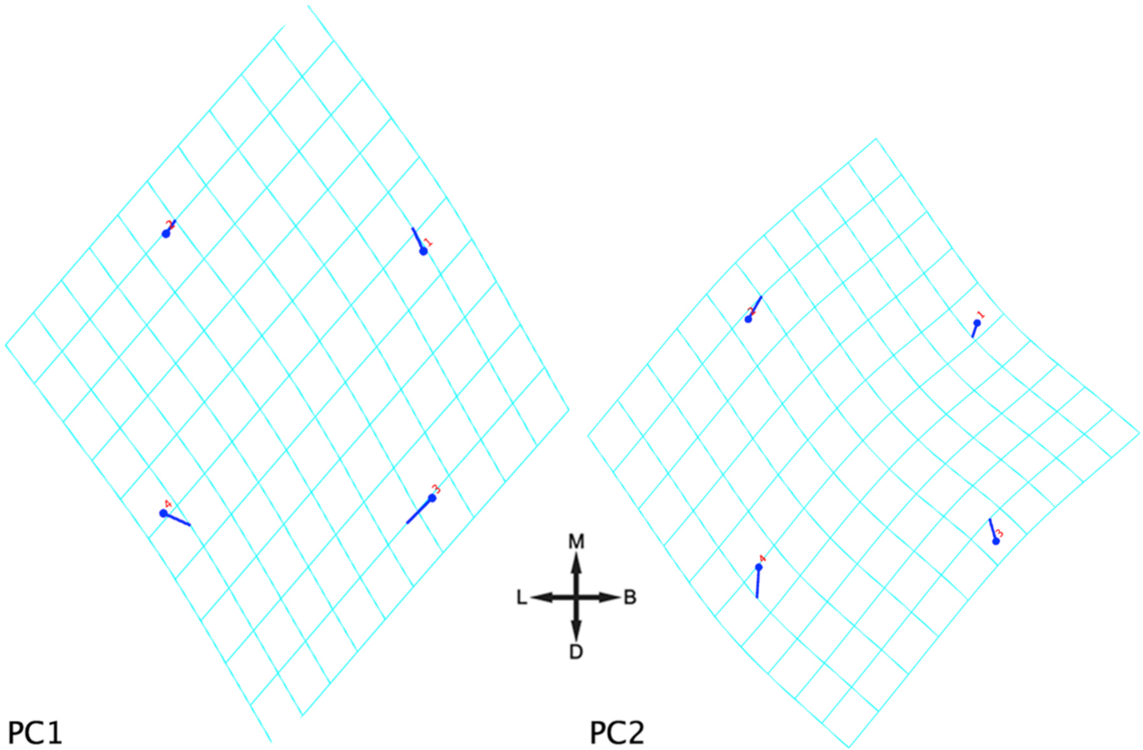


Fig. 9.4. Shape changes associated with PC1 (left) and PC2 (right) of M_2.

9.4.3 Interlandmark Distances (ILDs)

The means and standard deviations for the M_2 ILDs are tabulated in Table 9.8. The ILD for cusp 1-2 is significantly different in ancestry ($F = 6.5$; $p < 0.001$), though the only significant differences are between AW and both AA and AB. The ILD for cusp 1-3 is not significantly different in ancestry ($F = 0.5$; $p = 0.659$). Ancestry is significantly different for the ILD of cusp 1-4 (F = 13.6; $p < 0.001$) wherein only AH is not significantly different from both AA and AW. The ILD for cusp 2-3 is not significantly different in ancestry (F = 2.2; $p = 0.087$). Likewise, ancestry is not significantly different in the ILD for cusp 2-4 (F = 0.5; $p = 0.671$). Lastly, the ILD for cusp 3-4 is significantly different for ancestry (F = 16.6; $p < 0.001$); the only non-significant differences are between AA and both AB and AH. When significant differences occur, AW typically has the smallest dimensions of the groups. Furthermore, AA and AB consistently have the largest ILDs with AH having intermediate values.

Table 9.8. Means and standard deviations for ILDs by group for M_2. All measurements in mm.

	Cusp 1-2		**Cusp 1-3**		**Cusp 1-4**		**Cusp 2-3**		**Cusp 2-4**		**Cusp 3-4**	
	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd	Mean	sd
AA	5.6	0.6	5.1	0.7	7.7	0.6	7.9	0.7	5.8	0.7	5.8	0.7
AB	5.5	0.7	5.1	0.8	7.9	0.8	7.9	0.8	5.7	0.8	6.0	0.8
AH	5.4	0.7	5.1	0.8	7.6	0.9	7.7	0.9	5.8	0.8	5.7	0.8
AW	5.3	0.6	5.1	0.8	7.4	0.8	7.8	0.7	5.7	0.7	5.5	0.7

9.4.4 Principal Components of ILDs

The ILDs of M_2 were subjected to a PCA and yielded six PCs. The first four PCs contributed eigenvalues greater than one, which account for 88.6% of the variance and were retained for further analyses. The first PC accounts for 49.8% of the variance and is mostly loaded by the ILD for cusp 1-4. The second PC accounts for an additional 17.4% of the variance and is heavily loaded by the ILD for cusp 1-3. The length variations observed in M_2 are the same as those noted in M_1, though with less variability.

9.5 COMBINED MOLARS

Each of the individual molar datasets was combined to examine variation among the molars. Again, the morphometric PCs were simply compiled to retain the spatial relationship each PC represented, though the raw ILDs from each molar were subjected to a PCA. The PCA of the combined molar ILD dataset resulted in 28 PCs. Of the 28 PCs, the first 12 contain eigenvalues greater than one and were retained for further analyses. The first PC accounts for 28.5% of the variance and is most heavily loaded by the M^2 ILD for cusp 1-2, followed by the M_1 ILD for cusp 2-3. The second PC accounts for an additional 12% of the variance and was most heavily loaded by the M_1 ILD for cusp 3-5, followed by the M_1 ILD for cusp 1-5. The first PC is fairly evenly distributed with loadings from each of the molars, while the mandibular molars, specifically M_1, most heavily load PC2.

9.6 DISCRIMINANT FUNCTION ANALYSIS

Each of the dataset's correct classifications is listed by descending accuracy in Table 9.9. The individual classification matrix for each dataset is available in Appendix E. The combined molar shape PC dataset has the highest total correct classification at 55.5% and the M_2 shape and size dataset has the lowest total correct classification at 33.9%. Across each analysis, variables of M^1 are the most influential on the DFA coefficients, and comprise the majority of the CV1 coefficients. The second CV coefficients are mostly influenced by the variables of M_1. The maxillary first molar was the most variable between groups in both shape and in size, as the centroid size of M^1 was the only morphometric size variable stepwise selected in the combined molar shape PC and size DFA. Furthermore, the M^1 shape and size DFA has a higher total correct classification than the combined molar ILD dataset. In the combined molar datasets, each group classifies correctly more often than not. When misclassifications occur, AA misclassifies mostly as AH and least as AW. American blacks misclassify mostly as AA in the morphometric DFAs and AW in the ILD DFAs, but always misclassify least as AH. American Hispanics misclassify mostly as AA and least as AB. Lastly, AW misclassifies most commonly as AH and least frequently as AA. American whites have the highest mean across each DFA, followed by AB, AH, and lastly, AA. Comparisons of the CV plots for each individual analysis are available Appendix E. A comparison of the combined molar CV plots is shown in Figure 9.5. In each plot, AW and AB are the most distinct, while AA and AH consistently cluster near one another, which is corroborated by the relatively high misclassification between the two groups. Additionally, in both of the morphometric-based analyses, AW is unique to each group on CV2, but is intermediate between all groups on CV1. In the shape-only analysis, AW is closer to AH, but the inclusion of size in each additional analysis causes AW to be more dissimilar to AH. Finally, the ILD PC demonstrates the least group separation out of the combined analyses, which is consistent with the comparably low correct classifications shown in the combined ILD PC DFA.

The D^2 matrices for each of the individual tooth and combined analyses are listed in Appendix E. The combined analyses show the greatest distances between groups. Consistently, AB is the most dissimilar from AH, especially in the shape PC and size combined analysis. Across the board, the most two most similar groups are AA and AH. In fact, AA and AH are not significantly different from one another in any of the M_2 analyses, and in the shape PC analysis of M^2. In addition, the combined molar ILD analyses have smaller D^2 values between AA and AH than the morphometric variables, which indicates that these groups are more similar in size than in shape.

9.7 PRINCIPAL COORDINATE ANALYSIS

The perceptual plots for the individual molar PCOs are available in Appendix E. A comparison of the perceptual plots for each of the combined molar analyses is compiled in Figure 9.6. In every PCO, only two dimensions were available with eigenvalues greater than zero, and could be visualized. The R^2 values range from 0.88-0.98, which shows a good goodness-of-fit of the original distances. The PCOs for M_2 show the lowest R^2 values, which is likely due to that molar being the least variable. In each of the PCOs, AA and AH cluster near one another, showing their greater affinity with one another. Also, AH and AB are the most dissimilar from one another. The combined molar PCOs follow the same trends as the individual teeth with AA and AH clustering near one another and AH and AB being the most dissimilar. However, the morphometric based analyses separated AA and AH more than the ILD analyses, again demonstrating the shape variability between the groups.

Table 9.9. Correct classifications for each of the DFAs ordered by total correct classification. All values are percentages (%).

Analysis	**AA**	**AB**	**AH**	**AW**	**Total Correct**
Combined Molar Shape	38.6	66.1	55.6	62.8	55.5
Combined Molar Shape and Size	42.1	60.9	50.8	64.1	54.2
Combined Molar ILD	44.7	64.7	46.0	57.7	52.3
M^1 Shape and Size	48.7	47.5	51.6	47.6	48.9
Combined Molar ILD PC	49.6	50.4	39.9	55.8	48.3
M^1 ILD	48.7	52.4	47.0	39.2	46.4
M^1 ILD PC	48.7	48.6	45.2	40.5	45.3
M^1 Shape	27.6	50.5	55.3	41.9	45.0
M_1 Shape and Size	31.8	47.9	27.6	57.3	41.4
M_1 Shape	26.5	49.7	29.0	56.9	41.0
M_1 ILD	39.7	45.3	29.7	48.6	40.7
M_1 ILD PC	32.5	50.6	30.1	50.0	40.7
M^2 Shape	16.2	47.1	42.3	46.4	39.4
M^2 Shape and Size	36.5	40.1	29.3	48.5	38.6
M^2 ILD	50.0	36.1	22.5	46.2	37.7
M^2 ILD PC	43.8	34.0	25.4	48.2	37.3
M_2 Shape	8.8	44.6	23.1	57.3	35.4
M_2 ILD	19.0	52.1	14.0	50.7	34.8
M_2 ILD PC	12.2	51.6	11.7	55.7	34.1
M_2 Shape and Size	11.6	43.5	20.2	54.1	33.9
Method Mean	**33.9**	**49.2**	**34.8**	**51.5**	**42.5**
Method Range	**41.2**	**32.1**	**43.9**	**24.2**	**21.6**

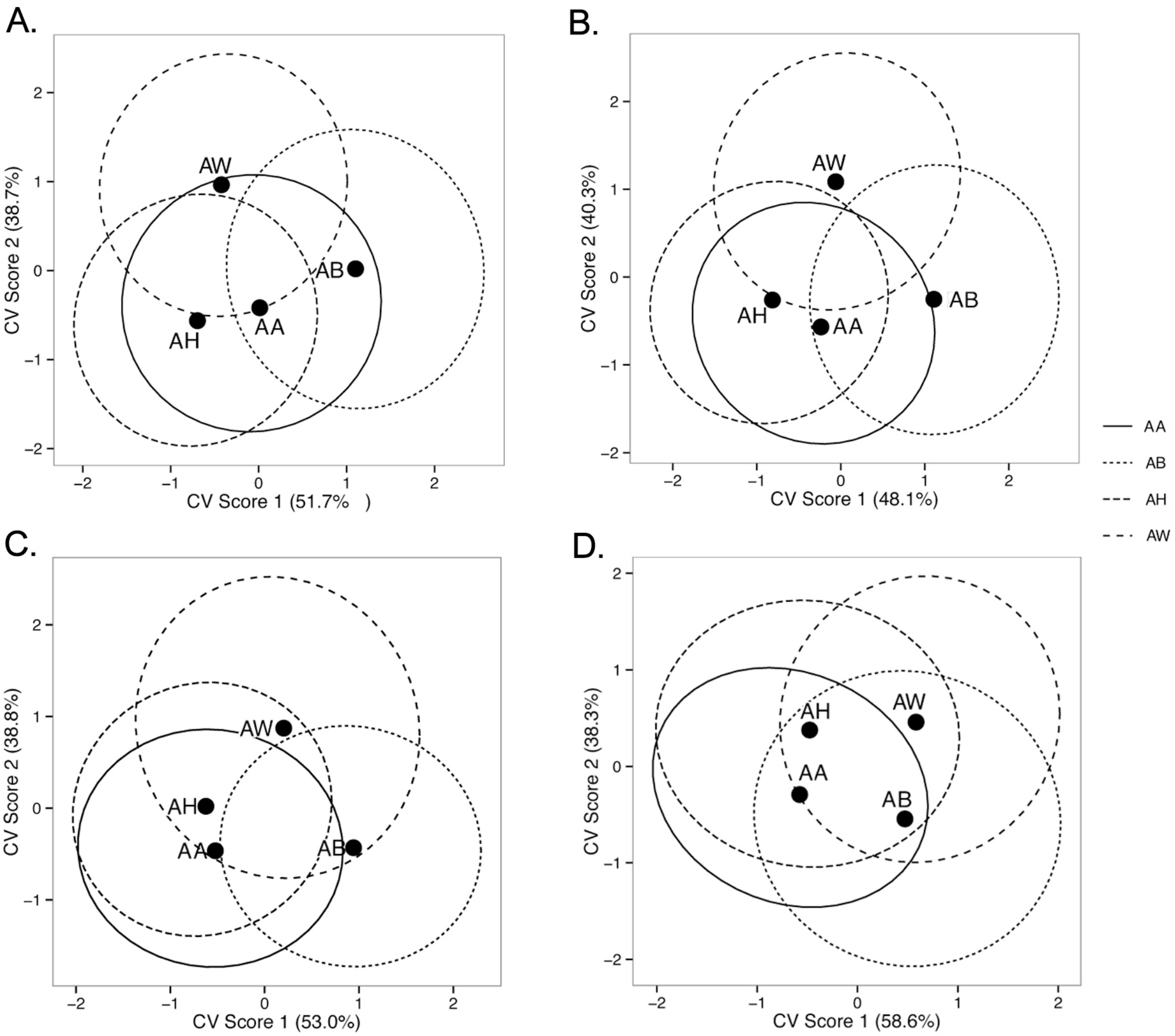


Fig. 9.5. Comparison of canonical variate plots from each of the combined analyses. The combined molar shape dataset is shown at A, the combined shape and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

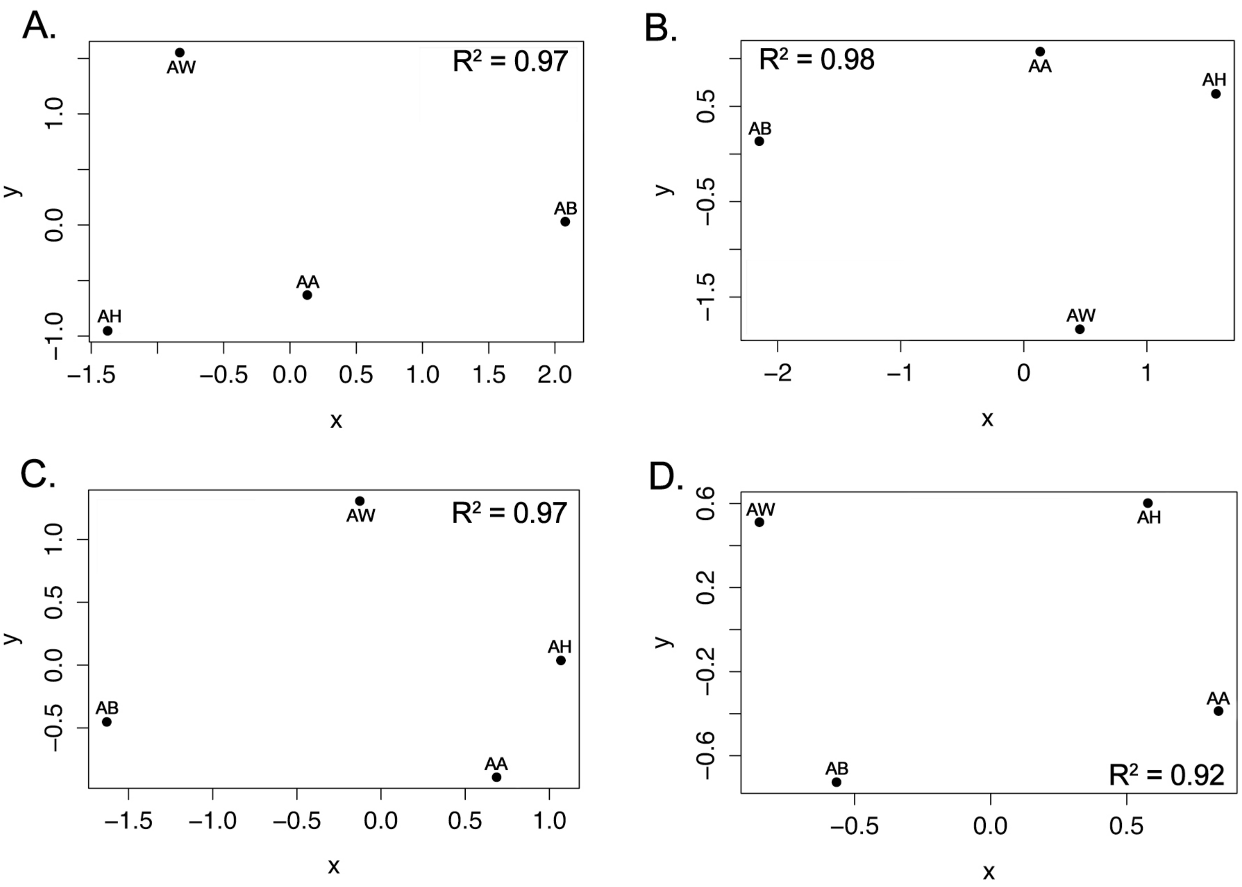
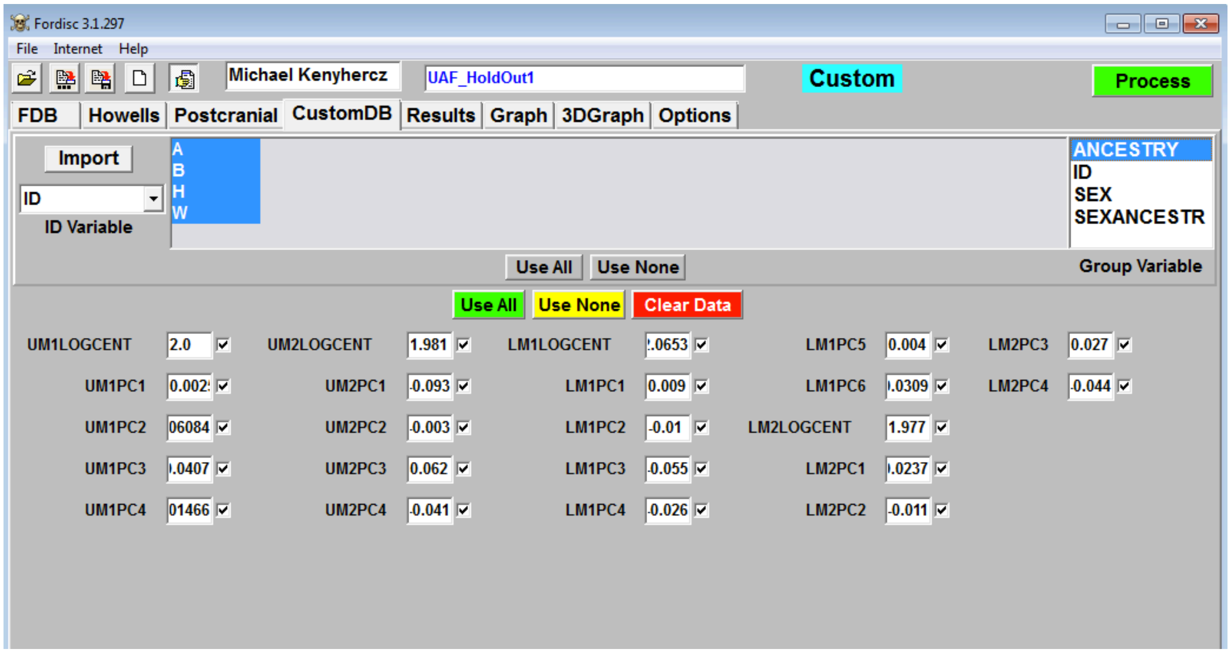


Fig. 9.6. Comparison of two-dimensional PCO perceptual plots for each combined dataset with individual R^2 values displayed. The PCO of the shape PC dataset is shown at A, shape PC and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

9.8 AN APPLIED EXAMPLE

The data from one individual, an American white male (the author), was withheld from the sample to use to test the models as an applied example. The data were digitized from a dental cast. The raw coordinate information was subjected to a GPA and the derived Procrustes Coordinates were subjected to a PCA. The log centroid sizes and PC scores for the holdout individual were then entered into a custom database in the computer program Fordisc 3.0 (Jantz and Ousley, 2005) (Fig. 9.7). The custom database was comprised of the shape PCs and centroid sizes from the original sample, minus the holdout. Forward stepwise selection was used to optimally select the variables that best discriminated between groups. The data were analyzed and the results show that the holdout individual is classified as American white (Fig. 9.8). The results page (Fig. 9.8) also shows the classification matrix for the DFA, the distance of the holdout individual from each centroid, and also posterior and typicality probabilities. Of note, the holdout individual did classify correctly as AW but is not atypical of any particular group and is only slightly closer to the AW centroid than the AB centroid (Fig. 9.9).



Michael Kenyhercz
UAF_HoldOut1
ID
A
B
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ANCESTRY
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SEXANCESTR

UM1LOGCENT 2.0 ☑
UM1PC1 0.002 ☑
UM1PC2 06084 ☑
UM1PC3 .0407 ☑
UM1PC4 01466 ☑
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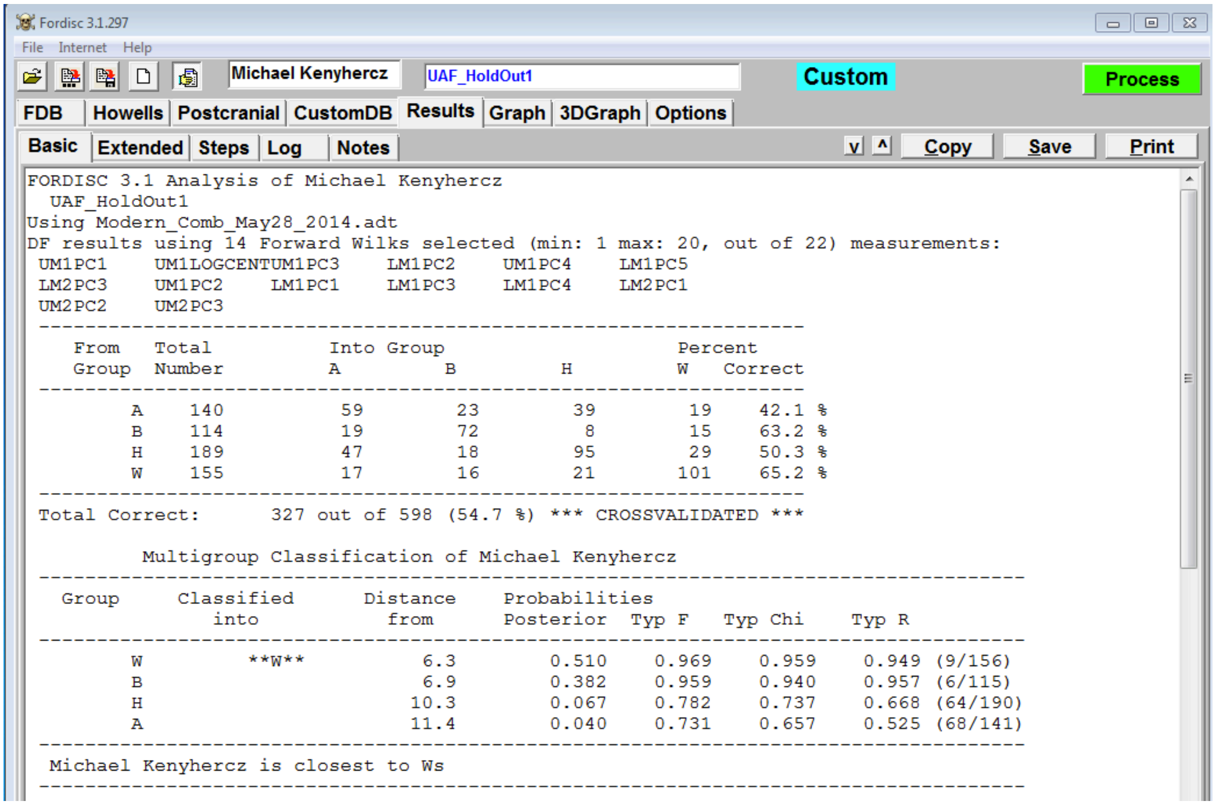
LM1PC4 -0.026 ☑
LM1PC5 0.004 ☑
LM1PC6 .0309 ☑
LM2LOGCENT 1.977 ☑
LM2PC1 .0237 ☑
LM2PC2 -0.011 ☑
LM2PC3 0.027 ☑
LM2PC4 -0.044 ☑

Fig. 9.7. Data entry screen for Fordisc 3.0. The information for the holdout AW male was entered and compared against the information from each ancestral group.



```
FORDISC 3.1 Analysis of Michael Kenyhercz
  UAF_HoldOut1
Using Modern_Comb_May28_2014.adt
DF results using 14 Forward Wilks selected (min: 1 max: 20, out of 22) measurements:
 UM1PC1    UM1LOGCENTUM1PC3    LM1PC2    UM1PC4    LM1PC5
 LM2PC3    UM1PC2    LM1PC1    LM1PC3    LM1PC4    LM2PC1
 UM2PC2    UM2PC3
 ------------------------------------------------------------------
    From   Total          Into Group                  Percent
    Group  Number         A         B         H         W   Correct
 ------------------------------------------------------------------
         A    140          59        23        39        19    42.1 %
         B    114          19        72         8        15    63.2 %
         H    189          47        18        95        29    50.3 %
         W    155          17        16        21       101    65.2 %
 ------------------------------------------------------------------
 Total Correct:      327 out of 598 (54.7 %) *** CROSSVALIDATED ***

          Multigroup Classification of Michael Kenyhercz
 ----------------------------------------------------------------------------------------
   Group     Classified      Distance    Probabilities
                into           from    Posterior  Typ F   Typ Chi    Typ R
 ----------------------------------------------------------------------------------------
         W         **W**          6.3        0.510    0.969    0.959    0.949 (9/156)
         B                        6.9        0.382    0.959    0.940    0.957 (6/115)
         H                       10.3        0.067    0.782    0.737    0.668 (64/190)
         A                       11.4        0.040    0.731    0.657    0.525 (68/141)
 ----------------------------------------------------------------------------------------
  Michael Kenyhercz is closest to Ws
 ----------------------------------------------------------------------------------------
```

Fig. 9.8. Results of the DFA of the AW male, classified as AW.

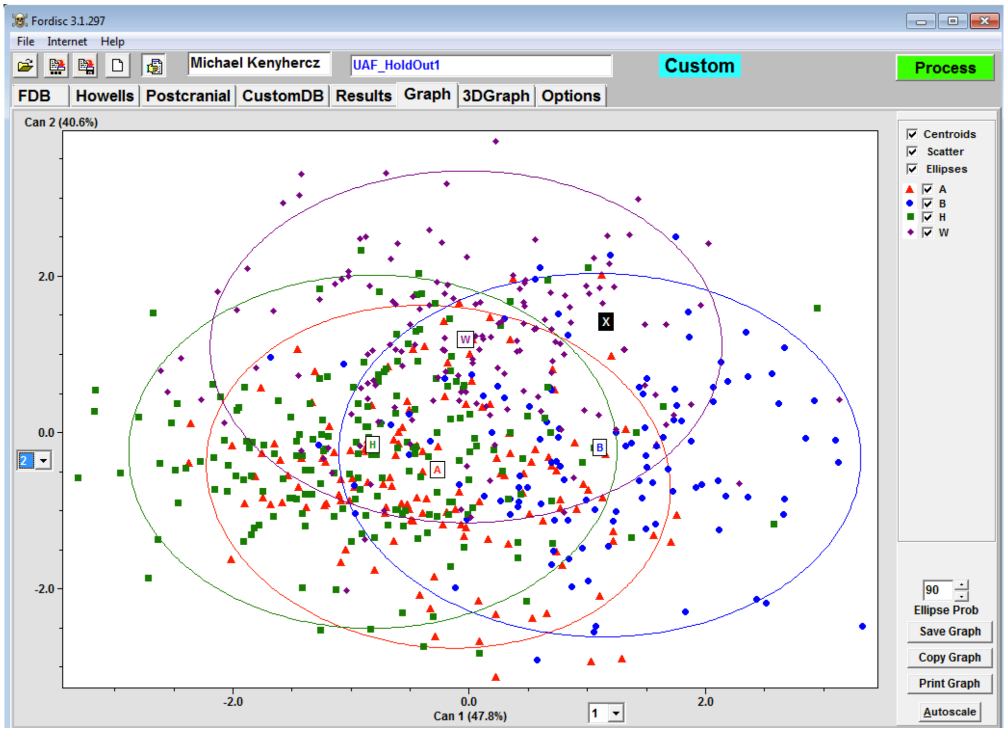
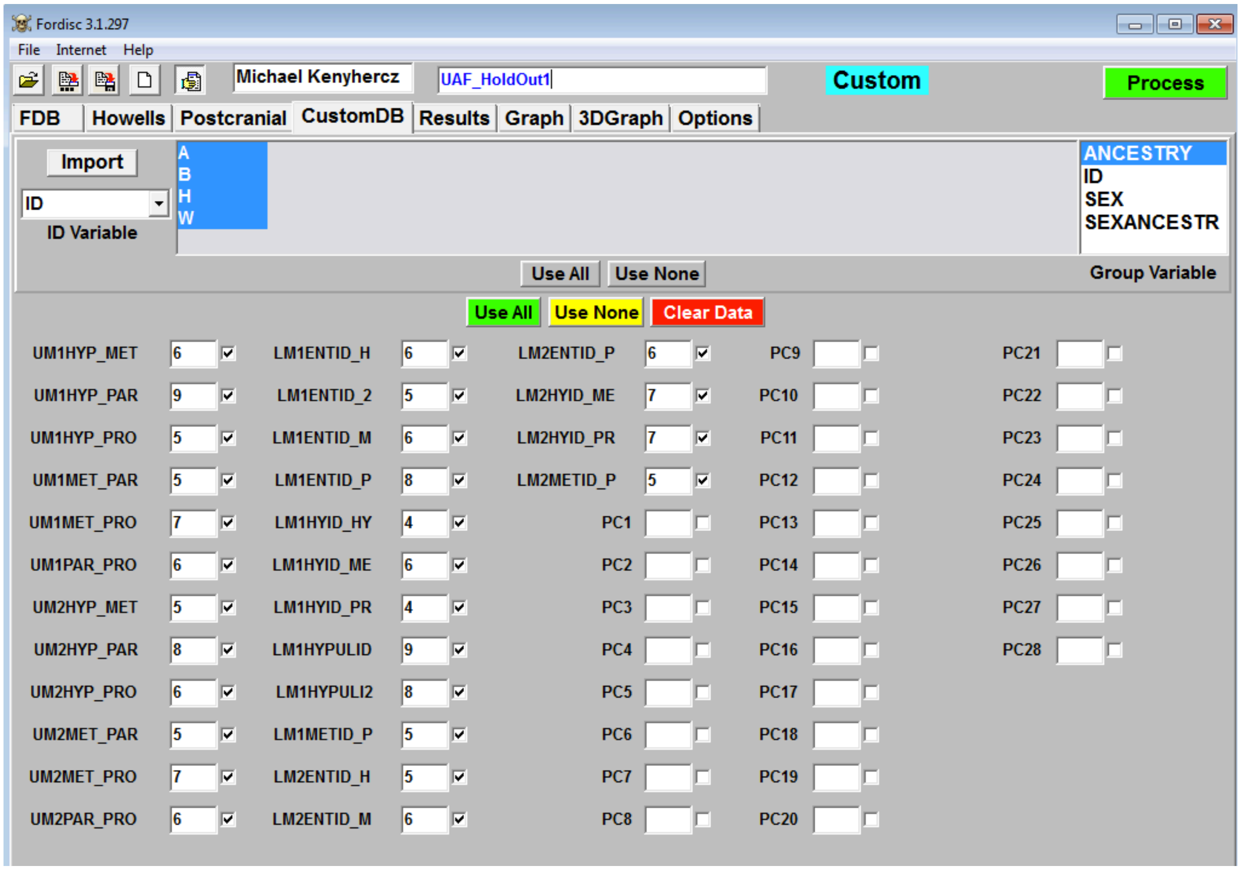


Fig. 9.9. CV Plot showing the location of the holdout AW male as an X.

Next, the ILDs from the same holdout were entered into a Fordisc 3.0 (Jantz and Ousley, 2005) custom database comprised of ILD data from the original sample (Fig. 9.10). Again, forward stepwise selection was used to optimize model performance. The holdout AW male again classified correctly as AW (Fig. 9.11). Further, the AW male holdout is atypical of both AA and AH with F typicalities below 0.05 and low posterior probabilities. The CV plot of the ILD DFA is similar to that of the morphometric dataset above, wherein the holdout individual is closest to the AW centroid, but is next closest to the AB centroid (Fig. 9.12).



Michael Kenyhercz

UAF_HoldOut1

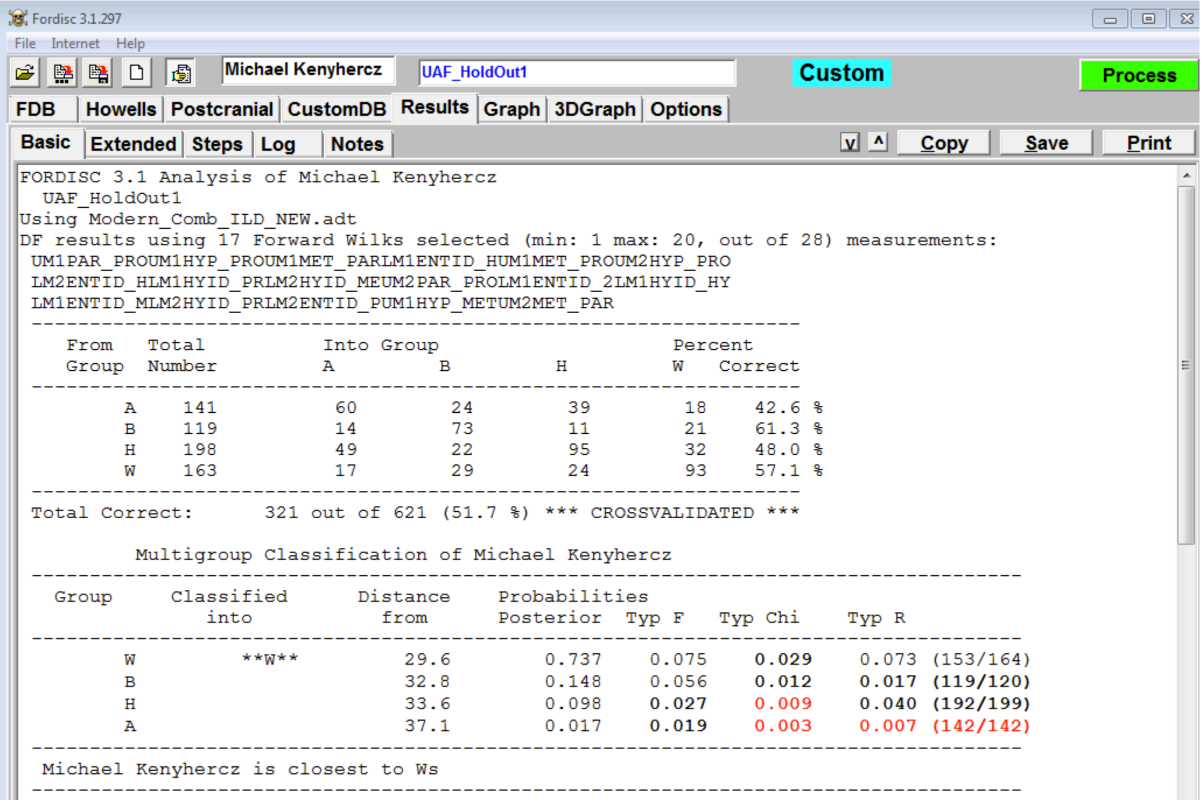
ID Variable: ID

A
B
H
W

Group Variable:
ANCESTRY
ID
SEX
SEXANCESTR

UM1HYP_MET	6 ☑	LM1ENTID_H	6 ☑	LM2ENTID_P	6 ☑	PC9	☐	PC21	☐
UM1HYP_PAR	9 ☑	LM1ENTID_2	5 ☑	LM2HYID_ME	7 ☑	PC10	☐	PC22	☐
UM1HYP_PRO	5 ☑	LM1ENTID_M	6 ☑	LM2HYID_PR	7 ☑	PC11	☐	PC23	☐
UM1MET_PAR	5 ☑	LM1ENTID_P	8 ☑	LM2METID_P	5 ☑	PC12	☐	PC24	☐
UM1MET_PRO	7 ☑	LM1HYID_HY	4 ☑	PC1	☐	PC13	☐	PC25	☐
UM1PAR_PRO	6 ☑	LM1HYID_ME	6 ☑	PC2	☐	PC14	☐	PC26	☐
UM2HYP_MET	5 ☑	LM1HYID_PR	4 ☑	PC3	☐	PC15	☐	PC27	☐
UM2HYP_PAR	8 ☑	LM1HYPULID	9 ☑	PC4	☐	PC16	☐	PC28	☐
UM2HYP_PRO	6 ☑	LM1HYPULI2	8 ☑	PC5	☐	PC17	☐		
UM2MET_PAR	5 ☑	LM1METID_P	5 ☑	PC6	☐	PC18	☐		
UM2MET_PRO	7 ☑	LM2ENTID_H	5 ☑	PC7	☐	PC19	☐		
UM2PAR_PRO	6 ☑	LM2ENTID_M	6 ☑	PC8	☐	PC20	☐		

Fig. 9.10. Data entry screen for Fordisc 3.0. The information for the holdout AW male was entered and compared against the information from each ancestral group.



```
FORDISC 3.1 Analysis of Michael Kenyhercz
  UAF_HoldOut1
Using Modern_Comb_ILD_NEW.adt
DF results using 17 Forward Wilks selected (min: 1 max: 20, out of 28) measurements:
 UM1PAR_PROUM1HYP_PROUM1MET_PARLM1ENTID_HUM1MET_PROUM2HYP_PRO
 LM2ENTID_HLM1HYID_PRLM2HYID_MEUM2PAR_PROLM1ENTID_2LM1HYID_HY
 LM1ENTID_MLM2HYID_PRLM2ENTID_PUM1HYP_METUM2MET_PAR
 ------------------------------------------------------------------
    From   Total          Into Group                  Percent
    Group  Number         A         B         H         W   Correct
 ------------------------------------------------------------------
         A    141          60        24        39        18     42.6 %
         B    119          14        73        11        21     61.3 %
         H    198          49        22        95        32     48.0 %
         W    163          17        29        24        93     57.1 %
 ------------------------------------------------------------------
 Total Correct:       321 out of 621 (51.7 %)  *** CROSSVALIDATED ***

          Multigroup Classification of Michael Kenyhercz
 -------------------------------------------------------------------------------------
   Group      Classified      Distance    Probabilities
                 into            from        Posterior  Typ F    Typ Chi    Typ R
 -------------------------------------------------------------------------------------
         W         **W**          29.6        0.737     0.075    0.029     0.073  (153/164)
         B                        32.8        0.148     0.056    0.012     0.017  (119/120)
         H                        33.6        0.098     0.027    0.009     0.040  (192/199)
         A                        37.1        0.017     0.019    0.003     0.007  (142/142)
 -------------------------------------------------------------------------------------
  Michael Kenyhercz is closest to Ws
 -------------------------------------------------------------------------------------
```

Fig. 9.11. Results of the DFA of the AW male, classified as AW.

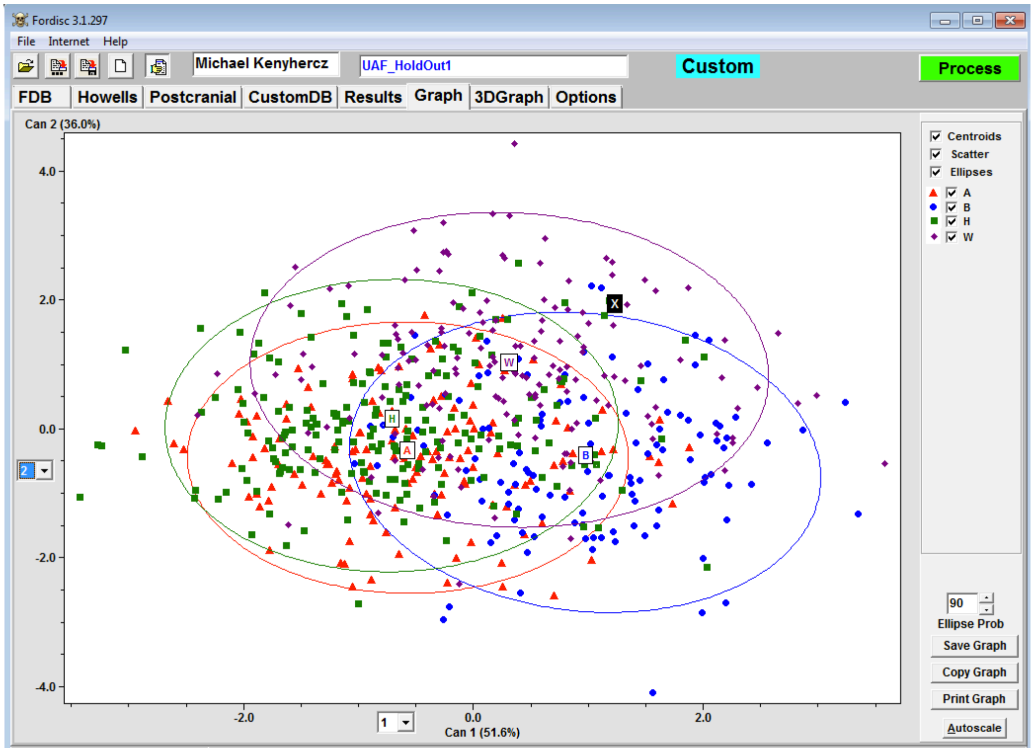


Fig. 9.12. CV Plot showing the location of the holdout AW male as an X.

9.9 THREE GROUP CLASSIFICATION EXAMPLE

The highest four group total correct classification was 55.5%, which is greater than chance (i.e., 25%) and could be used to supplement other commonly employed methods, though it is not particularly telling if only teeth remain. American Asians show the lowest total correct classifications and generally misclassify as AH. Given the overlap between AA and AH, and the comparatively small percentage of Americans identifying as AA (5% as compared to the 16.7% as AH), DFA was used to compare the three most common ancestries (AB, AH, and AW) in the U.S. using the morphometrics (with centroid size) and ILD datasets. The results from the DFAs are available in Table 9.10, the individual classification matrices are available in Appendix E, and a comparison of the CV plots is shown in Figure 9.13. The combined molar shape and size dataset has the highest total correct classification at 72.3%. In both the morphometric and ILD DFAs, AB has the highest correct classification and AW has the lowest. In each case, the groups classify mostly correctly, but AB and AH misclassify mostly as AW, while AW misclassifies mostly as AH. In both CV plots, AW is central to both AB and AH, though shows a closer centroid to AH.

Table 9.10. Correct classifications for each of the three group DFAs ordered by total correct classification. All values are percentages (%).

Analysis	AB	AH	AW	Total Correct
Combined Molar Shape and Size	76.3	73.0	68.4	72.3
Combined Molar ILD	70.6	67.2	62.0	66.2

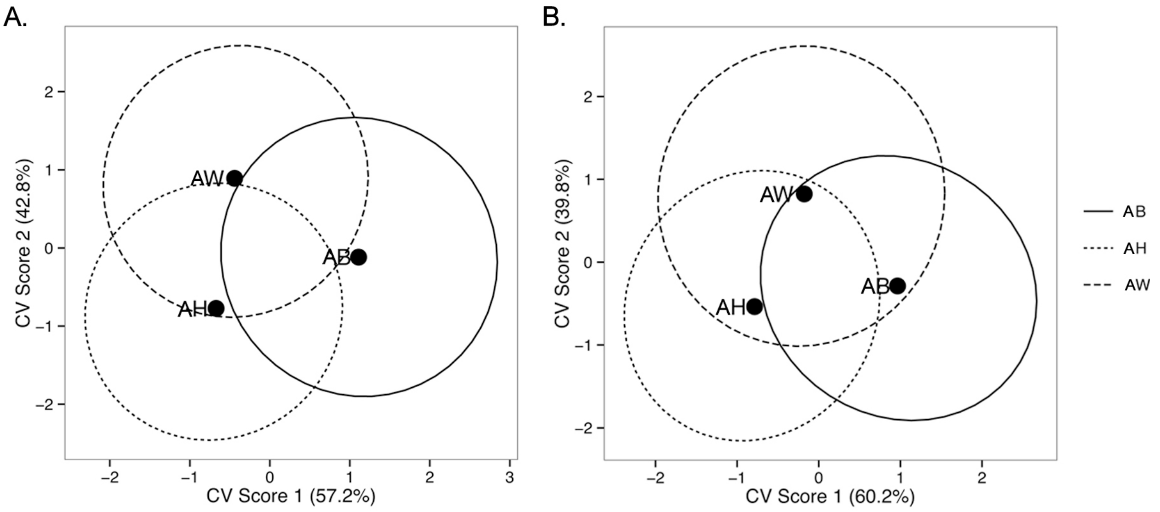


Fig. 9.13. Comparison of canonical variate plots the three group combined analyses. The combined molar shape dataset is shown at A and the ILD dataset at B.

9.10 DISCUSSION

The combined molar shape dataset offers the highest total correct classification of 55.5% and the single highest group correct classification with AB achieving 66.1%. The method mean for total correct classifications is 42.5%, though classifications range from 33.9-55.5%. American Asians have the lowest mean total correct classification, as well as the single lowest correct classification, while AW has the highest method mean classification. Furthermore, AH has the highest method range, which is expected due to their higher levels of intermarriage as compared to other groups (Passel et al., 2010; Taylor et al., 2012b). Conversely, AW has the lowest method range and the highest method mean; this homogeneity may be due to AW having the lowest levels of intermarriage. In fact, the reported levels of intermarriage are negatively correlated to method mean ($r = -0.96$, $p = 0.04$), wherein the lower the rate of intermarriage, the higher the method mean classification. In sum, the observed variation lends support to Hypothesis 5, wherein groups with lower intermarriage rates (AB and AW), have lower misclassification rates than groups with greater intermarriage rates (AA and AH).

The centroid size of M^1 is the most important molar size variable, as it was the only size variable stepwise selected in the combined molar morphometric DFA. Furthermore, the shape and size DFA of M^1 achieved greater total correct classifications than the model of the combined molar ILD PCs. With the exception of the DFA of M^1, the addition of centroid size generally causes a decrease in model performance. However, the ILD PC almost always generated lower correct classifications than the raw ILDs.

Individually, the polar molars are the best at discriminating between groups. In fact, in the DFA, the maxillary first molar analyses have the highest correct classifications, followed by each of the mandibular first molar analyses, then the maxillary second molar, and finally, the mandibular second molar, which offers the least discriminating power. Further, a combination of M^1 and M_1 variables are most prevalent in the canonical variate coefficient structures in both the morphometric and ILD analyses. Assuming Dahlberg (1945) was correct in his assessment of polar teeth containing the most genetic information in shape and size, the prevalence of the first molars in the analyses was expected.

The models created from the morphometric and ILD datasets were successful in correctly classifying an AW male holdout. The morphometric-based DFA shows greater separation of the groups, but has the holdout as being comparably more similar to AB than in the ILD-based DFA. Additionally, the ILD-based DFA shows the holdout as being atypical of both AA and AH, which is not the case in the morphometric-based DFA. In both instances, it was demonstrated how each of the datasets could be operationalized as a tool for classifying unknown individuals via both molar morphometrics and ILDs.

The three-group DFA shows improved classification over the four group DFA, which is likely due to the high rate of misclassification between AA and AH. The overlap between AA and AH can likely be attributed to the fact that the majority of these samples came from the same collection (the Economides collection, UNM), which prescribed “race” post-hoc via names, photographs, and addresses (Edgar et al., 2011). The three-group DFA shows greater correct classification than the four-group model at 72.3 percent, which is consistent with DFAs using craniometric (78.0 total correct classification) and cranial non-metric (75.4%) data between American blacks, Hispanics, and whites (Hefner et al., 2014).

In a practical application, it is recommended to utilize the combined molar shape variables when applying the model to an unknown individual. Across the board, the positive predictive values are greatest for American blacks and whites, and lowest for Asians. The model assumes that an unknown individual will have an equal prior probability as belonging to one of the four groups, however, if there is prior information that will better inform the model, the prior probabilities may be changed accordingly. In sum, the percentage of total correct classifications evaluate model performance and show any bias, which in the current model shows a bias for correct classification in American blacks and whites. Regardless of model performance, use of the proposed models allows a practitioner to submit admissible evidence to the court of law as outlined by Daubert v. Merrell Dow Pharmaceuticals, Inc (1993), which included known error rates.

9.11 SUMMARY

Total correct classifications range from 33.9% to 55.5%. While total correct classifications for the four modern U.S. groups are not particularly high, the groups are significantly different from one another, both morphometrically and metrically and can be operationalized to classify an unknown set of molars. In the event that only molars are available for analysis, the above-proposed models, both morphometric and metric, can be used to supply the researcher with a model and associated *p* values and error rates to qualify as admissible evidence. American Asians and AH most often misclassify as one another. American Asians have the lowest total correct classifications. The observed variation supports Hypothesis 5, in that groups with lower intermarriage rates show less within group variation and vice versa. The removal of AA in the DFAs improved classification to 72.6%, which is consistent with reported classification rates for craniometrics and cranial nonmetrics (Hefner et al., 2014). The polar teeth have the highest classifications out of any individual tooth, and generally, the morphometric analyses outperform the ILDs of the same dataset.

CHAPTER 10: DISCUSSION

10.1 REPEATABILITY, SEXUAL DIMORPHISM, AND ASYMMETRY

10.1.1 Repeatability

Molar cusp apices were proven to be confidently and repeatedly recorded. Morphologically, Nichol and Turner (1986) demonstrated through t-tests that most nonmetric character states could be confidently and repeatedly collected. Metrically, Bailit et al. (1968) and Potter et al. (1981) demonstrated, also through t-tests that MD and BL tooth measures could also be repeatedly collected confidently. Morphometrically, there is no real consensus on identifying the significance of repeated measures. Hartman (1989) suggested the use of a t-test on the scaled Procrustes coordinates, which was adopted by Hlusko (2002); Bernal (2007) suggested using ILDs generated from morphometric data to test repeatability via a t-test. Furthermore, Martinón-Torres et al. (2006) recommend using a Mantel test on a Procrustes coordinates matrix, which has been employed by other researchers (Gómez-Robles et al., 2007). Lastly, Kenyhercz et al. (2014a) compared scaled Procrustes coordinates with a Student's two-tailed t-test. However, oftentimes, tests of repeatability in a particular study are ignored (Yamada and Brown, 1990; Bailey, 2004; Bailey et al., 2008; Benazzi et al., 2009; Skinner et al., 2009). Instead of comparing ILDs or abstract x and y values, which hold no actual shape information, the 2D coordinates of repeated measures were converted to PC shape scores and compared via a t-test to test the overall shape. The repeated measures shape PCs show non-significant differences between measurement instances ($p = 0.14$) and moderately high agreement ($r = 0.68$). Similarly, the ICC on the repeated measures was non significantly different (ICC = 0.67, $p > 0.05$).

10.1.2 Sexual Dimorphism

In odontometrics, sexes are generally analyzed separately due to the effects of sexual dimorphism. Males generally display larger crown dimensions (Garn et al., 1966; Garn et al. 1968; Brace and Ryan, 1980), which can lead to the use of tooth size as a discriminator between sexes (Ditch and Rose, 1972). However, Harris and Dinh (2006) found that only the intercusp distance from the protocone to paracone has any significant differences between the sexes in term of relative cusp location, though their analyses only focused on first and second maxillary molars. Furthermore, it is standard practice to pool the sexes in dental morphological studies, as the character states are evaluated in reference to the entire dental complex (Turner et al., 1991). It then stands to reason that a morphometric approach that removes the influence of gross size through scaling would allow for sexes to also be pooled. To test whether sexes could be pooled, females and males were separated by ancestral group and tested against one another via a Student's two-tailed t-test for the PC1 shape variable of each molar. The only group to demonstrate significant differences in PC1 scores was American black in the M^1 PC1. American black males were shown to be more intermediate to the other groups in their PC1 distributions of M^1 as opposed to females, though both groups demonstrated PC1 means that were well below the means of each of the other groups. As discussed earlier in the population history of American blacks (section 2.1.3), there is a bias for black males to intermarry at a rate of two to one, especially to white females (Alba and Golden, 1986; Passel et al., 2010; Taylor et al., 2012). The perpetuation of positive assortative mating is then a likely factor in American black females demonstrating the lowest mean PC1 scores of M^1. However, American black males and females demonstrated no differences in PC1 scores of any of the other molars, nor did any other of the four groups demonstrate any sexual dimorphism.

10.1.3 Asymmetry

Fluctuating dental asymmetry has long been used as a measure of sustained developmental stress due to environmental conditions (Bailit et al., 1970; Doyle and Johnston, 1977; Harris and Nweeia, 1980; Khalaf et al., 2005; Barrett et al., 2012) as opposed to incident specific stressors that disrupt growth, such as linear enamel hypoplasias (Hoover et al., 2005). Moreover, researchers have found that more distal teeth within a field, especially maxillary teeth, demonstrate the greatest degree of asymmetry (Garn et al., 1966; Hershkovitz et al., 1993). What's more, the relative placement of the molar cusps form during the folding of the secondary enamel knot and are thus more susceptible to environmental influence (Townsend et al., 2003). While many of the previously mentioned studies focused on archaeological or historic samples, environmental stressors, such as differential access to nutrition and healthcare are still modern problems, stratified by socioeconomic status (Iceland and Wilks, 2006). Antisymmetry, DA, and FA were examined in accordance with Van Valen (1962). None of the groups demonstrated antisymmetry and showed negligible levels of DA and FA. However, even though the effect of DA and FA was small, American Hispanics generally displayed the greatest intensity of both. Using a paired sample t-tests on PC1 scores of each of the molars, American Hispanics are the only group to demonstrate asymmetry on M^1 antimeres. Each of the remaining molars is non-significant for asymmetry. According to Iceland and Wilks (2006), American Hispanics have the second highest incidence of poverty, which has been increasing more rapidly than any other group with a 6.6% jump in poverty between 2006 and 2010 (Taylor et al., 2012b). The comparatively disproportional access to income and healthcare may be responsible for the asymmetry observed in the American Hispanic's M^1, as this could introduce sustained developmental stress on the developing enamel knots.

10.2 AMERICAN ASIAN COMPARISON

Hypothesis 1 stated that American Asians will demonstrate intermediacy between East Asians and American whites and has been supported by the analyses in Chapter 5. American Asians were shown to be significantly different from each of the groups in the analysis. Still, American Asians demonstrate the greatest affinities with American Indians, American whites, and East Asians, which is expected given the population history in the United States. Similarly, in a craniometric study, Schmidt et al. (2011) found American Chinese immigrants to be unique but shared similarities with East Asian and American Indian populations. That being said, Schmidt et al. (2011) did not include any American whites in their analysis, but did include some European groups from the Howells dataset. Even though the Chinese immigrant sample shared the greatest affinities with northern Chinese groups, they also shared affinity with some of the European groups, namely Norse and Zalavar (Schmidt et al., 2011).

The observed affinity of the American Asian sample is due to several reasons. First, the affinity demonstrated between American Asians and American Indians in the present study is likely due to the shared Sinodonty dental complex, which was used to detail the migration out of Asia to the New World (Turner, 1990; Scott and Turner, 2008). The derived dental characteristics shared by modern American Asians and Indians, Native Alaskans, and East Asians outlines a clear lineage in the anthropological record. Secondly, the affinity between American Asians and East Asians is directly related to the fact that most of the American Asians have claimed Chinese heritage according to the U.S. Census Bureau (2013). Thirdly, American Asians have the highest incidence of intermarriage, particularly with American whites at 27.7% (Passel et al., 2010; Taylor et al., 2012a). Lastly, the American Asian and Indian samples both came from the same geographic location (Albuquerque, NM) and might be showing exaggerated similarity due proximity, or the way that ancestry was prescribed to that particular sample (Edgar et al., 2011)

The t-tests based on the shape variables for each tooth elucidated several trends. American Asians have comparable mean PC1 and PC2 scores with American Indians and East Asians. Conversely, American Asians have the most significantly different means from modern Thai and American whites. However, in the combined shape D^2, American Asians share the smallest value with American whites, followed by American Indians, and then East Asians, while modern Thais are the most dissimilar. Furthermore, the PCO shows that American Asians are intermediate between East Asians and American whites, though American Asians have *z* values more akin to those of East Asians.

Hillson (1996) stated that, metrically, Europeans and Asians have the smallest dentitions. Generally, American Asians have centroid sizes and ILD values that are intermediate between American whites, which show the smallest sizes in the current study, and East Asians, which have the second largest sizes. Further, Hanihara and Ishida (2005) demonstrated that European populations exhibit smaller sized teeth than East Asian groups. In the current study, the modern Thai have the largest teeth, which is consistent with Hanihara and Ishida (2005). Thais, however, have long been acknowledged as belonging to a dental complex known as Sundadonty (Turner, 1990), which also includes Australian Aboriginals, the group that has the largest dental dimensions (Hillson, 1996).

Harris and Dinh (2006) noted that breadth measures, particularly between cusps 1-2, were more stable than length measures. Despite Harris and Dinh's (2006) findings, the breadth measures are more variable than the length measures, especially in M^1. Though, it should be noted that Harris and Dinh (2006) only examined one population group (American whites). However, the stability of breadth measures within a population, along with the greater heritabilities of tooth size, particularly molar breadths (Alvesalo and Tigerstedt, 1974), explains the greater discriminatory power of the breadth ILDs in the analyses.

Each of the size-based analyses achieve higher total correct classifications than the shape only analysis, indicating that size is more variable than shape in terms of American Asian biohistory. In the shape analyses, American Asians are most similar to American whites. Although, the addition of size variables in each of the remaining analyses indicates that American Asians are most similar to American Indians. Thus, it may be the case that molar shape is less stable than the more derived size characteristics.

10.3 AMERICAN BLACK COMPARISON

In each of the combined analyses, American blacks prove to be significantly different from each of the comparison groups tested. American blacks are intermediate to the West African group and American whites, thus supporting Hypothesis 2. Currently, American blacks have an intermarriage rate of 17.1%, of which 11.9% is to American whites (Taylor et al., 2012a) that likely contributes to the observed gene flow. Additionally, the intermediacy of American blacks to West Africans and American whites has been shown through craniometrics (Spradley, 2006), cranial morphometrics (Spradley, 2013), dental odontometrics (Moss et al., 1967), and also through dental non-metrics (Edgar, 2007, 2009)

In terms of shape, American blacks have the greatest affinities with West Africans, followed by East Africans, and then American whites. The t-tests of the shape variables between each group and American blacks show some overarching trends. Firstly, American blacks most commonly have comparable, non-significantly different means with West Africans. Conversely, American blacks have the most significantly different means with North Africans and American whites. Still, in the PCO of the combined shape variables, American blacks are distinct from West Africans, indicating their uniqueness as a group.

Edgar (2009) found comparable D^2 values with the current study between American blacks, West Africans, and American whites using dental non-metric variables. Thus, the morphometric variables display the same biological affinity patterns as dental nonmetrics (Edgar, 2007, 2009) with American blacks demonstrating intermediacy between West Africans and American whites, as hypothesized. Furthermore, the lower first molar contributed the most shape variables with discriminating power in the combined shape analyses, a trend that was also noted nonmetrically by Edgar (2005).

The individual size based t-tests show similar trends as in the shape-only analyses. American blacks have the most significant differences from North Africans that generally have larger sizes (centroid size and ILDs), and American whites that show smaller values. In M^2, American blacks are not significantly different from either West Africans or American whites, though their centroid size is intermediate between the two groups. According to the Field Concept theory (Dahlberg, 1945), the more distal teeth within a morphogenetic field are less stable or fixed, which can explain the intermediacy of M^2 as compared to M^1. However, the greater variability of M^2 may be due to a greater sensitivity to admixture instead of a "weakening of the mechanisms of genetic control", as suggested by Harris and Dinh (2006, p. 526).

The inclusion of size increased the predictive value of the discriminant function with the shape variables, indicating the importance of size as a discriminator between populations. However, the ILD analyses show comparably lower classifications than the morphometric analyses. American blacks are generally characterized as having smaller labial teeth and larger buccal teeth as opposed to European-derived American whites (Harris and Rathbun, 1989, Schmidt, 2008). The trend for American blacks to have larger sized molars is consistent in the present study with American blacks falling in between West Africans and American whites in both centroid sizes and ILDs. Furthermore, American blacks have smaller centroid sizes and ILDs as compared to the other African populations, a trend also noted metrically by Harris and Rathbun (1989).

The reduction in American black molar size is likely the reason why the inclusion of size in the shape analyses increased the D^2 between American blacks and West Africans and decreased the D^2 between American blacks and whites. Just as in the American Asian biohistory analyses, breadth ILDs comprise the majority of the variables stepwise selected for analyses and most heavily loaded the PCs of the ILDs. The breadth ILDs are the most diagnostic between populations, and thus more stable, as previously noted by Harris and Dinh (2006) and more heritable by Avesalo and Tigerstedt (1974).

10.4 AMERICAN HISPANIC COMPARISON

As discussed in the previous chapters, shape and size conveyed different trends in affinity. It was hypothesized that American Hispanics would demonstrate intermediacy with the historic Spanish and Mexican groups due to population history, American whites due to intermarriage rates (Taylor et al., 2012), and American Indians due to proximity. Each comparative group is significantly different from American Hispanics with the exception of American Indians in the shape-based analysis. The similarity of the American Hispanic and Indian samples might be due to the close geographic proximity from which the sample had come from, or due to the way in which ancestry was prescribed to the particular collection from which the majority of both samples was collected (the Economides collection) (Edgar et al., 2011). The Economides dental collection consists of dental casts, radiographs, photographs, and dental records for nearly six thousand patients and from these records, ancestry was prescribed by two independent observers who evaluated each subject by at least three of the following: 1) name; 2) address; 3) skin color; 4) facial features; and 5) hair form and color (Edgar et al., 2011). Edgar et al. (2011) found that the independent observers had high agreement between classifications, though American Indian and American Hispanics generally had the most confusion. However, the present study only used individuals that were unanimously agreed upon as one particular ancestry by both observers.

The shape based analyses show that American Hispanics are the most similar to, and non-significantly different from, American Indians, followed by American whites, and then historic Spanish. The previously mentioned trends held for misclassification rates in the DFA, D^2 matrix, and PCO. On an individual molar scale, American Hispanics show the greatest differences with historic Mexicans and American whites. As judged by total number of significant differences between shape variables, M^2 is more variable than M^1, which is consistent with the theoretical assumptions of Dahlberg (1945) and the observations of Harris and Dinh (2006). However, in the combined size DFA, the majority of variables stepwise selected are from M_1. Willermet and Edgar (2009) also found that American Hispanics are more similar to American whites as opposed to Western Europeans (which, in the present case, is comprised of historic Spanish); although, Willermet and Edgar (2009) noted that American Indians are not as similar to American Hispanics as the present study has shown.

The size analyses indicate the same trends as the shape analyses with historic Mexican and American whites having the most differences with American Hispanics. Generally, American whites have smaller centroid sizes and ILDs and the historic Mexican sample has larger values than American Hispanics. Though the individual molars did not always show significant differences between American Hispanics and American Indians or whites, American Hispanics typically have size values that are intermediate between the two groups. Just as with the shape, M^2 has more significant differences than M^1, which is, again, consistent with Dahlberg (1945) and Harris and Dinh (2006).

Following suit of previous analyses, the addition of size to the shape variables improves overall discriminant function model performance and increases the positive predictive value of American Hispanics as compared to the shape only analysis. Additionally, the size analyses result in American Hispanics being significantly different from each of the other groups. Notably, size also causes the historic Spanish group to be more dissimilar from American Hispanics, though closer to American whites, undoubtedly due to the smaller sizes shared by each group's molars. Interestingly, the size analyses focus on M^1, as it was the only centroid size stepwise selected and accounted for the majority of the ILDs. The results demonstrate that, within a highly admixed population such as American Hispanics, size is more diagnostic than shape. Size, through odontometrics, has also shown to be variable in other admixed, or nebulously defined populations, such as the Canary Islanders (Irish and Hemphill, 2004), and in regional Indian tribes (Lukacs, 1985; Lukacs and Hemphill, 1993).

10.5 AMERICAN WHITE COMPARISON

Following suit of previous discussions, the size and shape variables of American whites show differing trends in affinity. It was hypothesized that American whites would demonstrate affinity to Europeans due to the homogeneity of dental characteristics reported for Europeans and the admixture of different European groups during the population history of American whites. Furthermore, given relatively high rates of intermarriage between American Hispanics and whites (Taylor et al., 2012a), it was hypothesized that these two groups would also show biological affinity. American whites are significantly different from each of the groups in both shape and size. Across the board, American whites are most distinct from the American Indian sample, and second-most dissimilar from the historic European group. Boas (1912) noted the dissimilarity of American born whites versus their European born parents through craniometrics. Furthermore, Kimmerle et al. (2008) found the need for population specific standards in age, sex, and stature estimation between American white and European populations, so it should follow that biological affinities will also present differences. However, even with noted differences, American whites are generally lumped together into a group described as European-derived, or Caucasoid (Harris and Rathbun, 1991; Yaaccob et al., 1996; Harris and Lease, 2005; Willermet and Edgar, 2009, to name a few). The significant differences shown in the present study, as well as recent findings on the secular changes in dental morphology in American populations (Ousley and Edgar, 2013) indicate a need to treat American whites as a uniquely distinct population group.

Consistently, American whites show the most significant shape differences with American blacks. The molars demonstrate more differences in lingual cusps, as opposed to mesial or distal cusps. The DFA of the shape analysis stepwise selected shape variables from each tooth, though M^2 is most heavily represented in the CV1 coefficients, while CV2 is most heavily influenced by shape variables of M_1. Kenyhercz et al. (2014) also noted the relative importance of M^2 and M_1 morphometric variables in discriminating between American black and white populations, though their research only included American blacks and whites.

The DFA shows that American whites classify mostly correctly and misclassify mostly as American Hispanic and least as American Asian. The D^2 matrix shows that American whites are significantly different from each of the groups, but closest to American Asians, then Hispanics, then blacks. The PCO shows American whites clustering nearest Hispanics, though they show unique *z* values, thus demonstrating their uniqueness as a group.

The size variables show different trends than the shape variables with American whites showing the least significant differences with the historic European group. Consistently, American whites have the smallest centroid sizes and ILD values as compared to the other American groups. However, historic Europeans oftentimes have even smaller sizes than American whites. Yet, American whites are intermediate in size between historic Europeans and the other American groups. Other researchers have previously reported on the relatively small dentitions of European populations (Hillson, 1996; Hanihara and Ishida, 2005; Harris and Lease, 2005). Still, American whites and historic Europeans have the least significant differences in any of the size-based analyses. Conversely, American Asians have the most significantly different sizes (almost unanimously larger) from American whites.

The DFA of the ILDs resulted in lower total correct classification and lower positive predictive value of American whites. The ILDs stepwise selected for the model were mostly from M^1. American whites misclassified mostly as either historic European or American black. The D^2 matrix shows American whites as significantly different from each of the groups, though most similar to American blacks and least similar to American Indians. Notably, the size variables caused an increase in similarity between American whites and historic Europeans as compared to the shape only analyses.

The combined shape and size DFA provide the most optimistic model results and the greatest positive predictive value for American whites. Shape and size variables were selected from each molar, with the exception of the centroid size of M_1. In fact, size and shape variables of M^2 account for the majority of the CV1 coefficients. The D^2 matrix indicates that American whites are significantly different from each of the other groups but are the closest to American Hispanics and then blacks. American whites are the most dissimilar from American Indians. Furthermore, the PCO shows American whites clustering near American Hispanics and are the closest of the U.S. groups to the historic European sample.

10.6 COMPARISON OF MODERN AMERICAN GROUPS

It was hypothesized that groups with greater allele-frequency differences and lower intermarriage rates will demonstrate less within group variation (such as American blacks and whites) than groups with lesser allele-frequency differences and higher intermarriage rates (like American Asians and Hispanics). Just as in previous analyses, the shape and size analyses illuminate different trends in affinity. Still, each of the combined analyses shows that each of the four groups is significantly different from one another. Further, the majority of the individual molar analyses also result in significant differences between each of the groups. Most non-significant mean differences occur between American Asians and Hispanics, both of which share the smallest D^2 values and consistently cluster with one another. The clustering of American Asians and Hispanics could be due proximity as the majority of the samples for these groups came from the same geographical locale (American Southwest), or also the ill-defined way in which ancestry was assigned post-hoc to each individual in the Economides collection (Edgar et al., 2011).

10.6.1 Shape

The shape-derived variables and analyses generally outperform the size analyses in both the individual and combined molar datasets. In fact, the combined shape variable DFA achieved the highest total correct classification at 55.5%. The shape variables of M^1 show the uniqueness of shapes expressed by American blacks and Hispanics as compared to other groups. The first PC of M^1, though significantly different for ancestry, is not different between American Asians and whites. The greatest difference in PC1 is between American blacks and Hispanics. American blacks have PC1 scores that represent a comparatively square-rhomboidal shape. American Hispanics demonstrate a trapezoidal M^1 shape by the more distobuccally placed protocone and lingually positioned metacone. Lastly in PC1, American Asians and whites are intermediate in shape expression between American blacks and Hispanics. Additionally, PC2 is significantly different in ancestry, though the shape only reflects the comparably longer and narrower M^1 shapes of American whites compared to the rest of the groups.

The shape variables of M^2 show the uniqueness of American blacks and whites in comparison to the other two groups. The M^2 PC1 of American whites shows an exaggerated rhomboidal shape through the distobuccally placed protocone and lingually placed hypocone as compared to other groups. American blacks have the most distinct mean PC2 mean, which corresponds to a rectangular M^2 shape that is not as mesiodistally compressed lingually, as in other groups.

The mandibular first molar shows the greatest differences between American Asians and whites in PC1 and American blacks and Hispanics in PC2. The first PC shows that American Asians have M_1 shapes that are mesiodistally compressed and have comparatively buccally placed hypoconulids. In comparison, American whites have PC1 scores that show longer teeth mesiodistally with a more closely associated hypoconulid and entoconid. The differences in PC2 shapes are mainly between American blacks and Hispanics. Comparatively, American blacks have much more mesiodistally-compressed molars, particularly on the lingual aspect, as compared to American Hispanics. Further, American blacks have a more lingually positioned hypoconulid as compared to the other groups.

Lastly, M_2 demonstrates significantly different shapes among ancestries in PC1, but not in PC2. The shape changes associated with PC1 are mainly between American whites and blacks, with American Asians and Hispanics falling intermediate. American whites have an M_2 shape that is buccolingually constricted and mesiodistally elongated, especially distally. The remaining groups have shorter and broader molars in comparison to American whites.

The shape variables typically achieve greater total correct classifications than the size-only analyses in both combined models and individual molar DFAs. The range of classifications for the shape variables DFAs range from 35.2% (M_2) to 55.5% (combined molars). In fact, aside from the combined molars, the polar molars discriminate between groups better than distal teeth. Furthermore, maxillary teeth outperform mandibular teeth of the same position. In a similar study by Klales et al. (2012), M^1 was shown to be the most important molar in discriminating between populations, though their research only included American Asians, blacks and whites. Still, the shape of M^1 is more variable than any of the other teeth and has the greatest total correct classification for any of the individual molar shape DFAs.

The variability of M^1 between groups is opposite of a recent publication by Kenyhercz et al. (2014a) that demonstrated M^2 to be more variable between groups, followed by M_1, though their research only compared American blacks and whites. However, Harris and Dinh (2006) noted that more mesial teeth are less variable, and thus more stable, which should then lead to better discrimination between groups by introducing less statistical noise. Using 29 dental morphological traits, Edgar (2013) compared American blacks, Hispanics, and whites and achieved total correct classifications ranging from 46.2 to 100%, though her analyses were based on pairwise comparison of groups as opposed to each group tested in one model, which is likely the cause of the unrealistically optimistic classification of 100%. Using the same analytical techniques as the present study, Kenyhercz et al. (2014a) achieved total correct classifications ranging from 62.7 to 87.9%, though, again, their comparisons were only between American blacks and whites.

10.6.2 Size

The centroid size for M^1 is significantly different for ancestry, though American blacks and whites have means that are not significantly different from one another. American whites have the smallest mean centroid size and American Asians have the largest. Further, American blacks have the greatest variability in M^1 size, as shown through their relatively larger standard deviations. Each of the ILDs is significantly different for ancestry, though pairwise comparison of groups revealed some non-significantly different means. In individual ILDs, American blacks and whites typically have similar breadth measures, which are smaller than the other two groups. Just as in the shape analyses, the M^1 lingual aspect demonstrates greatest variability for Hispanics due to the mesiodistally compressed lingual aspect of the molar. Due to the compressed relative location of the protocone and hypocone, the ILD for cusp 1-4 is the smallest in Hispanics even though they typically exhibit much larger ILDs as compared to other groups.

The centroid sizes of M^2 are also significantly different for ancestry. Again, American whites have the smallest centroid sizes, though they are not significantly different from those of American Hispanics. American Asians continue to show the largest centroid sizes. Just as in M^1 American blacks have the greatest standard deviation in centroid size, thus demonstrating the greatest variability in size. Each of the ILDs of M^2 is significantly different in ancestry except for the ILD for cusp 2-4. Generally, American whites are the most unique group with consistently smaller ILDs as compared to other groups. American Asians again demonstrate the largest ILD values. Similar to the M^1 ILDs, the ILD for cusp 1-4 is significantly smaller in American Hispanics as compared to American whites, thus corroborating the trend in the morphometric variables to see a reduction mesiodistally of the lingual aspect of the tooth, primarily in American Hispanics.

The centroid size of M_1 is significantly different in ancestry, though American Hispanics are not significantly different from either American Asians or blacks. However, following previously noted trends, American whites have significantly smaller centroid sizes as compared to the other groups. Each of the M_1 ILDs is significantly different in ancestry except for the ILDs for cusps 2-4 and 2-5. Consistently, American whites have smaller ILD values than the other groups, while American Asians have mostly larger ILDs as compared to the other groups. The distal breadth (cusp 3-4) shows the most variability, which is consistent with the morphometric variables that showed greater shape variation in the distal aspect of the tooth.

Lastly, the centroid sizes of M_2 are the least variable, but American whites still demonstrate the smallest values. Just as in the maxillary molars, American Hispanics have the greatest reduction in sizes from the first to second molar. Following the overarching trend, American whites have consistently smaller ILDs than the rest of the groups. American Asians and blacks typically have the largest ILD values. Additionally, the ILDs for M_2 have the least significant differences in ancestry out of any of the molars thus showing the low level of variability in this tooth.

The molars that varied the most between groups follow the same trends as in the shape analyses. Polar teeth are more effective at discriminating between groups than the more distal molars, and the mandibular molars are less effective at discrimination than their maxillary isomeres. Just as with the shape variables, American Asians and Hispanics are the most similar in terms of misclassification patterns and cluster analyses. However, the ILDs of M^1 demonstrate that American blacks and whites are the most similar groups.

Also in line with the shape analyses, the combined size analyses are more effective at discriminating between populations than individual molars. The DFA analyses are most heavily loaded on CV1 by the shape variables of M^1, specifically the ILD for cusps 1-4 and 2-4, demonstrating the importance of lengths as compared to breadths. The second CV is mostly loaded by the ILDs from M_1, especially for cusp 3-4, showing the importance of distal breadths of the mandibular molars. The combined ILDs show the similarity of American Asians and Hispanics as compared to other groups. The greatest differences are between American blacks and Hispanics that rarely misclassified as one another.

Generally, odontometrics have been used to examine microevolutionary processes in admixed populations abroad (Lukacs and Hemphill, 1993; Irish and Hemphill, 2004; Matsumura and Hudson, 2005) or on a worldwide scale (Flower, 1885; Garn et al., 1968; Hanihara and Ishida, 2005; Harris, 1997; Harris and Lease, 2005). However, very few studies have focused on odontometrics in modern American populations. Using raw buccolingual and mesiodistal measures and their residual apportionments, Harris and Rathbun (1991) achieved total correct classification of blacks, whites, and Asians that were comparable to the ILDs of the molars in the present study. However, Harris and Rathbun's (1991) sample lumped American blacks with Africans and American whites with Europeans and also utilized an Asian sample that lumped samples from across Asia. The Asian sample in Harris and Rathbun's (1991) study achieved the lowest correct classifications, which was explained by considering Asians more “odontometrically variable” (p. 135) than other groups. Still, each of the groups in the current study achieved higher total correct classifications from ILDs from the molars than those reported by Harris and Rathbun (1991).

Still, the ILDs consistently show the least variation between groups, as each of the ILD analyses has lower correct classifications than the shape-based analyses. It has previously been demonstrated by Townsend et al. (2003) that intercusp distances show only a moderate degree of heritability, which would explain their comparably lower classification rates. The intercuspal dimensions are not as stable because the molar cusps themselves are formed later in odontogenesis during the secondary knot formation (Townsend et al., 2003; Townsend et al., 2009). Furthermore, Townsend et al. (2009) have shown through twin studies that intercuspal dimensions are particularly sensitive to epigenetic factors. The amount of environmental impact on the formation of the secondary knot could then introduce more noise in the analysis of simply linear dimensions between cusps leading to lower classification rates.

10.6.3 Shape and Size

The combination of shape and size resulted in the second highest total correct classification in any of the analyses at 54.2%. Furthermore, in the single molar DFAs, the combination of shape and size outperform the analyses of just shape or size in the polar teeth but not the distal molars. However, even though the distal molars have lower total correct classification than the polar molars, the combination of both shape and size did increase the D^2 values between groups in both individual molars and the combined analyses, especially between American Asians and Hispanics. Furthermore, the shape and size analyses for individual teeth show more or less equal separation between the groups, with the exception of M_2. Still, the combined molar analyses demonstrated the uniqueness of American whites from the rest of the groups.

The ILD PCs, which was also speculated to attain shape and size differences performed worse than any of the molars in terms of classification, as well as in the combined molar analyses. Harris and Rathbun (1991) have also noted that the raw measures outperform the PCs of mesiodistal and buccolingual measures in several instances. Yet, Harris and Rathbun (1989) have shown that the PCs of the linear measurements are more informative than the raw measures themselves. It is likely that the greater differences in tooth dimensions from the entire arcade was more informative to get a sense of size apportionment in their analyses, as opposed to simply linear measures between relative cusp locations in the present study. However, describing the allocation of sizes within an arcade is perhaps a misleading use of the term shape, as shape refers to the geometric properties of an object invariant to scale (Bookstein, 1991). Furthermore, the linear dimensions between molar cusps are not as variable a range of numbers as would be present in measurements of the entire arcade. Kenyhercz et al. (2014a) have further concluded that the relative location of cusps is more informative than simply the linear distances between cusps, as well as the PCs derived from the linear measures in the molars.

Using a novel approach, Lease and Sciulli (2005) combined dental morphological and metric variables to discriminate between American blacks and whites using the deciduous dentition. They reported between 90.1 and 92.6% total correct classifications using logistic regression equations. Similar to the present study, combining the shape (morphological) and size (metrical) variables yielded the highest total correct classification. The combination of shape with size is more informative because of the varying trends that size and shape have on affinities between groups. For example, the shape only variables in the present study indicate the similarity between American Asians and Hispanics, which are sometimes not significantly different from one another. However, the addition of size increases the discriminating power between the two groups, wherein American Asians often demonstrated greater sizes than American Hispanics.

10.6.4 Individual Molar Variability

The overall trends show that the polar molars are better discriminators than distal members within the same field and that maxillary molars are better discriminators than mandibular molars. Following Dahlberg (1945), the polar teeth receive the most genetic information, thus giving the strongest trait expression and exhibiting the most stable teeth. Similarly, Osborn (1973) agreed that there was a primary tooth within regions and it was the determinant model, or demonstrated the greatest genetic potential. In any event, the first molars demonstrate the most variability among groups, and thus could be said to be the most stable teeth among populations. However, M_2 varies the least among populations in both shape and size and demonstrates the lowest discriminating power. In fact, not only are distal teeth within a field more variable, more distal cusps within the same molar are also more variable, which has been previously noted by Corruccini (1979), as well as Harris and Dinh (2006).

The current study has corroborated previous authors' claims concerning the increased variability of maxillary and mandibular distal teeth and distal regions of each particular molar, with the exception of M_2. In each analysis, the distal molar regions vary more than the mesial regions, which is consistent with Dahlberg (1945) and Osborn

(1973). In addition to the more distal cusps demonstrating more variation, the lingual aspect of the molars exhibits more variation than the buccal aspect. Within M^1, it would be counterintuitive for the protocone to exhibit as much variation as it does, however, as pointed out by Butler (1978), the protocone is not actually the primary cusp in the tritubercular model as originally proposed by Osborn, but is actually the second cusp developed evolutionarily. Gómez-Robles et al. (2007) have also noted the more variable lingual aspect of M^1. However, M_1, whose cusps are ordered correctly in terms of evolutionary development, did exhibit more variation in the distal aspect of the molar, which consistent with both Field theory (Dahlberg, 1945) and the Clone model (Osborn, 1973). The more distal cusps form later than the mesial cusps (Christensen and Kraus, 1965), which would allow more outside influence, leading to greater variation observed.

In the combined models, M^1 contributes the most to the shape only analysis, followed by M_1 and is least impacted by M_2. In the shape and size model, the only size variable selected was centroid size from M^1. Additionally, the combined molar ILD DFA is mostly influenced by variables from M^1 and then by M_1. In sum, the variables that best discriminate between groups are the polar molars in both shape and size. However, Alvesalo and Tigersted (1974) have previously noted the greater hetitabilities of M^1 dimensions over M_1 dimensions, especially concerning buccolingual dimensions, which explains the discriminatory power of M^1 in the current study. Greater heritabilities of the first molars, in conjunction with the Field theory (Dahlberg, 1945) and Clone model (Osborn, 1973) could then describe why the shapes and sizes of both maxillary and mandibular first molars best discriminate among populations. If allele-frequency differences and intermarriage rates are low between groups, and thus conceivably gene flow, it stands to reason that the first molars would discriminate best between populations, which has been demonstrated through the analyses.

The variability of the second molar, especially M^2, is likely due to its later development, which occurs after birth (Hillson, 1996) and would then have more time to be affected by environmental conditions. The variation of M^2 is noted in the current study as more important for discriminating between modern U.S. populations and possible parental populations. Thus, the relatively later formation of the second molar contributes to the observed variation between the modern U.S. groups and parental populations due to the sustained environmental impact.

10.6.5 Comparison to Other Research in U.S. Biological Affinity

The majority of the recent research in the attempts to quantify and classify biological affinity, or ancestry, in the United States has focused on the discrimination between American blacks and whites using different elements and classification statistics (Edgar, 2005; Lease and Sciulli, 2005; Kenyhercz, 2011; Kindschuh et al., 2012; Hefner and Ousley, 2014; Kenyhercz et al., 2014a). More recently, research has started to focus on discriminating among American blacks, Hispanics, and whites (Spradley et al., 2008; Hurst, 2012; Edgar, 2013; Hefner et al., 2014; Hefner and Ousley, 2014; Kenyhercz et al., 2014b). Using cranial metric and nonmetric data, Hefner et al. (2014) were able to classify American blacks, Hispanics, and whites up to 89.6% correctly. Using only cranial nonmetrics, Hefner and Ousley (2014) were able to achieve 87.8% total correct classification between the same three groups using different classification statistics. To compare the efficacy of using molar morphometrics to the previous mentioned accuracies, the combined molar shape and size variables were tested with American Asians removed and resulted in a total correct classification of 72.3%. The three-group total correct classification is on par with correct classifications based on only craniometrics (72.3%) and cranial nonmetrics (75.4%) as reported by Hefner et al. (2014).

Furthermore, the combined molar shape and size D^2 values were compared to distance measures from cranial nonmetrics from Hefner et al. (2014). The distance matrices were each subjected to a PCO to visualize the distances. Each of the R^2 values is greater than 0.95 indicating good goodness-of-fit to the original distances, though only two dimensions provided eigenvalues greater than zero. The comparison of projected distances is available in Figure 10.1. Each of the PCOs shows essentially the same plot with American whites being the most unique group, though showing greater affinity with American Hispanic than American black. Each of the PCOs shown corroborates one another.

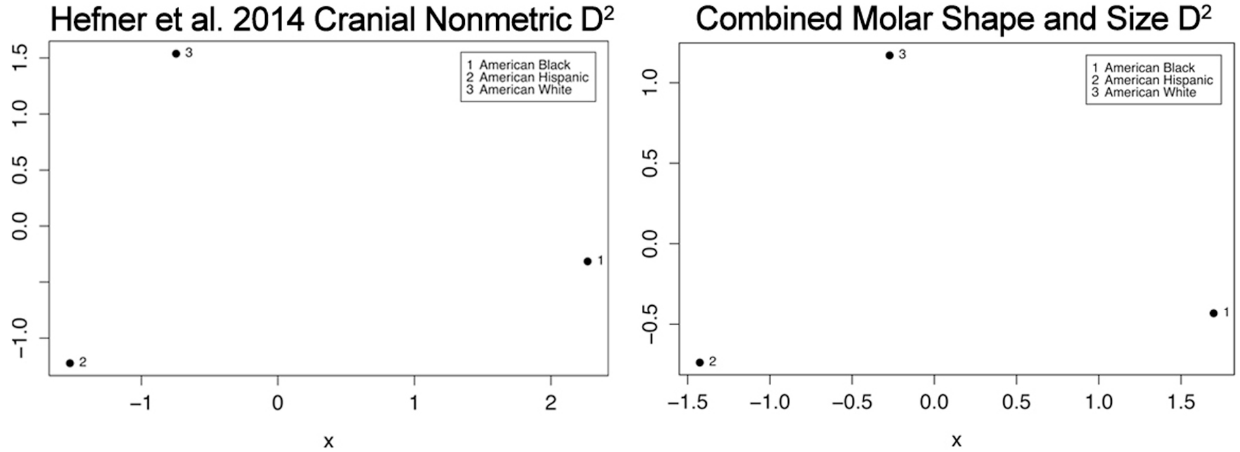


Fig. 10.1. Comparison of PCO plots showing distances between American blacks, Hispanics and whites. D^2 values from cranial nonmetrics on the left and the combined molar shape and size D^2 is on the right.

Regardless, the current study is the only one to date that examines the biological affinity of the big four modern American groups. Using Fordisc 3.0 (Jantz and Ousley, 2005) and craniometrics from positively identified individuals from the Forensic Databank, a four-way DFA was performed on American Asian, black, Hispanic, and white males. The DFA resulted in a total correct classification of 77.3% using 15 forward stepwise selected variables. The CV plot for the craniometric analysis has been combined with that of the combined molar shape variable CV plot for comparison in Figure 10.2. While the craniometrics performed better in terms of total correct classifications, the relationships among groups are quite similar. In each analysis, American whites are the most distinct from each group and American Asians and Hispanics cluster near one another. The similarity between the two graphs demonstrates that the method proposed in the current study is applicable as it shows similar trends to currently applied methods.

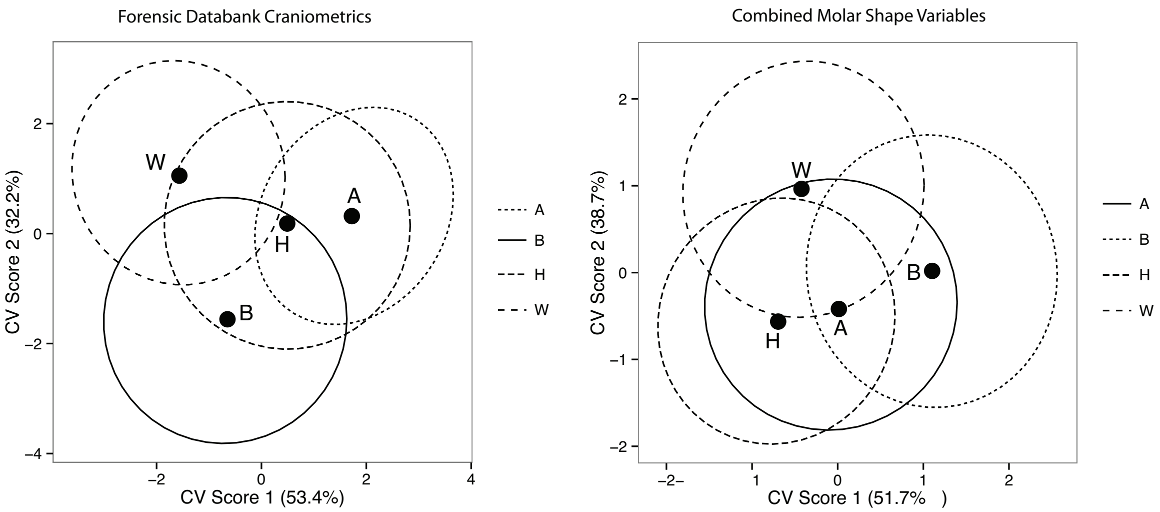


Fig. 10.2. Comparison of CV plots from craniometrics on modern American crania (left) and modern American molars (right).

10.7 BIOLOGICAL AFFINITY IN THE UNITED STATES

Each of the four modern U.S. groups was found to be a significantly unique group as compared to data from potential parental populations. Even though it is well understood that race is a sociological construct (Smedley, 1993; AJPA, 1996; Marks, 1996; AAA, 1998), the social stigmas surrounding race have acted as a barrier for gene flow, thus contributing to the uniqueness of each group. Rosenfeld (2008) noted that members of one social group were 100 times more likely to marry endogamously. Furthermore, Kalmijn (1998) described that the endogamy bias in the U.S. is likely due to the fact that marriage candidates have a preference for spouses similar to themselves, third parties often interfere in exogamy, and, lastly, there is a bias in access to other social groups. The bias in access to social groups has been demonstrated by the racially segregated residence patterns in the U.S. (Iceland and Wilks, 2006) wherein social groups tend to stay in clusters with members of the same group (Massey and Denton, 1993). Additionally, Iceland and Wilks (2006) did note that American Asians and Hispanics were less segregated residentially from American whites than American blacks were, which coincides with these groups higher intermarriage rates with American whites (Taylor et al., 2012a).

Moreover, the identification of belonging to a particular social group affords more political influence for disparate groups, though the definition of these groups has been in flux historically (Omi and Winant, 1994). The greater agency afforded by social identification to a particular group reinforces the "racial common sense" and "racial expectations" experienced within groups (Omi and Winant, 1994; Winant, 2000). Social and geographic stratification, mate preference, and social pressures have all led to the limited gene flow between the four groups in the United States. For each of these aforementioned reasons, the likely factor for the observed differences in molar morphometrics is positive assortative mating, the same conclusion that Ousley et al. (2009) have also arrived through craniometric analyses.

Lastly, it might be the case that the similarities noted in groups may be due to parallelism (Schluter et al., 2004) wherein the relative location of molar cusps evolved independently under similar selective forces, such as the positive assortative mating as postulated above or similarities in diet. Assuming that the environmental pressures are consistent across the groups, the relative location of molar cusps may have a biomechanical component related to the environment, such as diet.

Still, it is necessary to address ascertainment, or sampling bias. The skeletal populations of the collection represent a nonrandom sample that may not adequately represent the larger population. Additionally, the effect of sample size will directly impact ascertainment bias (e.g., larger sample sizes will have a larger ascertainment bias) (Rogers and Jorde, 1996). Due to the nature of discriminant function, each specimen is forced into a previously prescribed group category, which is only as meaningful as the label placed upon it (Rencher, 1995). A larger sample size for a particular group will thus influence the means for each population and thus their discriminatory power. However, to lessen ascertainment bias, the prior probabilities were set as equal to not influence the model, though this does not explicitly negate the issue of the differences in group means due to sample sizes as previously discussed.

CHAPTER 11: CONCLUSIONS

11.1 REPEATABILITY, SEXUAL DIMORPHISM, AND ASYMMETRY

Coordinate data from molar cusp apices can be consistently and confidently collected via a 3D digitizer (Chapter 4.1). The only instance of sexual dimorphism noted between shape variables is between American black females and males in M^1 (Chapter 4.2). Lastly, asymmetry between molar antimeres is low with only American Hispanics demonstrating significant differences between the antimeres of M^1, however, no other tooth or group showed any significant asymmetric differences (Chapter 4.3). Thus, the molars can be confidently employed in morphometric studies wherein the cusp tips are utilized as landmarks to define a shape. Furthermore, the sexes can be pooled for analyses due to the removal of overall size and the antimeres can be used interchangeably without a loss in data fidelity.

11.2 AMERICAN ASIAN COMPARISON

American Asians demonstrate significant differences from each of the groups in their population biohistory analyses (Chapter 5). Still they share the greatest affinities with American Indians, American whites, and East Asians. Thus the hypothesis that American Asians will demonstrate intermediacy between East Asians and American whites (Hypothesis 1) has been supported. Given ancestral lineages known about East Asians and American Indians (Turner, 1990; Scott and Turner, 2008), the similarity between American Asians and American Indians is not surprising. Furthermore, the majority of the American Asian and Indian samples came from the same collection that was comprised of individuals living in the same location (southwest New Mexico), which would lead to less restricted gene flow. Additionally, American Asians have the highest intermarriage rate with

American whites (Taylor et al., 2012a), the gene flow thus leading to their intermediacy between American Indians/East Asians and American whites. Finally, the analyses that include size demonstrate more variability than shape alone, indicating that size may be more informative than size in discriminating American Asians from other groups.

11.3 AMERICAN BLACK COMPARISON

American blacks are significantly different from each of the groups in biohistory analyses (Chapter 6). Following what is known of their population history and reported intermarriage rates (Taylor et al. 2012a), American blacks are intermediate between West Africans and American whites. Thus Hypothesis 2, which stated that American blacks would demonstrate intermediacy between West Africans and American whites, has been supported. Just as in the American Asian biohistory, the inclusion of size shows the uniqueness of American blacks to other groups. Interestingly, they demonstrate molar sizes that are between West Africans that have larger molars, and American whites that have smaller molars. The variability and intermediacy of the size again demonstrates that size might be more plastic than shape.

11.4 AMERICAN HISPANIC COMPARISON

In terms of shape, American Hispanics and American Indians do not demonstrate any significant differences, however, with the inclusion of size, they prove to be a unique group (Chapter 7). The similarity between American Hispanics and Indians was likely due to the samples coming from the same area (Legendre, 1993) and also the way in which ancestries were prescribed to individuals in the Economides collection (Edgar et al., 2011). The results do not lend support for Hypothesis 3, wherein it was postulated that American Hispanics would demonstrate intermediacy between historic Spanish and Mexican and

American whites. Just as in the previous analyses, the inclusion of size increased the discriminating power of the shape variables. Generally, in both shape and size, American Hispanics are intermediate between American Indians and whites. American Hispanics do share the second highest intermarriage rate with American whites (Taylor et al., 2012a), which like contributes to the intermediacy observed.

11.5 AMERICAN WHITE COMPARISON

American whites are significantly different from each of the groups in the biohistory analyses. In size, American whites are generally more similar other American groups, but are most distinct in shape from American blacks (Chapter 8). American whites are most similar to the historic European group in the size-based analyses wherein both groups have the smallest molars; however, they are dissimilar in the shape-based analyses. Again, the importance of size in discriminating between modern group and parental groups has been shown. Due to the greater affinities of American whites to other modern U.S. groups, the results do not lend support to Hypothesis 4, which stated that American whites would be most similar to the historic European group. Unlike previous groups, M^2 plays a more central role in discriminating between populations, a trend also noted by Kenyhercz et al. (2014a). In both the present study and Kenyhercz et al. (2014a), M^2 is more of an exaggerated rhomboidal shape, whereas other groups were either hyper-variable or rectangular in comparison. Consistent with previous trends, the analysis of both size and shape of the combined molars yields the greatest discriminating power and shows that American whites are most similar to American Hispanics and blacks and least similar to American Indians. Thus, American whites should be treated as a unique population group instead of being lumped together into a broader “European” or “Caucasian” category.

11.6 COMPARISON OF MODERN AMERICAN GROUPS

Each of the big four groups is significantly different from one another. However, American Asians and Hispanics consistently misclassify as one another more commonly than any of the other group misclassifications. American whites have the smallest method ranges and the highest mean total correct classifications, thus indicating their greater homogeneity. Conversely, greater heterogeneity is shown in American Hispanics and Asians where both groups show the lowest mean classifications and highest method ranges. The observed variation lends support to Hypothesis 5, which states that groups with greater allele-frequency differences and lower intermarriage rates will be less variable and vice versa.

The polar molars demonstrate greater variability between groups than the distal molars; additionally, the maxillary teeth have more variability than the mandibular teeth. The combined molar analyses, specifically the morphometric-derived analyses, have the most optimistic model performances, while the M_2 analyses present the poorest model performances.

The current study is the first of its kind to compare each of the four major groups in the United States. Because there have been no comparable studies, the current study's data were compared to craniometrics of modern U.S. samples via Fordisc 3.0 (Jantz and Ousley, 2005). The craniometrics and combined molar shape variables present similar trends (Chapter 10); for example, American whites, in each instance, are the most unique and homogenous of the modern American groups. In any event, each of the four modern U.S. groups has proven to be significantly different from one another, likely due to restricted gene flow through cultural barriers leading to positive assortative mating. Shape and size have demonstrated different trends in affinity between groups, and almost always, the inclusion of size in a shape analysis improves model performance. However, the morphometric shape and size analyses virtually always out perform the ILD analyses, which indicates that the relative spatial locations of cusp apices are more informative than simply linear dimensions between points.

11.7 FUTURE IMPLICATIONS

The data collection technique and subsequent analyses proposed in the current study have implications far outside of measuring modern population variation. Currently, molar morphometrics are most commonly applied to paleoanthropological contexts (Hartman, 1989; Hlusko, 2002; Bailey, 2004; Gómez-Robles et al. 2007; Bailey et al., 2008), though many of these studies are based upon utilizing outline analyses and sliding landmarks in addition to relative cusp location. The currently proposed methodology of digitizing molar cusp apices offers a means of rapid and consistent data collection that will generate a simple and easily interpretable model of the molars. What's more, the data can be compared to other populations, to examine both micro- (admixed, modern populations) and macro-evolutionary (paleoanthropological lineages) processes. So long as that each of the homologous cusps is visible and locatable (not too heavily worn), data can be collected and compared to examine both shape and size changes. For example, the proposed methodology may be used in a macro-evolutionary context, wherein molar cusp morphometrics can be compared across the ancestral lineages of *Homo* and *Australopithecus* to examine trends in molar shape over time, which could further be related to other known data, such as dietary preference and specific environmental conditions. The proposed methodology is especially useful in paleoanthropological contexts because oftentimes, teeth are all that remains and the method is non-invasive and easily implementable.

In addition to questions of population history, phenetics, or cladistics, the currently proposed method can also be used as a means to study fluctuating dental asymmetry, again, in terms of both shape and size. The proposed method could examine asymmetrical shape differences to examine levels of population stress. For example, American Hispanics and blacks are generally in a lower socioeconomic status, which would cause differential (less) access to nutrition and healthcare, which might express differences in molar antimeres.

Lastly, given the fact that the combined molar analyses outperform single molar models, it stands to reason that incorporating more teeth will further improve results. However, the issue with other teeth, primarily anterior teeth, is finding homologous landmarks that can be confidently and repeatedly collected. A potential solution to the homologous landmark identification issue may be to collect the points at which the maximum mesiodistal and buccolingual landmarks as determined by the caliper placement, as well as other landmarks, such as the apex of the cervical enamel junction. Additionally, in modern teeth where the differential wear between specimens is minimal, the z value for the specific landmarks can be reintroduced to add a three-dimensional aspect to each respective landmark. The relative spatial location of landmarks has proven to be more useful than simply linear measures as a means to study variation between admixed populations.

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APPENDIX A

CLASSIFICATION AND D^2 MATRICES FOR AMERICAN ASIAN POPULATION BIOHISTORY

Table A.1. Combined molar shape PCs linear discriminant function results using 7 forward stepwise selected variables: M^1 PC1, M^1 PC3, M^2 PC2, M_1 PC1, M_1 PC2, M_2 PC2, M_2 PC3.

From Group	**Total Number**	**Into Group (%)**						
		AA	**AI**	**EA**	**NA**	**SEA**	**Th**	**AW**
AA	140	**28.6**	25.0	12.1	7.9	4.3	4.3	17.9
AI	19	21.1	**47.4**	0.0	5.3	5.3	0.0	21.1
EA	23	13.0	0.0	**34.8**	0.0	34.8	13.0	4.3
NA	19	5.3	10.5	0.0	**47.4**	5.3	15.8	15.8
SEA	22	4.5	0.0	31.8	13.6	**9.1**	40.9	0.0
Th	21	4.8	0.0	28.6	14.3	9.5	**42.9**	0.0
AW	165	8.5	12.7	3.6	12.7	3.0	3.0	**56.4**

Total correct: 175 out of 409 (42.8%) Cross-validated

Table A.2. Combined molar shape PC and size linear discriminant function results using 8 forward stepwise selected variables: M^1 PC1, M^2 centroid size, M^2 PC1, M^2 PC2, M^2 PC3, M_1 PC1, M_1 PC2, M_1 PC3.

From Group	**Total Number**	**Into Group (%)**						
		AA	**AI**	**EA**	**NA**	**SEA**	**Th**	**AW**
AA	140	**27.9**	24.3	11.4	9.3	4.3	5.0	17.9
AI	19	31.6	**47.4**	0.0	10.5	0.0	0.0	10.5
EA	23	4.3	0.0	**43.5**	0.0	30.4	17.4	4.3
NA	19	0.0	10.5	5.3	**52.6**	5.3	10.5	15.8
SEA	22	4.5	0.0	31.8	9.1	**36.4**	9.1	9.1
Th	21	4.8	0.0	9.5	14.3	4.8	**66.7**	0.0
AW	165	9.7	10.3	1.2	9.7	5.5	1.2	**62.4**

Total correct: 193 out of 409 (47.2%) Cross-validated

Table A.3. Combined molar ILD linear discriminant function results using 8 forward stepwise selected variables: M^1 1-3, M^1 2-3, M^2 1-4, M_1 1-2, M_1 1-4, M_1 2-4, M_2 2-3, M_2 2-4.

From Group	Total Number	Into Group (%)						
		AA	AI	EA	NA	SEA	Th	AW
AA	122	**27.9**	20.5	6.6	9.8	14.8	3.3	17.2
AI	38	10.5	**68.4**	0.0	5.3	5.3	0.0	10.5
EA	23	4.3	13.0	**34.8**	4.3	17.4	17.4	8.7
NA	21	0.0	4.8	4.8	**57.1**	14.3	9.5	9.5
SEA	23	0.0	0.0	26.1	0.0	**34.8**	12.0	26.1
Th	44	4.5	2.3	9.1	13.6	4.5	**65.9**	0.0
AW	166	7.2	15.7	9.0	9.0	7.8	4.2	**47.0**

Total correct: 195 out of 437 (44.6%) Cross-validated

Table A.4. Combined molar ILD PC linear discriminant function results using 7 forward stepwise selected variables: PC1, PC3, PC4, PC5, PC6, PC8, PC11.

From Group	Total Number	Into Group (%)						
		AA	AI	EA	NA	SEA	Th	AW
AA	122	**35.2**	20.5	7.4	5.7	11.5	3.3	16.4
AI	38	15.8	**63.2**	5.3	0.0	5.3	0.0	10.5
EA	23	8.7	0.0	**26.1**	4.3	34.8	17.4	8.7
NA	21	14.3	4.8	4.8	**52.4**	4.8	14.3	4.8
SEA	23	8.7	4.3	34.8	0.0	**17.4**	8.7	26.1
Th	44	6.8	0.0	13.6	18.2	0.0	**59.1**	2.3
AW	166	8.4	8.4	3.6	13.3	4.8	2.4	**59.0**

Total correct: 212 out of 437 (48.5%) Cross-validated

Table A.5. Mahalanobis D^2 matrix based on the shape PCs of the combined molars for American Asian biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	AA	AI	EA	NA	SEA	Th	AW
AA	-						
AI	1.24	-					
EA	1.92	5.07	-				
NA	3.43	5.16	3.63	-			
SEA	2.41	6.15	**0.73**	4.06	-		
Th	6.21	10.13	2.80	5.09	3.18	-	
AW	0.58	1.87	2.95	3.26	2.83	8.13	-

Table A.6. Mahalanobis D^2 matrix based on the shape PCs and centroid sizes of the combined molars for American Asian biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	AA	AI	EA	NA	SEA	Th	AW
AA	-						
AI	1.18	-					
EA	2.85	6.21	-				
NA	4.05	5.45	6.05	-			
SEA	3.21	7.16	**0.90**	5.99	-		
Th	6.86	10.32	4.13	6.65	5.00	-	
AW	1.67	3.87	4.29	5.74	3.85	11.07	-

Table A.7. Mahalanobis D^2 matrix based on the ILDs of the combined molars for American Asian biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	AA	AI	EA	NA	SEA	Th	AW
AA	-						
AI	1.10	-					
EA	1.62	3.97	-				
NA	2.84	6.12	3.77	-			
SEA	1.66	4.03	**0.36**	4.41	-		
Th	5.41	8.25	3.53	5.10	4.33	-	
AW	0.77	2.36	2.64	3.32	2.62	8.52	-

Table A.8. Mahalanobis D^2 matrix based on the ILD PCs of the combined molars for American Asian biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	AA	AI	EA	NA	SEA	Th	AW
AA	-						
AI	1.36	-					
EA	2.32	5.43	-				
NA	3.65	6.45	5.11	-			
SEA	2.56	5.23	**0.43**	6.07	-		
Th	5.92	10.24	4.01	4.98	6.21	-	
AW	1.62	4.07	4.22	4.11	3.95	9.17	-

APPENDIX B

CLASSIFICATION AND D^2 MATRICES FOR AMERICAN BLACK POPULATION BIOHISTORY

Table B.1. Combined molar shape PC linear discriminant function results using 7 forward stepwise selected variables: M^1 PC1, M^1 PC3, M^2 PC3, M_1 PC1, M_1 PC2, M_1 PC3,M_2 PC1.

From Group	**Total Number**	**Into Group (%)**					
		B	**EA**	**NA**	**SA**	**W**	**WA**
AB	95	**49.5**	13.7	9.5	7.4	6.3	13.7
EA	21	9.5	**38.1**	9.5	14.3	14.3	14.3
NA	63	3.2	15.9	**50.8**	17.5	9.5	3.2
SA	14	7.1	0.0	28.6	**42.9**	0.0	21.4
AW	167	13.2	4.8	4.8	0.0	**67.7**	9.6
WA	67	16.4	16.4	3.0	9.0	11.9	**43.3**

Total correct: 235 out of 427 (55.0%) Cross-validated

Table B.2. Combined molar shape PC and size linear discriminant function results using 8 forward stepwise selected variables: M^1 PC1, M^1 PC3, M_1 centroid size, M_1 PC1, M_1 PC2, M_1 PC3, M_2 centroid size, M_2 PC1.

From Group	**Total Number**	**Into Group (%)**					
		B	**EA**	**NA**	**SA**	**W**	**WA**
AB	95	**56.8**	7.4	6.3	6.3	10.5	12.6
EA	21	14.3	**38.1**	9.5	14.3	14.3	9.5
NA	63	6.3	9.5	**57.1**	19.0	7.9	0.0
SA	14	14.3	7.1	21.4	**42.9**	0.0	14.3
AW	167	13.8	5.4	2.4	1.8	**62.9**	13.8
WA	67	16.4	10.4	3.0	10.4	11.9	**47.8**

Total correct: 241 out of 427 (56.4%) Cross-validated

Table B.3. Combined molar ILD linear discriminant function results using 11 forward stepwise selected variables: M^1 1-2, M^1 1-3, M^2 1-2 M_1 1-2, M_1 1-3, M_1 1-4, M_1 2-4 M_1 3-4, M_2 1-2, M_2 2-4, M_2 3-4.

From Group	**Total Number**	**Into Group (%)**					
		B	**EA**	**NA**	**SA**	**W**	**WA**
AB	124	**39.5**	6.5	1.6	7.3	24.2	21.0
EA	23	21.7	**39.1**	13.0	13.0	8.7	4.3
NA	63	1.6	17.5	**58.7**	15.9	6.3	0.0
SA	15	6.7	20.0	26.7	**40.0**	0.0	6.7
AW	167	16.8	5.4	3.6	3.6	**61.1**	9.6
WA	73	19.2	6.8	4.1	13.7	15.1	**41.1**

Total correct: 233 out of 465 (50.1%) Cross-validated

Table B.4. Combined molar ILD PC linear discriminant function results using 11 forward stepwise selected variables: PC1, PC3, PC4, PC5, PC6, PC7, PC8.

From Group	**Total Number**	**Into Group (%)**					
		B	**EA**	**NA**	**SA**	**W**	**WA**
AB	124	**43.5**	8.1	4.0	6.5	20.2	17.7
EA	23	8.7	**47.8**	8.7	17.4	13.0	4.3
NA	63	1.6	15.9	**58.7**	19.0	3.2	1.6
SA	15	13.3	0.0	33.3	**40.0**	6.7	6.7
AW	167	20.4	10.8	2.4	1.2	**53.9**	11.4
WA	73	19.2	16.4	2.7	17.8	11.0	**32.9**

Total correct: 22 out of 465 (47.7%) Cross-validated

Table B.5. Mahalanobis D^2 matrix based on the shape PCs of the combined molars for American black biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	**B**	**EA**	**NA**	**SA**	**W**	**WAB**
AB	-					
EA	2.91	-				
NA	4.18	3.20	-			
SA	4.18	**2.71**	2.02	-		
AW	4.11	4.32	6.07	8.33	-	
WA	2.56	1.92	4.45	2.86	3.42	-

Table B.6. Mahalanobis D^2 matrix based on the shape PCs and centroid sizes of the combined molars for American black biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	**B**	**EA**	**NA**	**SA**	**W**	**WAB**
AB	-					
EA	2.37	-				
NA	5.79	2.85	-			
SA	4.42	**2.28**	2.36	-		
AW	4.07	4.07	8.04	8.85	-	
WA	2.84	2.38	6.16	3.47	3.63	-

Table B.7. Mahalanobis D^2 matrix based on the ILDs of the combined molars for American black biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	**B**	**EA**	**NA**	**SA**	**W**	**WAB**
AB	-					
EA	3.42	-				
NA	6.37	3.00	-			
SA	3.38	**2.38**	2.78	-		
AW	1.28	5.09	7.97	6.86	-	
WA	1.38	3.31	6.57	3.35	3.05	-

Table B.8. Mahalanobis D^2 matrix based on the ILD PCs of the combined molars for American black biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	**B**	**EA**	**NA**	**SA**	**W**	**WAB**
AB	-					
EA	3.52	-				
NA	6.07	3.91	-			
SA	3.46	**3.34**	2.12	-		
AW	1.25	3.78	8.02	6.15	-	
WA	1.70	3.79	6.51	3.30	2.11	-

APPENDIX C

CLASSIFICATION AND D^2 MATRICES FOR AMERICAN HISPANIC POPULATION BIOHISTORY

Table C.1. Combined molar linear discriminant function results using 4 forward stepwise selected variables: M^1 PC1, M_1 PC1, M_1 PC2, M_1 PC3.

From Group	Total Number	Into Group (%)				
		AI	**AH**	**Sp**	**Mex**	**AW**
AI	19	**52.6**	26.3	5.3	0.0	15.8
AH	192	22.4	**37.0**	16.7	5.7	18.2
Sp	10	10.0	10.0	**30.0**	30.0	20.0
Mex	25	0.0	0.0	28.0	**72.0**	0.0
AW	164	22.6	17.7	14.0	6.7	**39.0**

Total correct: 166 out of 410 (40.5%) Cross-validated

Table C.2. Combined molar linear discriminant function results using 6 forward stepwise selected variables: M^1 Log Centroid Size, M^1 PC1, M^1 PC3, M^2 PC2, M_1 PC3, M_2 PC1.

From Group	Total Number	Into Group (%)				
		AI	**AH**	**Sp**	**Mex**	**AW**
AI	19	**63.2**	21.1	5.3	0.0	10.5
AH	192	24.5	**45.8**	8.3	6.3	15.1
Sp	10	0.0	0.0	**30.0**	20.0	50.0
Mex	25	0.0	8.0	8.0	**84.0**	0.0
AW	164	12.2	14.0	21.3	4.9	**47.6**

Total correct: 202 out of 410 (49.3%) Cross-validated

Table C.3. Combined molar linear discriminant function results using 11 forward stepwise selected variables: M^1 1-3, M^1 1-4, M^1 2-3, M^2 1-2, M^2 1-4, M^2 2-3, M_1 1-3, M_1 3-4, M_2 2-3, M_2 2-4, M_2 3-4.

From Group	Total Number	Into Group (%)				
		AI	**AH**	**Sp**	**Mex**	**AW**
AI	19	**57.9**	26.3	10.5	0.0	5.3
AH	200	22.0	**43.0**	8.5	9.0	17.5
Sp	11	9.1	9.1	**27.3**	9.1	45.5
Mex	27	0.0	3.7	11.1	**81.5**	3.7
AW	167	6.0	13.8	15.6	9.0	**55.7**

Total correct: 215 out of 424 (50.7%) Cross-validated

Table C.4. Combined molar linear discriminant function results using 11 forward stepwise selected variables: PC1, PC3, PC4, PC5, PC6, PC7, PC8, PC10, PC11, PC12.

From Group	**Total Number**	**Into Group (%)**				
		AI	**AH**	**Sp**	**Mex**	**AW**
AI	19	**57.9**	31.6	5.3	0.0	5.3
AH	200	29.5	**32.0**	15.0	6.5	17.0
Sp	11	0.0	9.1	**27.3**	18.2	45.5
Mex	27	3.7	0.0	14.8	**77.8**	3.7
AW	167	5.4	16.2	18.6	5.4	**54.5**

Total correct: 190 out of 424 (44.8%) Cross-validated

Table C.5. Mahalanobis D^2 matrix based on the shape PCs of the combined molars for American Hispanic biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	**AI**	**AH**	**Sp**	**Mex**	**AW**
AI	-				
AH	**0.35**	-			
Sp	**1.80**	1.48	-		
Mex	4.97	5.17	**1.36**	-	
AW	1.34	0.53	**1.21**	4.72	-

Table C.6. Mahalanobis D^2 matrix based on the shape PCs and centroid size of the combined molars for American Hispanic biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	**AI**	**AH**	**Sp**	**Mex**	**AW**
AI	-				
AH	1.53	-			
Sp	6.14	3.29	-		
Mex	8.06	6.66	5.59	-	
AW	4.05	1.96	**1.21**	8.29	-

Table C.7. Mahalanobis D^2 matrix based on the ILDs of the combined molars for American Hispanic biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	AI	AH	Sp	Mex	AW
AI	-				
AH	1.58	-			
Sp	5.75	3.12	-		
Mex	9.60	7.12	6.14	-	
AW	4.43	2.03	2.19	7.81	-

Table C.8. Mahalanobis D^2 matrix based on the ILD PCs of the combined molars for American Hispanic biohistory. Values not significantly different at $p > 0.05$ are in bold.

Group	AI	AH	Sp	Mex	AW
AI	-				
AH	**1.04**	-			
Sp	5.19	2.85	-		
Mex	9.08	8.25	6.81	-	
AW	4.32	1.68	1.93	8.77	-

APPENDIX D

CLASSIFICATION AND D^2 MATRICES FOR AMERICAN WHITE POPULATION BIOHISTORY

Table D.1. Combined molar shape PC linear discriminant function results using 13 forward stepwise selected variables: M^1 PC1, M^1 PC2, M^1 PC3, M^2 PC1, M^2 PC2, M^2 PC3, M_1 PC1, M_1 PC2, M_1 PC3, M_1 PC4, M_1 PC5, M_2 PC1, M_2 PC3.

From Group	**Total Number**	**Into Group (%)**					
		AA	**AI**	**AB**	**EU**	**AH**	**AW**
AA	140	**23.6**	17.1	15.7	9.3	21.4	12.9
AI	38	15.8	**52.6**	5.3	0.0	21.1	5.3
AB	119	10.1	10.9	**42.0**	16.0	6.7	14.3
EU	41	7.3	2.4	19.5	**51.2**	7.3	12.1
AH	193	11.4	15.5	7.8	6.7	**46.1**	12.4
AW	167	7.2	9.0	9.0	9.6	12.0	**53.3**

Total correct: 302 out of 698 (43.3%) Cross-validated

Table D.2. Combined molar shape PC and size linear discriminant function results using 15 forward stepwise selected variables: M^1 Log centroid size, M^1 PC1, M^1 PC2, M^1 PC3, M^2 Log centroid size, M^2 PC1, M^2 PC2, M^2 PC3, M_1 PC1, M_1 PC2, M_1 PC3, M_1 PC4, M_2 Log centroid size M_2 PC1, M_2 PC3.

From Group	**Total Number**	**Into Group (%)**					
		AA	**AI**	**AB**	**EU**	**AH**	**AW**
AA	140	**28.6**	14.3	13.6	8.6	22.1	12.9
AI	38	10.5	**52.6**	10.5	0.0	21.1	5.3
AB	119	10.1	14.3	**47.1**	9.2	6.7	12.6
EU	41	4.9	0.0	17.1	**58.5**	4.9	14.6
AH	193	16.6	15.0	5.7	7.3	**42.5**	13.0
AW	167	4.2	5.4	11.4	10.8	10.8	**57.5**

Total correct: 318 out of 698 (45.6%) Cross-validated

Table D.3. Combined molar ILD linear discriminant function results using 9 forward stepwise selected variables: M^1 1-2, M^1 1-3, M^1 1-4, M^1 2-3, M^1 2-4, M_1 1-4, M_1 2-4, M_1 3-4, M_2 1-2.

From Group	**Total Number**	**Into Group (%)**					
		AA	**AI**	**AB**	**EU**	**AH**	**AW**
AA	145	**36.6**	24.1	4.8	9.0	15.2	10.3
AI	19	21.1	**36.8**	10.5	10.5	21.1	0.0
AB	124	9.7	9.7	**35.5**	19.4	7.3	18.5
EU	44	9.1	6.8	11.4	**47.7**	11.4	13.6
AH	201	16.9	18.4	7.5	7.0	**34.3**	15.9
AW	167	8.4	8.4	16.2	16.2	8.4	**42.5**

Total correct: 265 out of 700 (37.9%) Cross-validated

Table D.4. Combined molar linear discriminant function results using 9 forward stepwise selected variables: PC1, PC4, PC5, PC6, PC7, PC8, PC9, PC10, PC11.

From Group	**Total Number**	**Into Group (%)**					
		AA	**AI**	**AB**	**EU**	**AH**	**AW**
AA	145	**31.7**	15.9	13.1	10.3	17.9	11.0
AI	19	26.3	**26.3**	21.1	0.0	21.1	5.3
AB	124	8.9	12.9	**45.2**	17.7	0.8	5.6
EU	44	11.4	4.5	15.9	**50.0**	2.3	15.9
AH	201	13.9	19.4	6.5	8.5	**35.3**	16.4
AW	167	6.0	6.0	18.6	13.8	15.0	**40.7**

Total correct: 268 out of 700 (38.3%) Cross-validated

Table D.5. Mahalanobis D^2 matrix based on the shape PCs of the combined molars for American white biohistory. All values are significantly different at $p > 0.05$.

Group	**AA**	**AI**	**AB**	**EU**	**AH**	**AW**
AA	-					
AI	1.54	-				
AB	1.77	3.50	-			
EU	3.80	8.04	3.36	-		
AH	1.01	1.96	3.38	5.33	-	
AW	2.26	4.11	2.87	4.40	2.54	-

Table D.6. Mahalanobis D^2 matrix based on the shape PCs and centroid sizes of the combined molars for American white biohistory. All values are significantly different at $p > 0.05$.

Group	**AA**	**AI**	**AB**	**EU**	**AH**	**AW**
AA	-					
AI	1.78	-				
AB	2.57	4.66	-			
EU	5.31	10.72	4.25	-		
AH	1.16	2.51	3.66	6.22	-	
AW	3.06	5.39	2.89	5.05	2.81	-

Table D.7. Mahalanobis D^2 matrix based on the ILDs of the combined molars for American white biohistory. Values not significantly different at $p > 0.05$ are shown in bold.

Group	AA	AI	AB	EU	AH	AW
AA	-					
AI	**0.71**	-				
AB	1.73	2.38	-			
EU	2.20	3.28	0.82	-		
AH	0.63	**0.76**	2.00	2.51	-	
AW	1.63	2.43	1.11	1.64	1.37	-

Table D.8. Mahalanobis D^2 matrix based on the ILD PCs of the combined molars for American white biohistory. Values not significantly different at $p > 0.05$ are shown in bold.

Group	AA	AI	AB	EU	AH	AW
AA	-					
AI	**1.04**	-				
AB	2.01	3.35	-			
EU	3.19	6.18	2.86	-		
AH	0.71	1.27	2.90	3.86	-	
AW	1.97	3.46	1.81	2.78	1.57	-

APPENDIX E

CLASSIFICATION AND D^2 MATRICES FOR MODERN AMERICAN GROUPS

Table E.1. M^1 shape PC linear discriminant function results using 3 forward stepwise selected variables: PC1, PC2, PC3.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	152	**27.6**	20.4	29.6	22.4
AB	204	14.7	**50.5**	12.3	22.5
AH	219	17.4	10.5	**55.3**	16.9
AW	229	14.4	27.1	16.6	**41.9**

Total correct: 362 out of 804 (45.0%) Cross-validated

Table E.2. M^1 shape PC and centroid size linear discriminant function results using 4 forward stepwise selected variables: Log Centroid Size, PC1, PC2, PC3.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	152	**48.7**	13.8	24.3	13.2
AB	204	14.7	**47.5**	13.2	24.5
AH	219	21.9	10.5	**51.6**	16.0
AW	229	10.0	28.8	13.5	**47.6**

Total correct: 362 out of 804 (48.9%) Cross-validated

Table E.3. M^1 ILD linear discriminant function results using 5 forward stepwise selected variables: Cusp 1-2, 1-3, 1-4, 2-3, 3-4.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	152	**48.7**	14.5	27.0	9.9
AB	208	16.8	**52.4**	11.1	19.7
AH	217	27.2	13.4	**47.0**	12.4
AW	237	13.9	33.8	13.1	**39.2**

Total correct: 378 out of 814 (46.4%) Cross-validated

Table E.4. M^1 ILD PC linear discriminant function results using 2 forward stepwise selected variables: PC1, PC2.

From Group	Total Number	Into Group (%)			
		AA	AB	AH	AW
AA	152	**48.7**	12.5	28.3	10.5
AB	208	16.3	**48.6**	12.0	23.1
AH	217	30.4	11.5	**45.2**	12.9
AW	237	13.1	29.5	16.9	**40.5**

Total correct: 369 out of 814 (45.3%) Cross-validated

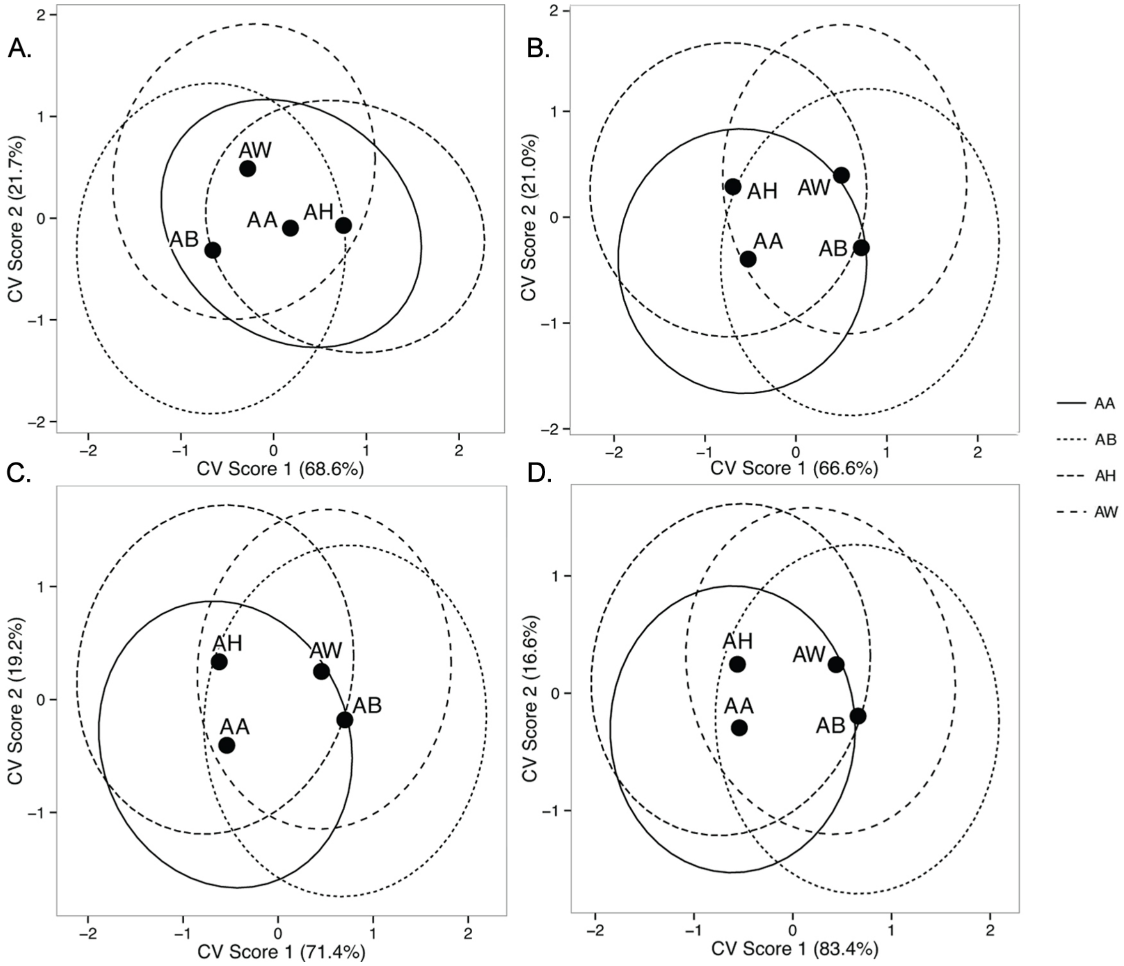

Fig. E.1. Comparison of canonical variate plots from each of the M^1 analyses. The molar shape dataset is shown at A, the shape and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

Table E.5. Mahalanobis D^2 matrix based on shape variables of M^1. All values significantly different at $p > 0.05$.

Group	**AA**	**AB**	**AH**	**AW**
AA	-			
AB	0.95	-		
AH	0.60	2.06	-	
AW	0.69	0.80	1.41	-

Table E.6. Mahalanobis D^2 matrix based on shape and size variables of M^1. All values significantly different at $p > 0.05$.

Group	**AA**	**AB**	**AH**	**AW**
AA	-			
AB	1.83	-		
AH	0.78	2.32	-	
AW	1.68	0.80	1.73	-

Table E.7. Mahalanobis D^2 matrix based on ILDs of M^1 All values significantly different at $p > 0.05$.

Group	**AA**	**AB**	**AH**	**AW**
AA	-			
AB	1.73	-		
AH	0.65	2.01	-	
AW	1.45	0.51	1.37	-

Table E.8. Mahalanobis D^2 matrix based on ILD PCs of M^1. All values significantly different at $p > 0.05$.

Group	**AA**	**AB**	**AH**	**AW**
AA	-			
AB	1.46	-		
AH	0.30	1.69	-	
AW	1.26	0.24	1.00	-

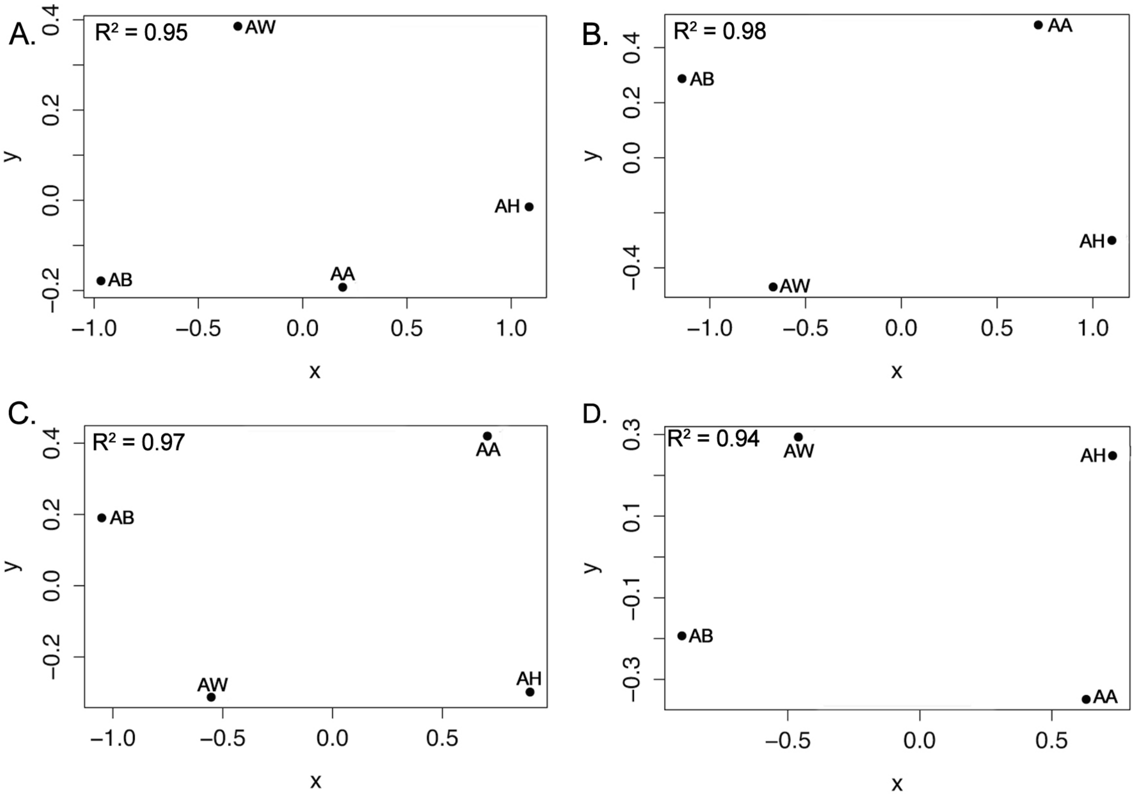

Fig. E.2. Comparison of two-dimensional PCO perceptual plots for each M^1 dataset with individual R^2 values displayed. The PCO of the M^1 shape PC dataset is shown at A, M^1 shape PC and size dataset at B, the M^1 ILD dataset at C, and the M^1 ILD PC dataset at D.

Table E.9. M^2 shape PC linear discriminant function results using 3 forward stepwise selected variables: PC1, PC2, PC3.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	148	**16.2**	26.4	39.9	17.6
AB	187	10.2	**47.1**	17.6	25.1
AH	208	14.9	15.9	**42.3**	26.9
AW	196	9.2	27.6	16.8	**46.4**

Total correct: 291 out of 739 (39.4%) Cross-validated

Table E.10. M^2 shape PC and centroid size linear discriminant function results using 4 forward stepwise selected variables: Log Centroid Size, PC1, PC2, PC3.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	148	**36.5**	21.6	27.7	14.2
AB	187	19.3	**40.1**	14.4	26.2
AH	208	31.3	13.9	**29.3**	25.5
AW	196	10.7	25.5	15.3	**48.5**

Total correct: 285 out of 739 (38.6%) Cross-validated

Table E.11. M^2 ILD linear discriminant function results using 3 forward stepwise selected variables: Cusps 1-2, 1-3, 3-4.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	146	**50.0**	19.9	11.6	18.5
AB	191	26.2	**36.1**	11.0	26.7
AH	209	28.2	21.1	**22.5**	28.2
AW	199	16.1	24.1	13.6	**46.2**

Total correct: 281 out of 745 (37.7%) Cross-validated

Table E.12. M^2 ILD PC linear discriminant function results using 4 forward stepwise selected variables: PC1, PC2, PC3, PC4.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	146	**43.8**	18.5	25.3	12.3
AB	191	25.7	**34.0**	13.6	26.7
AH	209	30.6	17.7	**25.4**	26.3
AW	199	12.1	25.6	14.1	**48.2**

Total correct: 278 out of 745 (37.3%) Cross-validated

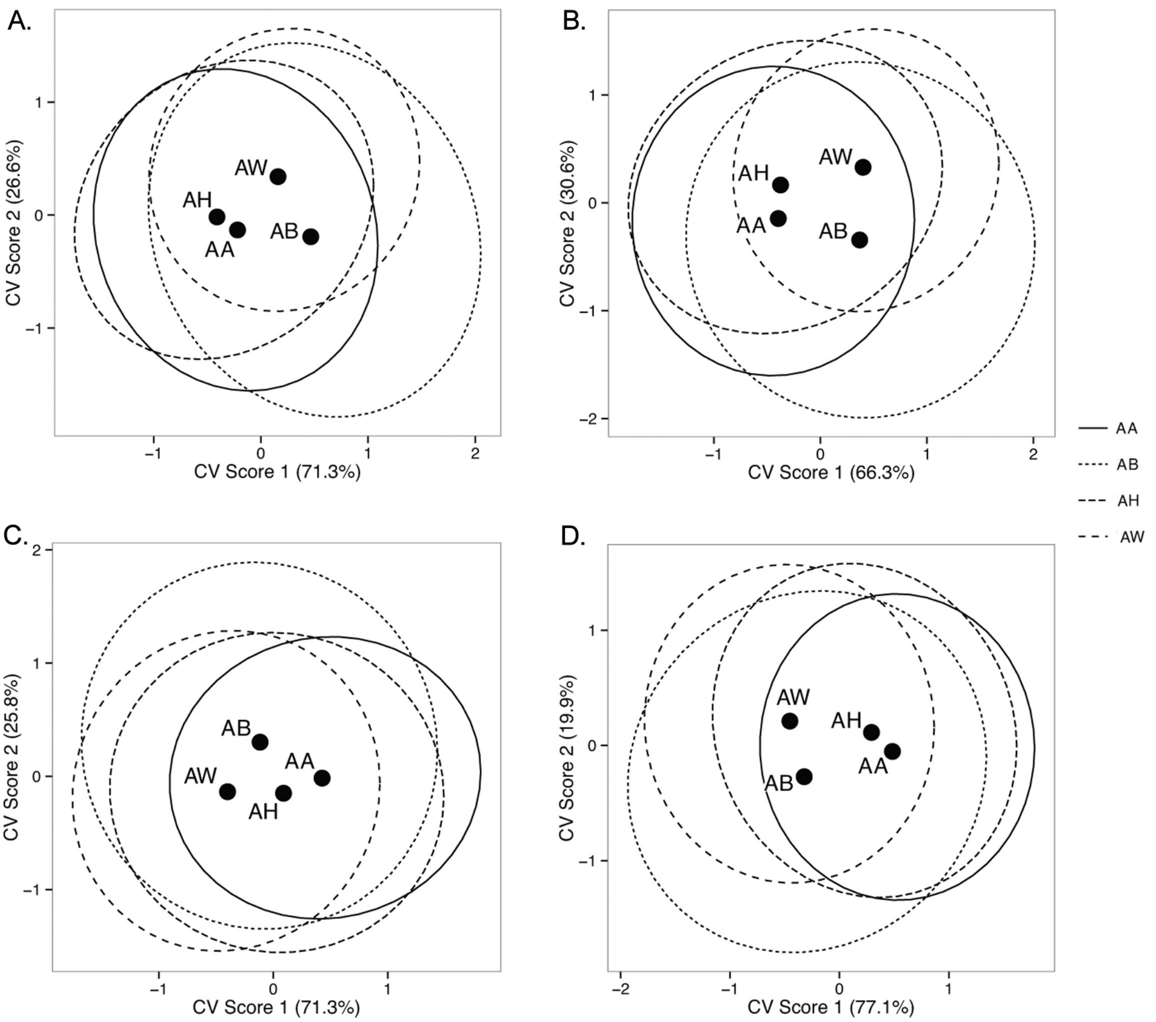

Fig. E.3. Comparison of canonical variate plots from each of the M^2 analyses. The molar shape dataset is shown at A, the shape and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

Table E.13. Mahalanobis D^2 matrix based on shape variables of M^2. Values not significantly different at $p > 0.05$ listed in bold.

Group	AA	AB	AH	AW
AA	-			
AB	0.48	-		
AH	**0.07**	0.80	-	
AW	0.37	0.38	0.46	-

Table E.14. Mahalanobis D^2 matrix based on shape PCs and centroid size of M^2. All values are significantly different at $p > 0.05$.

Group	AA	AB	AH	AW
AA	-			
AB	0.65	-		
AH	0.14	0.82	-	
AW	0.86	0.46	0.65	-

Table E.15. Mahalanobis D^2 matrix based on ILDs of M^2. All values are significantly different at $p > 0.05$.

Group	AA	AB	AH	AW
AA	-			
AB	0.40	-		
AH	0.15	0.25	-	
AW	0.70	0.28	0.26	-

Table E.16. Mahalanobis D^2 matrix based on ILD PCs of M^2. All values are significantly different at $p > 0.05$.

Group	AA	AB	AH	AW
AA	-			
AB	0.69	-		
AH	0.15	0.58	-	
AW	0.99	0.27	0.59	-

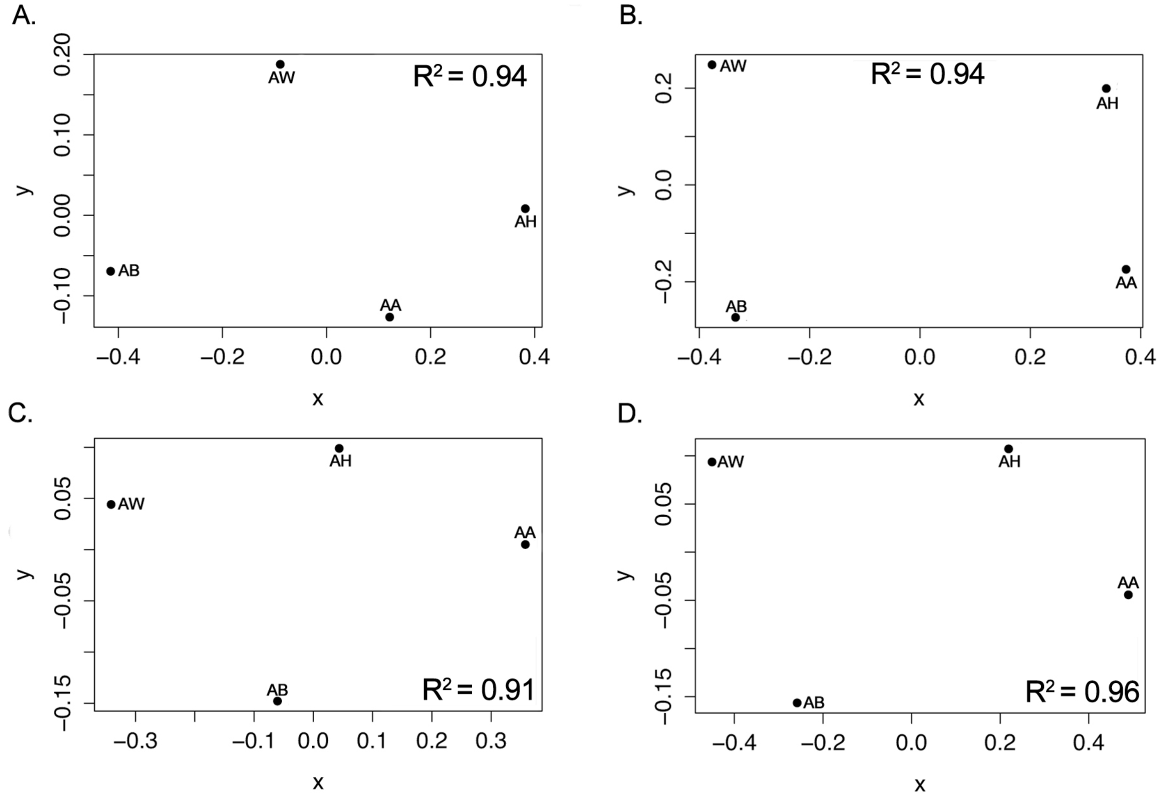

Fig. E.4. Comparison of two-dimensional PCO perceptual plots for each M^2 dataset with individual R^2 values displayed. The PCO of the shape PC dataset is shown at A, shape PC and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

Table E.17. M_1 shape PC linear discriminant function results using 4 forward stepwise selected variables: PC1, PC2, PC3, PC4.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	151	**26.5**	26.5	27.2	19.9
AB	167	18.0	**49.7**	11.4	21.0
AH	217	23.0	18.9	**29.0**	29.0
AW	211	11.4	14.2	17.5	**56.9**

Total correct: 306 out of 746 (41.0%) Cross-validated

Table E.18. M_1 shape PC and centroid size linear discriminant function results using 5 forward stepwise selected variables: Log Centroid Size, PC1, PC2, PC3, PC4.

From Group	Total Number	Into Group (%)			
		AA	AB	AH	AW
AA	151	**31.8**	25.8	27.8	14.6
AB	167	22.8	**47.9**	7.2	22.2
AH	217	26.3	17.1	**27.6**	29.0
AW	211	9.5	15.2	18.0	**57.3**

Total correct: 309 out of 746 (41.4%) Cross-validated

Table E.19. M_1 ILD linear discriminant function results using 4 forward stepwise selected variables: Cusps 1-5, 3-4, 3-5, 4-5.

From Group	Total Number	Into Group (%)			
		AA	AB	AH	AW
AA	151	**39.7**	20.5	25.8	13.9
AB	170	22.9	**45.3**	8.8	22.9
AH	219	27.9	16.9	**29.7**	25.6
AW	222	9.9	21.6	19.8	**48.6**

Total correct: 310 out of 762 (40.7%) Cross-validated

Table E.20. M_1 ILD PC linear discriminant function results using 5 forward stepwise selected variables: PC1, PC2, PC3, PC4, PC5.

From Group	Total Number	Into Group (%)			
		AA	AB	AH	AW
AA	151	**32.5**	26.5	32.3	17.9
AB	170	18.2	**50.6**	9.4	21.8
AH	219	22.8	17.8	**30.1**	29.2
AW	222	10.4	20.7	18.9	**50.0**

Total correct: 310 out of 762 (40.7%) Cross-validated

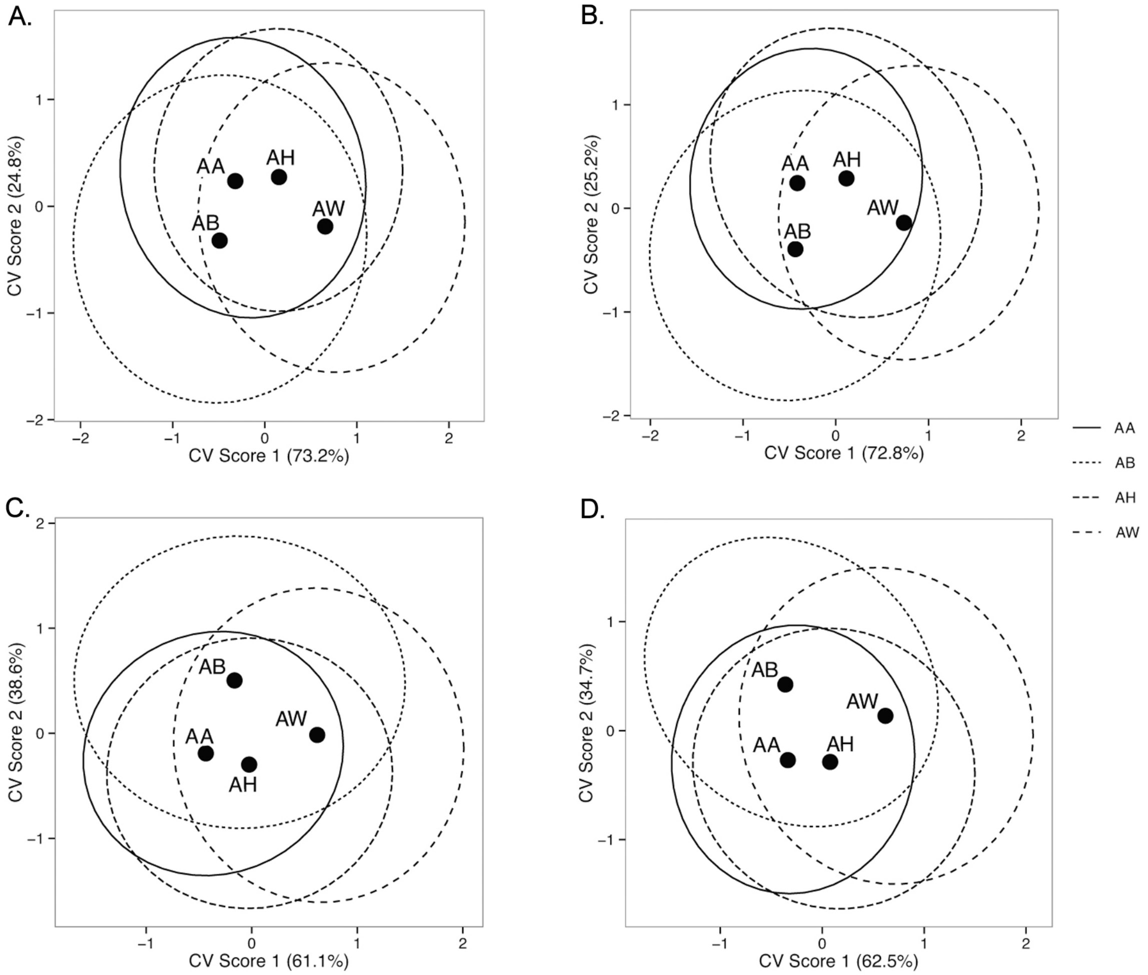

Fig. E.5. Comparison of canonical variate plots from each of the M_1 analyses. The molar shape dataset is shown at A, the shape and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

Table E.21. Mahalanobis D^2 matrix based on shape variables of M_1. All values are significantly different at $p > 0.05$.

Group	**AA**	**AB**	**AH**	**AW**
AA	-			
AB	0.36	-		
AH	0.26	0.77	-	
AW	1.14	1.37	0.48	-

Table E.22. Mahalanobis D^2 matrix based on shape PCs and centroid size of M_1. All values are significantly different at $p > 0.001$.

Group	AA	AB	AH	AW
AA	-			
AB	0.42	-		
AH	0.32	0.77	-	
AW	1.47	1.44	0.59	-

Table E.23. Mahalanobis D^2 matrix based on ILDs of M_1. All values are significantly different at $p > 0.01$.

Group	AA	AB	AH	AW
AA	-			
AB	0.56	-		
AH	0.19	0.66	-	
AW	1.14	0.88	0.50	-

Table E.24. Mahalanobis D^2 matrix based on ILDs of M_1. All values are significantly different at $p > 0.01$.

Group	AA	AB	AH	AW
AA	-			
AB	0.50	-		
AH	0.22	0.70	-	
AW	1.08	1.05	0.50	-

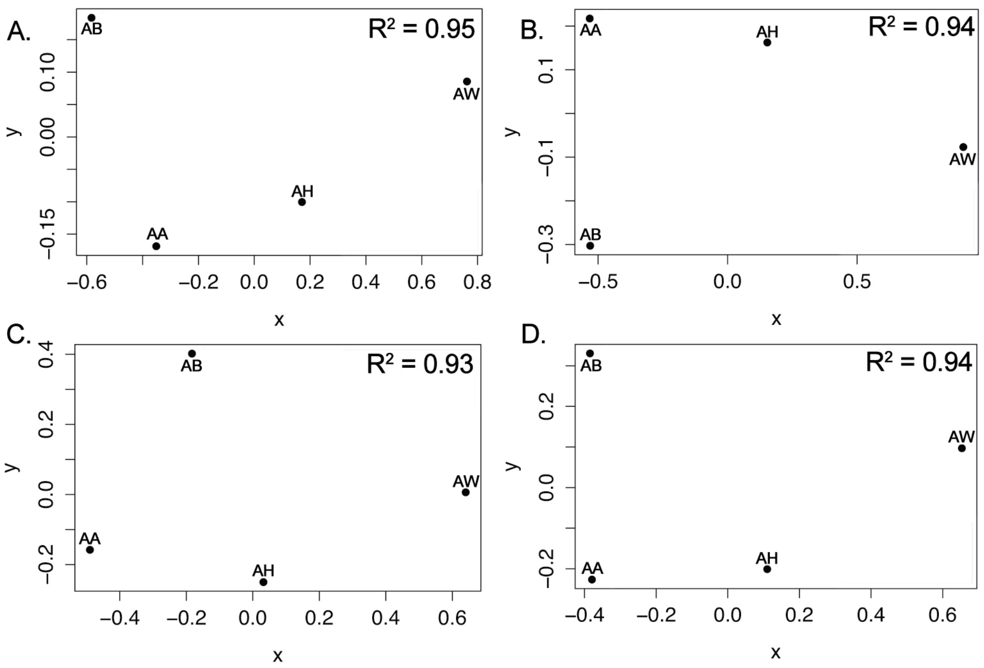

Fig. E.6. Comparison of two-dimensional PCO perceptual plots for each M_1 dataset with individual R^2 values displayed. The PCO of the shape PC dataset is shown at A, shape PC and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

Table E.25. M_2 shape PC linear discriminant function results using 3 forward stepwise selected variables: PC1, PC2, PC3.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	147	**8.8**	36.7	23.1	31.3
AB	184	5.4	**44.6**	21.2	28.8
AH	208	7.2	35.6	**23.1**	34.1
AW	218	11.0	15.1	16.5	**57.3**

Total correct: 268 out of 757 (35.4%) Cross-validated

Table E.26. M_2 shape PC and centroid size linear discriminant function results using 4 forward stepwise selected variables: Log centroid size, PC1, PC2, PC3.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	147	**11.6**	34.7	24.5	29.3
AB	184	13.0	**43.5**	17.9	25.5
AH	208	12.5	34.1	**20.2**	33.2
AW	218	12.4	13.3	20.2	**54.1**

Total correct: 257 out of 757 (33.9%) Cross-validated

Table E.27. M_2 ILD linear discriminant function results using 2 forward stepwise selected variables: Cusp 2-3, 3-4.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	147	**19.0**	34.0	12.9	34.0
AB	188	15.4	**52.1**	7.4	25.0
AH	214	17.3	31.3	**14.0**	37.4
AW	219	15.5	26.5	7.3	**50.7**

Total correct: 267 out of 768 (34.8%) Cross-validated

Table E.28. M_2 ILD PC linear discriminant function results using 2 forward stepwise selected variables: PC1, PC2.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	147	**12.2**	46.9	10.9	29.9
AB	188	11.7	**51.6**	5.3	31.4
AH	214	11.2	33.6	**11.7**	43.5
AW	219	12.3	25.1	6.8	**55.7**

Total correct: 262 out of 768 (34.1%) Cross-validated

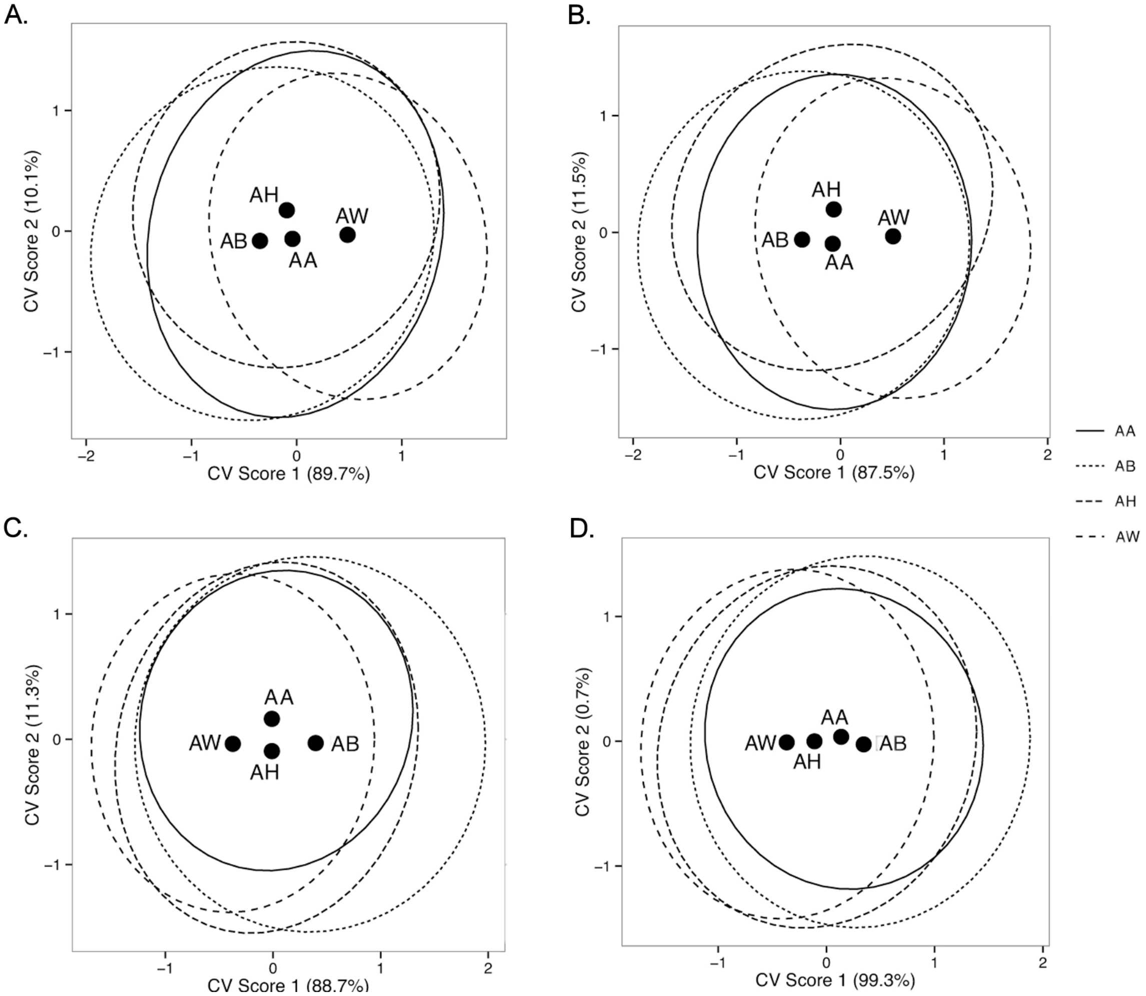

Fig. E.7. Comparison of canonical variate plots from each of the M_2 analyses. The molar shape dataset is shown at A, the shape and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

Table E.29. Mahalanobis D^2 matrix based on shape variables of M_2. Values not significantly different at $p < 0.05$ in bold.

Group	**AA**	**AB**	**AH**	**AW**
AA	-			
AB	**0.10**	-		
AH	**0.06**	0.13	-	
AW	0.28	0.69	0.37	-

Table E.30. Mahalanobis D^2 matrix based on shape and size variables of M_2. Values not significantly different at $p < 0.05$ in bold.

Group	**AA**	**AB**	**AH**	**AW**
AA	-			
AB	**0.10**	-		
AH	**0.09**	0.16	-	
AW	0.35	0.77	0.38	-

Table E.31. Mahalanobis D^2 matrix based on the ILDs of M_2. Values not significantly different at $p < 0.05$ in bold.

Group	**AA**	**AB**	**AH**	**AW**
AA	-			
AB	0.20	-		
AH	**0.07**	0.17	-	
AW	0.17	0.60	0.14	-

Table E.32. Mahalanobis D^2 matrix based on the ILD PCs of M_2. Values not significantly different at $p < 0.05$ in bold.

Group	**AA**	**AB**	**AH**	**AW**
AA	-			
AB	**0.05**	-		
AH	**0.06**	0.21	-	
AW	0.25	0.51	0.07	-

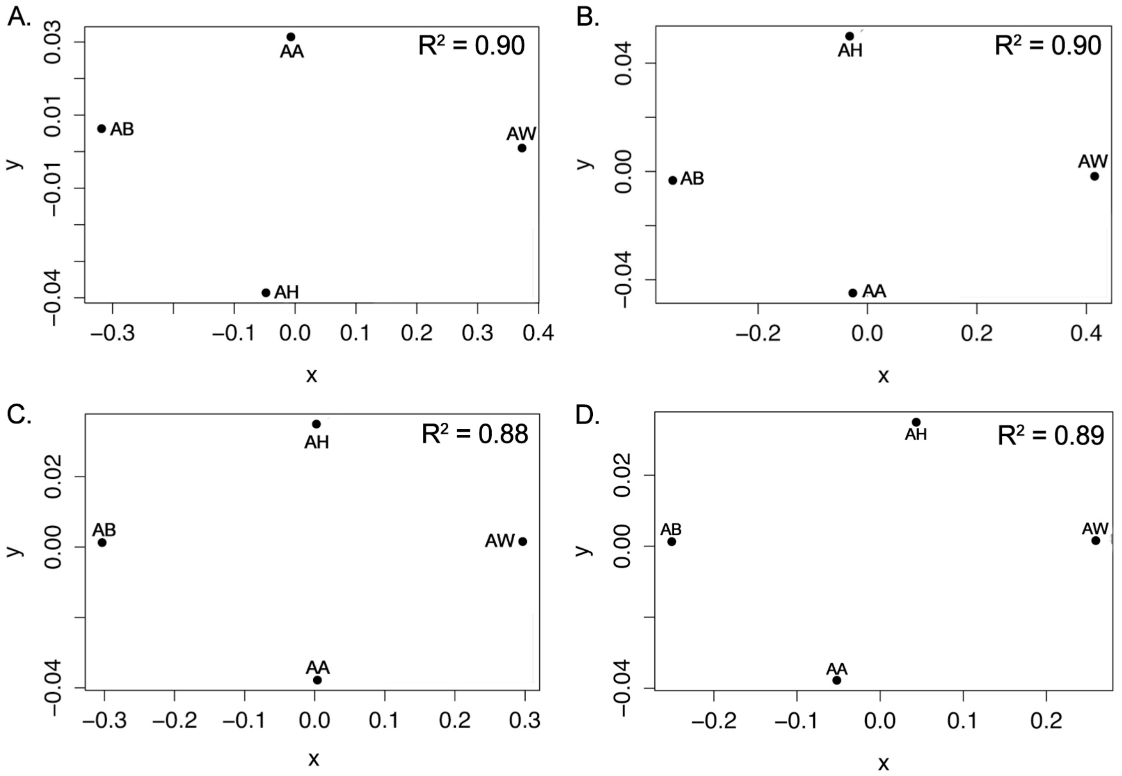

Fig. E.8. Comparison of two-dimensional PCO perceptual plots for each M_2 dataset with individual R^2 values displayed. The PCO of the shape PC dataset is shown at A, shape PC and size dataset at B, the ILD dataset at C, and the ILD PC dataset at D.

Table E.33. Combined molar shape PC linear discriminant function results using 13 forward stepwise selected variables: M^1 PC1, M^1 PC2, M^1 PC3, M^2 PC1, M^2 PC2, M^2 PC3, M_1 PC1, M_1 PC2, M_1 PC3, M_1 PC4, M_1 PC5, M_2 PC2, M_2 PC3.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	140	**38.6**	20.7	26.4	14.3
AB	115	15.7	**66.1**	7.0	11.3
AH	189	20.1	10.1	**55.6**	14.3
AW	156	11.5	10.9	14.7	**62.8**

Total correct: 333 out of 600 (55.5%) Cross-validated

Table E.34. Combined molar linear shape PC and centroid size discriminant function results using 13 forward stepwise selected variables: M^1 Centroid size, M^1 PC1, M^1 PC2, M^1 PC3, M^2 PC2, M^2 PC3, M_1 PC1, M_1 PC2, M_1 PC3, M_1 PC4, M_1 PC5, M_2 PC2, M_2 PC3.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	140	**42.1**	16.7	27.9	13.6
AB	115	18.3	**60.9**	7.0	13.9
AH	189	24.9	8.5	**50.8**	15.9
AW	156	10.9	10.9	14.1	**64.1**

Total correct: 325 out of 600 (54.2%) Cross-validated

Table E.35. Combined molar ILD linear discriminant function results using 15 forward stepwise selected variables: M^1 cusp 1-3, 1-4, 2-4, 3-4; M^2 cusp 1-2; M_1 cusp 1-3, 2-3, 2-4, 2-5, 3-4, 3-5, 4-5, M_2 2-3, 2-4, 3-4.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	141	**44.7**	14.9	27.0	13.5
AB	119	10.9	**64.7**	10.9	13.4
AH	198	24.7	11.1	**46.0**	18.2
AW	163	12.3	19.6	10.4	**57.7**

Total correct: 325 out of 621 (52.3%) Cross-validated

Table E.36. Combined molar ILD PC linear discriminant function results using 5 forward stepwise selected variables: PC1, PC4, PC5, PC7, PC12.

From Group	**Total Number**	**Into Group (%)**			
		AA	**AB**	**AH**	**AW**
AA	141	**49.6**	18.4	25.5	6.4
AB	119	17.6	**50.4**	10.1	21.8
AH	198	26.8	13.1	**39.9**	20.2
AW	163	7.4	21.5	15.3	**55.8**

Total correct: 300 out of 621 (48.3%) Cross-validated

Table E.37. Mahalanobis D^2 matrix based on the combined molar shape variables. Each value is significantly different at $p < 0.001$.

Group	AA	AB	AH	AW
AA	-			
AB	1.85	-		
AH	1.17	3.59	-	
AW	2.31	3.27	2.53	-

Table E.38. Mahalanobis D^2 matrix based on the combined molar shape and size variables. Each value is significantly different at $p < 0.001$.

Group	AA	AB	AH	AW
AA	-			
AB	2.38	-		
AH	1.26	3.74	-	
AW	2.91	3.25	2.66	-

Table E.39. Mahalanobis D^2 matrix based on the combined molar ILDs. Each value is significantly different at $p < 0.001$.

Group	AA	AB	AH	AW
AA	-			
AB	2.31	-		
AH	0.69	2.73	-	
AW	2.34	2.29	1.64	-

Table E.40. Mahalanobis D^2 matrix based on the combined molar ILD PCs. Each value is significantly different at $p < 0.001$.

Group	AA	AB	AH	AW
AA	-			
AB	1.22	-		
AH	0.54	1.75	-	
AW	1.91	1.06	1.19	-

Table E.41. Three group combined molar linear shape PC and centroid size discriminant function results using 15 forward stepwise selected variables: M^1 Centroid size, M^1 PC1, M^1 PC2, M^1 PC3, M^2 PC1, M^2 PC2, M^2 PC3, M_1 PC1, M_1 PC2, M_1 PC3, M_1 PC4, M_1 PC5, M_2 Centroid size, M_2 PC1, M_2 PC3.

From Group	**Total Number**	**Into Group (%)**		
		AB	**AH**	**AW**
AB	114	**76.3**	11.4	12.3
AH	189	11.6	**73.0**	15.4
AW	155	12.9	18.7	**68.4**

Total correct: 331 out of 458 (72.3%) Cross-validated

Table E.42. Three group combined molar ILD discriminant function results using 15 forward stepwise selected variables: M^1 1-2, 1-3, 1-4, 1-5, 2-3, 2-4; M^2 1-2, 1-3, 1-4; M_1 1-4, 2-4, 3-4, 3-5; M_2 2-3, 3-4.

From Group	**Total Number**	**Into Group (%)**		
		AB	**AH**	**AW**
AB	119	**70.6**	13.4	16.0
AH	198	15.7	**67.2**	17.1
AW	163	19.0	19.0	**62.0**

Total correct: 318 out of 480 (66.3%) Cross-validated