A Geometric Morphometric Analysis of Contemporary Hispanic Populations from Mexico and Colombia

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Introduction

Within contexts such as natural disasters, humanitarian efforts, and other forensic investigations, the timely and accurate development of the biological profile (sex, age, ancestry, and stature of skeletonized remains) is vital to the identification of decedents. The standardization of population-specific criteria is imperative to improving the current methods used for identification. Part of the challenge faced with creating the biological profile is the estimation of ancestry. The goal is to provide an estimate of biogeographic provenience by using either macromorphoscopic/nonmetric or macromorphometric/metric methods. Forensic anthropologists frequently utilize *FORDISC (3.1)*, a computer program to derive ancestry estimations by inputting cranial measurements and conducting discriminant function analyses (DFA) that classify an unknown individual into one of 13 reference groups.

In the U.S., the Hispanic demographic includes individuals from South and Central America, Mexico, Cuba, Puerto Rico, and other Latino/Spanish-speaking persons. However, in *FORDISC,* the "Hispanic" reference group is comprised only of U.S.-born Hispanics, Mexicans, and Central Americans (Jantz and Ousley 2005). The 2010 U.S. Census Bureau reports that Hispanics make up nearly 17% of the total U.S. population—approximately 55.4 million people. Individuals originating from Hispanic countries are often referred to as "tri-hybrid", descended from the three continental-level ancestral groups—European, African, and Native/Indigenous (Bertoni *et al.* 2003). Therefore, *FORDISC* often misclassifies Hispanic individuals because: (1) the current reference group lacks robust data from a majority of Hispanic populations; and (2) the "Hispanic" designator does not reflect the "tri-hybrid" nature of this unique demographic (Spradley *et al.* 2008). As such, *FORDISC* collapses the genetic admixtures and population histories from a multitude of Hispanic countries into a single group. This detail is of critical importance when considering the human rights crisis occurring along the U.S./Mexico border. Not all Latin American countries share the same colonial histories and not all migrants originate from Mexico or Central America (Anderson 2008).

The primary objective of this research is to examine craniometric variability in **547 documented individuals from three contemporaneous Latin American populations represented by Colombian, Mexican, and migrant samples** in order to ascertain whether it is possible to distinguish closely related Hispanic groups. Geometric morphometric (GM) analyses have recently gained traction in the field of biological and forensic anthropology because they allow users to explore shape-related variation independent of size, which potentially improves the forensic determination of ancestry (Humphries *et al.* 2013). Previous research by Spradley (2014) supports the notion that a finer degree of classification is possible using GM-derived data for ancestry estimation. Ultimately, the use of methods that are not population-specific will remain problematic when employed in areas where remains are likely to be of Hispanic origin because the admixture from the three ancestral groups is too variable to be represented by a single category.

Table 1. Mahalanobis Distances among the Colombian, Mexican, and Migrant samples

Group	Colombia	Mexico	Migrant
Colombia	—	—	—
Mexico	3.34	—	—
Migrant	6.29	6.76	—

Materials and Methods

The Colombian sample consists of **191 (F = 58; M = 133)** individuals from the Antioquia province in Colombia (Universidad de Antioquia). The Mexican sample consists of **133 (F = 48; M = 85)** individuals from the Federal District in Mexico (Universidad Nacional Autónoma de México). The migrant sample consists of **223 (F = 30; M = 193)** positively identified border crossers from the Pima County Office of the Medical Examiner in Tucson, Arizona. Collectively, all the samples represent individuals **18-102 years of age**, who died in the late 20th and early 21st centuries. *MorphoJ*, a program written for GM analyses, was used to interpret the data (Klingenberg 2011). Within *MorphoJ*, a Generalized Procrustes Analysis (GPA) was performed to scale, rotate, and transform the data onto a common coordinate system; this eliminates the effects of size and allows males and females to be pooled together. In order to explore shape-related variation for statistical discrimination between the groups, a Canonical Variate Analysis (CVA) was performed on the GPA-modified coordinates; this test maximizes variation among groups to detect which craniofacial landmarks best distinguish the groups. Wireframe graphs of each canonical variate are provided to better visualize cranial morphology; the light blue outline represents the average shape of all the samples and the dark blue outline represents shape changes (Figure 2 and 3).
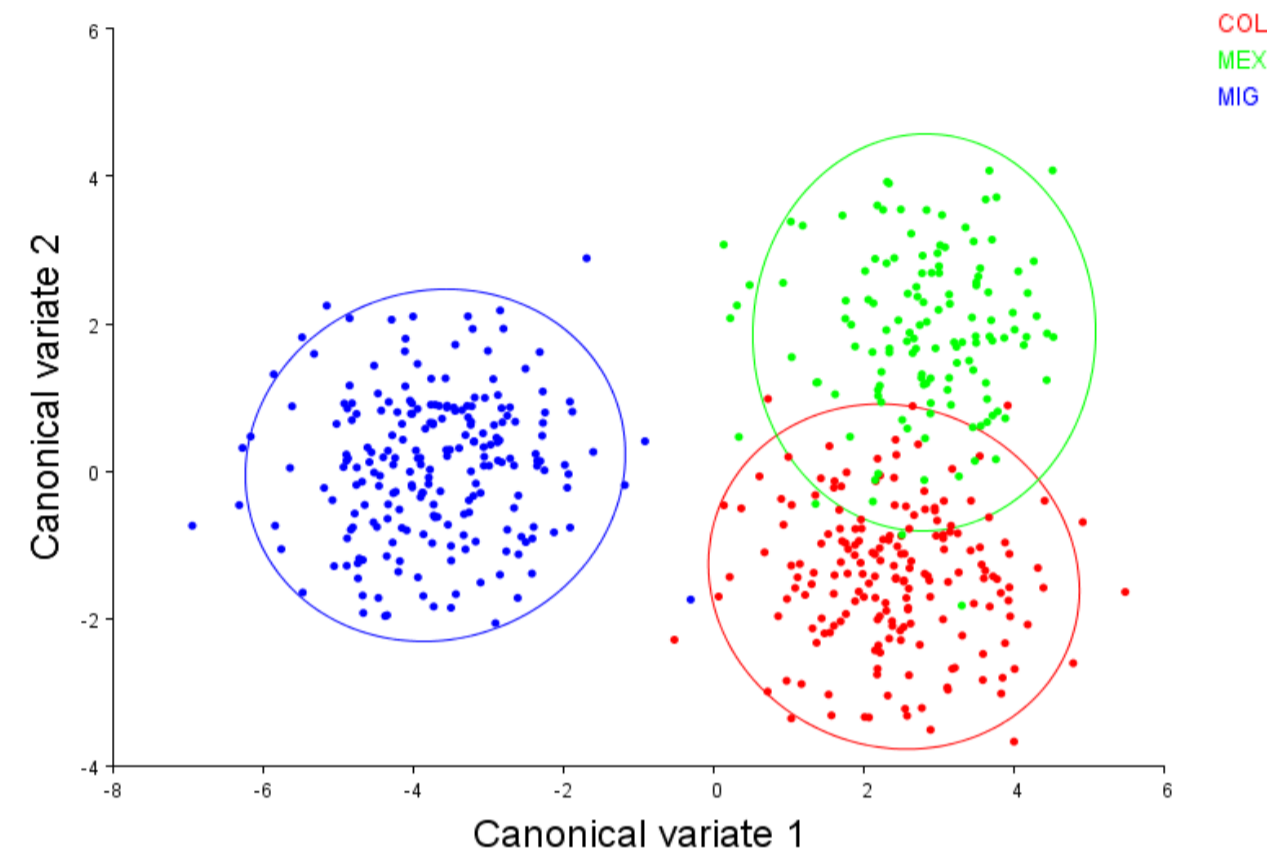
Results

Figure 1. Canonical variates plot of Colombian, Mexican, and Migrant samples
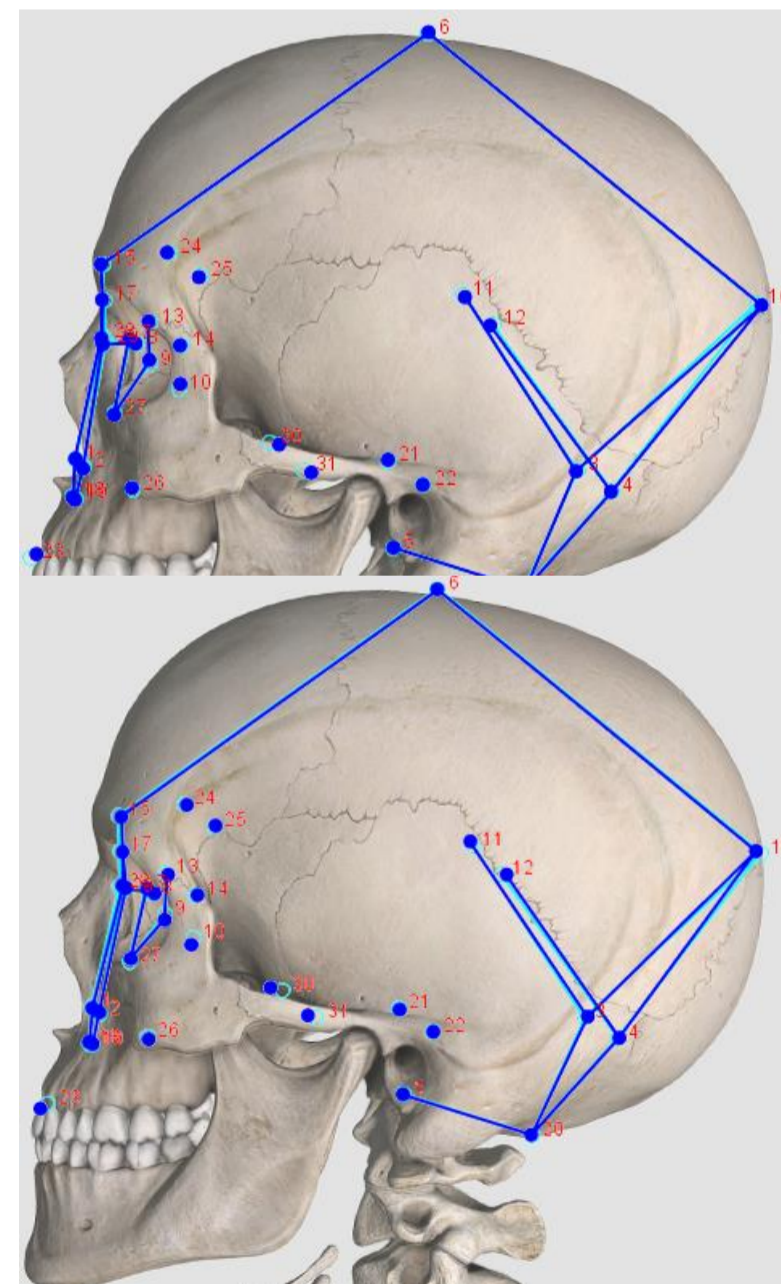

Figure 2. Wireframe graphs displaying morphological shape changes along CV1 (Mexico and Colombia, top; Migrant, bottom)
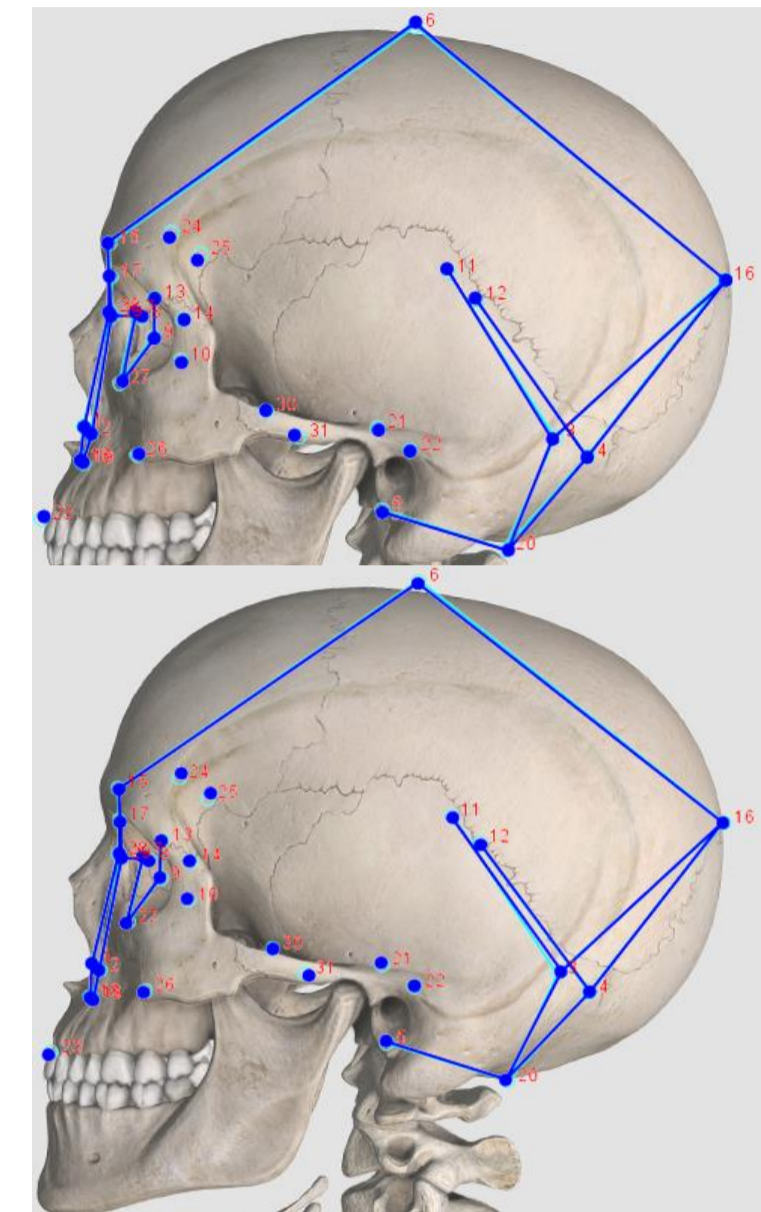

Figure 3. Wireframe graphs displaying morphological shape changes along CV2 (Colombia, top; Mexico, bottom)

Discussion and Conclusion

Few studies have performed GM analyses on Hispanic populations; this is the first investigation to perform such analyses on Colombian, Mexican, and migrant samples. Mahalanobis distances produced from the CVA are shown in Table 1 and are all significantly different (p-value <0.0001). According to these distances, the Colombian and Mexican samples are most similar to one another and suggest that the migrant sample is most divergent from all other groups. Figure 1 displays the canonical variate (CV) plot, showing the separation of the migrants. CV1 separates the migrant sample from the Mexican and Colombian samples (accounting for 85% variation). CV2 separates the Mexican and Colombian samples from one another with the migrant sample plotting intermediately (accounting for 15% variation). Along CV1, shape variation in the positive direction shows that the Mexican and Colombian samples show a more anteriorly projecting glabella and nasion and a more posteriorly located prosthion, suggesting overall smaller cranial bases. Shape variation in the negative direction displays a more anteriorly projecting prosthion and lamba and a posteriorly located glabella, suggesting shorter cranial lengths for the migrant sample (Figure 2). Along CV2, shape variation in the positive direction separates the Mexican and Colombian group based on a more inferior bregma, glabella, and prosthion and a superiorly placed basion, suggesting lower cranial vaults in the Mexican sample; conversely, shape variation in the negative direction displays a more superior bregma, prosthion and inferiorly placed basion in the Colombian sample, suggesting a higher cranial vaults in the Colombian group (Figure 3).

Overall, these distances suggest statistically significant morphological dissimilarity between all samples, most notably in the Migrant sample. Both Mexico and Colombia receive large genetic contributions from the European and Native/Indigenous ancestral groups and the individuals comprising the Migrant sample may originate from populations with genetic ancestry that are not fully represented by Mexico or Colombia, which may explain the Migrant separation. Ultimately, results suggest it is possible to infer group membership in a CVA analysis, and this could be implemented to estimate ancestry with a fine degree of precision. GM methods show immense promise and should be considered as forensic anthropologists revise the methods used to construct forensic ancestry.

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