H19 Biological Variation Among Hispanic (Spanish-Speaking) Peoples of the Americas

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The goal of this presentation is to present the biological variation that exists among Hispanic (Spanish-speaking) peoples of the Americas and how this variation allows for the development of better standards in ancestry identification.

The purpose of this paper is to demonstrate the biological variation that exists among Hispanic (Spanish-speaking) peoples of the Americas. This paper will also attempt to show that craniometric data from different geographic areas in Latin America and Mexico could aid in the determination of the geographic origin of unknown individuals identified as Hispanic. Additionally, this paper will explore postcranial variation of Hispanic groups when compared to American Blacks and Whites. The impact of this research can aid in the development of better craniometric standards for use in ancestry identification on an international level. For example, FORDISC 3.0 will have more appropriate samples for use in Latin America and other parts of the world.

The determination of ancestry or group affiliation is one of the primary factors in a forensic anthropological analysis. Craniometric data is commonly used as a means of ancestry determination. However, sample specific standards may not always be readily available for a particular group. In the United States, "Hispanic" refers to individuals originating from Mexico, Puerto Rico, Cuba, South or Central America, or other Hispanic/Latino origin (U.S. Census Bureau 2003) and therefore does not have precise genetic meaning. In general, Hispanics are hybrid populations composed of various African, Native American and European genetic backgrounds. Caribbean Hispanics may have large African components, while Mexican Hispanics may have large Native American components. For example, Ross *et al*. 2004, using geometric morphometric methods, found Cuban Americans nearer to American Blacks, indicating the term Hispanic as too broad.

When analyzing biological variation from skeletal metrics, a commonly used method is biological distance or Mahalanobis D^2, a measure of population divergence based on polygenic traits (Buikstra *et al*. 1990). Samples used in this analysis are Guatemalans, Argentineans, American Hispanics and American Whites. All samples are modern and forensic in nature. The D^2 distances among all groups are all significant at the .001 level, indicating that group centroids are significantly different. The D^2 distance matrix indicates that the smallest distances, therefore the most similarities are found between American White and American Hispanic females, followed by males from the same groups. Argentinean males are more similar to American Hispanic males and furthest from Guatemalan males. Overall, Guatemalans are most differentiated from all other groups. When the first two canonical means are plotted they show, again, that Guatemalan males are furthest from the centroids and therefore more differentiated from the other groups. CAN 1 separates the sexes and indicates that American White males have taller, wider and longer cranial vaults. CAN 2 indicates that Guatemalan males have more facial forwardness, a wider face with wide nasal aperture, a wide palate and a wide interorbital breadth.

While all groups exhibit differences, Guatemalans appear to be most differentiated from all other groups. The most likely explanation for these results is that the Guatemalan sample is comprised of Indigenous individuals, i.e. more or less pure Native Americans, while Argentinean and American Hispanics have more European admixture. Additionally, craniometric data of known individuals from different groups could potentially aid in identifying more specific geographic origins of individuals who die in U.S. border crossings.

Biological Variation, Hispanic, Craniometric