



Physical Anthropology Section – 2011

H73 Craniometric Variation in the Caribbean and Latin America as Influenced by the Trans-Atlantic Slave Trade

Ashley L. Humphries, BA*, North Carolina State University, Department of Sociology & Anthropology, 334 1911 Building, Campus Box 8107, Raleigh, NC 27695

After attending this presentation, attendees will have a better understanding of the craniometric diversity within Caribbean and Latin America as influenced by the Trans-Atlantic slave trade.

This presentation will impact the forensic science community by highlighting the importance of investigating biological diversity in regional samples. Such investigations are paramount in refining identification methods, which would allow forensic anthropologists to determine ancestry more accurately and aid in narrowing the pool of missing persons during an investigation.

Timely and accurate identification of unidentified remains is integral to the progression of medico-legal and human rights investigations. Determination and/or estimation of sex, age, stature, and ancestry narrows the list of missing persons, potentially leads to the positive identification of unidentified remains, aids in the success of

criminal investigations, and provides family and friends with closure. As the application of forensic anthropology increases worldwide, the need for population specific methods and population specific research has become more paramount, particularly those concerned with ancestry. Until recently, ancestral categories have been loosely based on linguistics, regional, and/or continental affinity. For example, the terms Hispanic and African provide broad categories which assign a missing person as coming from a Spanish speaking population or the entire continent of Africa. Increasingly, investigations have shown that humans are far more diverse than these broad categories account for and have shown that modern statistical methods can more narrowly identify intra-regional variation as well as answer broader questions concerning human migration and expansion (Ousley 2010, Spradley et al. 2008, Kenyhercz et al. 2010, Ross et al. 2003, Ross et al. 2008).

During the 16th and 19th centuries, nearly 10 million African slaves were transported to the Americas drastically changing the biological composition of the region. This event brought together Europeans, indigenous Americans, and various African groups to create a blend of cultural and biological diversity. One approach to investigating this biological diversity is through the comparison of cranial inter-landmark distances.

In order to investigate the biological diversity found within the Caribbean and Latin America and elucidate the specific African origins, several samples of African origin, contemporary Mexicans (n=21), nineteenth-century Cubans (n=23), contemporary Panamanians (n=12), contemporary Afro-Antillean Panamanians (n=6), and contemporary Ecuadorians (n=54) were compared using traditional craniometrics. The African data include the Teita from Southeast Kenya (n=83), the Dogon tribe from Mali West Africa (n=99), the Zulu from South Africa (n=101), the Bushman from South Africa (n=90), individuals from Angola (n=68), individuals from São Tomé (n=5). All African data (excluding Angola and São Tomé) were collected by W.W. Howells and can be easily accessed online at <http://konig.la.utk.edu/howells.htm>. Inter-landmark distances (ILDs) from the Howells data were collected using the traditional 2D caliper-derived methods. On nearly all of the remaining crania, 3D data was collected using a Microscribe digitizer in which the traditional ILDs were simultaneously recorded. To evaluate group similarities and differences, Mahalanobis D^2 were calculated using SAS

9.13 (2001). Mahalanobis D^2 is a function of the group means as well as pooled variances and covariances that measures the degree of differentiation observed between the considered populations. Results show that all African groups are significantly different from one another at the <0.05 level (nearly all with p -values <0.0001). Interestingly, Afro-Antillean Panamanians are not significantly different from Angolans (p -value=0.1793, D^2 =3.27) or the S. Tome sample (p -value=0.4904, D^2 =4.69). However, this may be the result of a small sample size and evokes further investigation as S. Tome and Angola were controlled for long periods of time during the slave trade by the Portuguese. While Mexico was significantly different from all African samples, Mexico was not significantly different from the Afro-Antillean Panamanians (p -value=0.1950, D^2 =2.15) and contemporary Panamanians (p -value=0.0818, D^2 =1.68), possibly suggesting a similar indigenous and African origin. While exploratory, these results indicate that not only are the various African populations significantly different from one another, this diversity has also contributed to the diversity evident in the Caribbean and Latin America.

Ancestry, Craniometrics, Mahalanobis Distance