ABSTRACT

HUMPHRIES, ASHLEY L. Craniometric Variation in the Caribbean and Latin America as Influenced by the Trans-Atlantic Slave Trade: An Examination of the Angolan Influence. (Under the direction of Dr. Ann H. Ross)

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 2009, Spradley et al. 2008, 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 nearly all African groups are significantly different from one another at the <0.05 level (many with p-values <0.0001). Interestingly, Afro-Antillean Panamanians are not significantly different from Angolans (p-value=0.119, D^2=2.12) or the São Tomé sample (p-value=0.293, D^2=3.14). However, this may be the result of a small sample size and evokes further investigation as São Tomé and Angola were controlled for

long periods of time during the slave trade by the Portuguese. Mexico was not significantly different from the Afro-Antillean Panamanians (p-value=0.08, D^2=2.77) possibly suggesting a similar indigenous and/or African origin. There 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. This research contributes to African Diaspora studies.

Craniometric Variation in the Caribbean and Latin America as Influenced by the Trans-Atlantic Slave Trade: An Examination of the Angolan Influence

by
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APPROVED BY:

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DEDICATION

This research is dedicated my grandmother, who’s strength has always inspired me.

BIOGRAPHY

Ashley Lynn Humphries obtained her B.A. in anthropology and minor in dance studies at the University of South Florida. As a child she enjoyed digging in the dirt (her mother lost countless spoons this way), playing with bugs and reptiles, and learning to be a ballerina. As she grew older her fondness of bugs and reptiles turned into a fascination with biology and after taking an anatomy course during high school, she developed an interest in the human form. However, when she graduated from high school, Ashley, like many others, had no clue what she wanted to do with her life or the possibilities that were out there. Her well-loved pastime of dancing remained with her throughout her childhood and so, with uncertainty of what she wanted to pursue during her undergraduate career, Ashley began her studies as a dance major. She struggled with this decision for quite some time and didn't quite feel that dance was her calling. After randomly taking an introduction course in physical anthropology, she immediately felt that this field, which she knew so little about at the time, was her calling and promptly switched majors. Little did she know that it would lead to so many wonderful opportunities and turn into such a passion (and that those years spent digging in the backyard would be put to good use during archaeological fieldwork).

During her time at North Carolina State University she participated in research projects, forensic casework, and community outreach. These experiences have shaped her interests within the field, which include the study of human skeletal variation of past and present populations through biocultural and evolutionary interpretations. She is interested in research that addresses questions of human migration, human variation, and the interaction

between skeletal biology and the environment. Ashley is eager to begin her doctoral studies in the Fall of 2011 at the University of South Florida's Applied Anthropology program.

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This thesis was accomplished with the help of many people. First and foremost I would like to thank my advisor, Dr. Ann Ross, who provided me with data and guided me through the thesis process. She has been a wonderful mentor and outstanding advocate for her students. She has provided me with numerous experiences and opportunities that will influence my career for years to come. I would also like to thank my thesis committee members, Dr. D. Troy Case and Dr. Scott Fitzpatrick for their valuable feedback and guidance. In addition, I would like to thank Dr. Hugo Cardoso from the Bocage Museum in Lisbon, Portugal and Drs. Eugenia Cunha and Ana Luisa Santos from the University of Coimbra for access to the Angolan and São Tomé collections.

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INTRODUCTION

Between the sixteenth and nineteenth centuries, nearly 10 million African slaves were transported to the Americas drastically changing the biological composition of the region. The Trans-Atlantic slave trade resulted in the largest forced migration of people in recorded history. This event, fueled by a European desire to establish plantations for growing important commodities such as tobacco and sugar cane, as well as missionization and the search for precious metals, brought together Europeans, indigenous Americans, and various African groups that led to a blend of cultural and biological diversity (Rawley 1981, Curtain 1969, Skidmore and Smith 1992).

The Trans-Atlantic slave trade had a tremendous effect on the New World and it is essential for contemporary ethnohistorians, culturalists, linguists, and archaeologists to understand the biological influences prevalent in the Americas, especially those originating from Africa. Physical anthropologists can provide information regarding human biological origins that may otherwise be unattainable. One approach to investigating this biological diversity is through the comparison of cranial inter-landmark distances. While craniometric research has been conducted to investigate the biological origins of North American African-Americans, little attention has been paid to the Caribbean and Latin America where nearly 91% of enslaved Africans destined for the Americans were transported (Curtin 1969, Rawley 1981).

The human skeleton, in particular the skull, has long been recognized for its ability to provide information regarding biological relatedness and the origins of human populations

(Relethford and Blangero 1990, Relethford 2001, Sparks and Jantz 2002, Ubelaker and Jantz 1986). This study utilizes craniometric landmark data as a biological proxy to investigate the biological diversity of the Caribbean and Latin America and includes a newly available skeletal sample of Angolans (from west-central Africa), who are reported to have had a significant influence in colonial America (Blakey 2001, Curtin 1969, Rawley 1981, Salas et al. 2004). The present study evaluated the cranial diversity of skulls from Cuba, Panama, Ecuador, Mexico, West Africa, West-Central Africa, and South Africa. The specific goals of this research are as follows:

- To test the null hypothesis that there is no significant difference among the groups using craniometric data to trace the geographical African origins present in the Caribbean and Latin American.
- To test the null hypothesis that there is no genetic Angolan (or West-Central African) influence in the Caribbean and Latin America.
- To investigate the pattern of variation in the Caribbean and Latin America as influenced by African groups.
- To examine the variation in admixture. Higher F_{ST} values are expected as a result of heterogeneity. The morphological diversity in the Caribbean and Latin America is expected to reflect their heterogeneous histories (indigenous, African, European), which is also noted in molecular studies.

The African continent has been found to be very heterogeneous and this heterogeneity can be observed geographically, culturally, archaeologically, and linguistically (Herskovits 1928a, Howells 1973, Keita 2004, Kittles and Keita 1999, Relethford 1994, Rightmire 1970, Rightmire 1971, Roseman 2004, Wolpoff and Caspari 1997, Workman et al. 1963). Therefore, this heterogeneity is expected to contribute to the morphological diversity in the contemporary New World and aid in identifying specific African origins within the Caribbean and Latin America. Historical, biological, and genetic evidence suggests that enslaved Africans forced to immigrate to the New World largely originated from West and West Central Africa (Cobb 1939, Herskovits 1928a, Herskovits 1928b, Herskovits 1930, Herskovits 1969, McMillin 2004, Parra et al. 2001, Parra et al. 1998, Rawley 1981, Salas et al. 2004). However, the large categorization "west-African" is often used to describe the individuals brought to the Americas for slave labor. Yet, there was a large geographical source of slaves along the west coast of Africa. The individuals who shipped from the variety of slave ports along the west coast of Africa came from many different cultural and linguistic groups that ultimately influenced their breeding populations and thus, contributed to making them distinctly different populations.

In general, Angolans, who originate from west-central Africa, are underestimated and underrepresented in literature concerning the Caribbean and Latin America. This may be the result of researchers using the all-encompassing term "west-Africans" and not making distinctions between individual group contributions. It is important to have knowledge of the specific African groups that were transported to various parts of the New World as their cultural affiliations, beliefs, and linguistic designations ultimately influenced the ways in

which they transformed and adapted to the New World. Increasingly, research has shown that humans are far more diverse than previous population designations account for and craniometric measurements using multivariate statistics can help identify group similarities, differences, and relationships (Howells 1973, Ross et al. 2002a).

Where Angola is mentioned in the literature it is primarily confined to Brazil, where most Angolan slaves were destined (Klein 1972). However, this does not preclude an Angolan influence in the Caribbean and Latin America. As such, this project expands our knowledge set of various biological contributions from African populations. Evidence does suggest that Angolans were present in the Caribbean. For example, Afro-Cuban religions are reported to have been influenced by several African religious practices. Of particular interest to this study is the religious practice of Palo Monte which is influenced by Kongo, an ethnic group included in Northern Angola (Singleton 2005).

Data collected on the biological diversity in the Caribbean and Latin America through craniometric techniques will prove useful in future studies as it will aid archaeological, ethnohistorical, linguistic, and cultural research to elucidate the origins of people forcefully transported to the Caribbean and Latin America during the sixteenth and seventeenth centuries. Understanding the genetic African origin of the Americas is integral to the progress of African diaspora research, will facilitate a multidisciplinary approach to biological diversity, and provide answers related to questions concerning individual and national identity.

Vital to African diaspora research is the examination of the extent to which African heritage influenced the ways in which Africans and their descendants constructed their

material world (Singleton 2005). However, this can prove very difficult as establishing specific African influences have been debated. For example, as noted by Singleton (2005), scholars have argued about the geographical and cultural origins of cultural traditions associated with African diaspora archaeological material. Artifacts can be interpreted in many ways and make it difficult to determine their historical or migratory origins. The analysis of skeletal remains provides biological data to help support or refute the interpretations of material culture, cultural data, and linguistic data. Biological origins are important to understanding the past and present identity of people and may also shed light on biocultural adaptations, as well as provide insight for biomedical studies. As such, craniometric analyses that elucidate the origins of individuals may substantiate and/or provide context for archaeological, cultural, linguistic, biomedical, and nutritional evaluations.

In addition to elucidating the origins of the African diaspora within the Caribbean and Latin America, craniometric analyses can help anthropologists to understand contemporary patterns of variation that are useful in medico-legal circumstances. 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, especially in cases of mass disasters and genocide, 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 et al. 2009, Spradley et al. 2008, Ross et al. 2004a, Ross et al. 2008). This research not only provides insight to the biological anthropological aspects of the African diaspora, it also contributes to anthropological research by documenting the range and relationship of variation in the Caribbean and Latin America.

The scope of this study is not human variation in general, but the human variation that was produced as a result of the Trans-Atlantic Slave Trade, which consequently brought together the cultural, linguistic, and biological aspects of several distinct groups, the Europeans, Indigenous Americans, and a variety of African groups. In addition, anthropological studies of cranial variation seek to relate theoretical models of population genetics with data on human behavior and population history, which ultimately allow us to address large-scale issues regarding expansions and migrations in the past, such as the biological effects of the slave trade on contemporary population structures (Relethford and Lees 1982). This research will promote such analyses as it will provide the foundation upon which to do so. As Blakey (2001) has criticized, bioarchaeological diaspora studies have a

tendency to have little relevance to the communities whose history they reconstruct. This study will not only describe the biological variation in the Caribbean and Latin America but it will also provide insight about the origins of several groups in the Americas, which is an integral part of understanding and creating human identity past and present. Origin studies not only shed light on personal and national identity, but it is also the basis for a vast range of disciplines including archaeology, cultural anthropology, and biomedicine. The following literature review will provide the historical and theoretical framework central to the craniometric, biological investigation of the African diaspora.

REVIEW OF THE LITERATURE

I. Craniometric Variation

The history of craniometric analyses can be traced to the beginning of American physical anthropology. In its infancy, craniometric studies were focused on typological racial assessments and were largely descriptive. Early anthropological studies, such as those conducted by Morton (1844) were focused on ranking races and determining antiquity of racial types. These studies were influenced by the social, political, and religious conditions that prejudiced early scientific inquiry. According to Gould (1981), scientific change through time is the alteration of cultural contexts that influence science since it is a socially embedded activity. Through geographical discovery, Europeans encountered people who were very different from themselves and they sought to explain these differences. There were a variety of theories used to explain the human variation early research encountered. For example, prior to evolutionary theory, some researchers justified "racial ranking" through the view of degeneration from Adam and Eve's perfection and argued that races declined to different degrees, whites the least and blacks the most (Gould 1981:39). Others argued that human groups were different species that were descendants of "different Adams" (Gould 1981). It wasn't until the 1950s that physical anthropological studies began to slowly transform from merely categorizing and comparing data to fit within fixed typological classifications to answering questions about evolutionary change, functional anatomy, and population history (Saunders and Rainey 2008).

With the introduction of genetics and a better understanding of evolutionary mechanisms, the division of breeding populations into fixed racial groups was unsupported (Armelagos et al. 1982, Saunders and Rainey 2008). Studies of human variation have transformed considerably since the early typology research. We now have a better understanding of global diversity and have access to powerful multivariate statistical programs.

The theoretical foundation that provides justification for using craniometric analyses to investigate gene flow among indigenous Americans, Europeans, and Africans is that metric analysis of cranial form is supported through repeatability and heritability of inter-landmark distances (Pietrusewsky 2008). Central to supporting craniometric analyses is the fact that genetic loci are shared between all human populations and are a reflection of biological relatedness. The morphological expressions of craniometric traits are, in part, genetically controlled and therefore, allow us to understand human patterns of relationships, migration, and evolutionary trajectories (Ubelaker and Jantz 1986, Sparks and Jantz 2002, Relethford 2004a).

Craniometric analysis is the quantitative study and analysis of cranial form. The human skeleton, especially the cranium, is useful in bioarchaeology and physical anthropology because skeletal form and structure have a genetic basis (Ubelaker and Jantz 1986, Sparks and Jantz 2002, Relethford 2004a). As such, the analysis of craniometric data can provide an indirect reflection of genetic variation within and between human groups. Craniometric studies have increasingly been applied to investigate geographical variation,

identify biological relationships, detect migration patterns, identify ancestral origins, understand functional adaptation, and investigate evolutionary forces.

The foundation for craniometric studies lies in the fact that phenotypic cranial morphology is genetically influenced. However, cranial variation is the result of both intrinsic and extrinsic factors. Therefore, the biological distance and relatedness among populations are the result of the phenotypic expression of genetically inherited traits and environmental influences. Genetic and environmental factors may influence suites of traits through common developmental pathways; however, genetics clearly play a major role in the expression of craniofacial growth and the expression of phenotypic traits (Carson 2006, Kohn 1991, Devor 1987). So, while the environment plays a role in the morphology of the cranium, it does not completely mask the genetic factors; and while secular change may occur and alter the morphological expression of the cranium, biological distance and relatedness should still be able to be detected. Sparks and Jantz (2002) reanalyzed the findings published by Boas in 1912 that emphasized the plasticity of the skull in response to environmental changes. After using advanced statistical methods that were not available to Boas during the time of his original analyses, Sparks and Jantz (2002) concluded that there is a high genetic component, relative to environmental influences, that impact the morphology of the skull.

Biological genetic variation and the morphology of the skull are dependent on the genes present in the population and their frequencies (Kohn 1991). Therefore, the introduction of the various European and African gene pools (from different breeding

populations) to the New World should be expressed through cranial morphology within the Caribbean and Latin America.

Numerous studies have shown that morphological variation expressed by craniometric analyses is a valuable tool for examining trends in human variation as it relates to the biological distance between populations and identifying ancestral origins (Spradley 2006, Ross 2004, Relethford and Lees 1982). The morphological variation that can be expressed through differences in cranial measurements contributes to theories of human migration, human variation, biological relatedness, and evolutionary trajectories.

When investigating craniometric variation, two main types of data are collected, two-dimensional and three-dimensional. Both of these types of data collection require locating a suite of craniometric landmarks. Landmarks, according to Richtsmeier et al. (2002), are precise locations on biological forms that hold some developmental, functional, structural, or evolutionary significance. Therefore, the basis of morphometric research lies in the fact that landmark data can provide a spatial map of cranial form and/or homologous points that can be compared between two or more objects. Within craniometric studies, these points are standard landmarks that are defined for anatomically modern humans. Detailed descriptions of these landmarks can be found in Howells (1973) and White (2000).

According to Bookstein (1991), there are three different types of landmarks, type 1, type 2, and type 3. Type 1 landmarks are described as points located at the juxtaposition of different tissues. For example, a type 1 landmark would be located at the intersection of the sutures in the skull such as the sagittal and frontal sutures, which come together at the landmark bregma. Type 2 landmarks are points of maximum curvature. For example, muscle

attachment processes on bones. Type 3 landmarks are extreme points in various dimensions and are identified in relation to the axes of the entire structure. An example of a type three landmark includes euryon, a paired point that is instrumentally determined on opposite sides of the skull that form the termini of the line of maximum cranial breadth (Buikstra and Ubelaker 1994).

Two-dimensional and three-dimensional data are valued in anthropology because the equipment used to collect the data is fairly inexpensive and portable. Two-dimensional data are simple distances and linear dimensions defined by craniometric landmarks and are often referred to as "traditional craniometrics." These variables can be measured directly on the cranium using handheld calipers, or a digitizer that collects both x, y, and z coordinates of a particular landmark and the distances (in mm) between landmarks. Three-dimensional craniometric data has been gaining popularity during the last ten years and involves the use of a 3D digitizer, such as the Microscribe Series or Polhemus digitizers. Three-dimensional craniometric data is specifically useful because it allows for the x and y coordinates from the traditional inter-landmark distances to be analyzed spatially with respect to the z coordinate.

While developments in three-dimensional coordinate data for evaluating cranial variation have shown positive results (Ross and Williams 2008, Slice 2005), analyses of two-dimensional inter-landmark distances remain useful in evaluating biological distances. This is particularly true as many available datasets do not include 3D coordinate data and would therefore render thousands of imperative cranial measurements useless for examining human variation. The current study utilizes two-dimensional inter-landmark distances to investigate the biological diversity in the Caribbean and Latin America due to the availability of

traditional inter-landmark distances across the samples. Size and shape analyses in traditional craniometrics rely on the application of multivariate statistical methods. These methods include, but are not limited to, discriminant function analysis, canonical variate analysis, and generalized distances (Rohlf and Marcus 1993, Lynch et al. 1996, Ross and Kimmerle 1999).

One problem reported in craniometric data collection is observer error. Hillgrissom et al. (2008) suggest that one should collect a sample dataset with repeated trials to verify precision. In addition, one must take precautions when collecting the three-dimensional data as it involves the addition of the z-coordinate. Any shift in the specimen while collecting the three-dimensional data could result in error for the x, y, and z coordinates and the inter-landmark measurements.

Another problem in craniometric data collection is determining what landmark data should be collected. Landmark collection is dependent upon research design and what questions the researcher is trying to answer. Richtsmeier and colleagues (2002) stress that if data is collected solely based on a hypothesis, the researcher may neglect some features that have the potential to provide crucial information. However, crucial data may be misinterpreted if landmarks influenced by external forces are included. For example, Schillaci and Stojanowski (2005) only collected facial dimensions because the population of interest, prehistoric Pueblo Indians, practiced cradle-boarding. Since cradle-boarding changes the morphology of the cranial vault, those points should be eliminated from study as cradle-boarding and other forms of cranial modification masks the genetic variation. When selecting landmarks for inclusion in a study, one must keep in mind which landmarks are and are not

of biological relevance and if the landmarks could have been influenced by something other than genetic potential, such as cultural practices.

II. Craniometric Variation Research

Craniometric analyses can provide a wealth of information regarding both past and present populations. One of the wider applications of craniometric analysis is evaluating biological distance. By comparing cranial form based on the linear measurements obtained from caliper derived standard craniometric landmarks, relatedness between different groups or populations can be evaluated. For example, cluster analyses in conjunction with other statistical testing can produce information regarding phylogeny and evolutionary trajectories. Craniometrics can provide biological information to investigate the evolutionary, cultural, and environmental forces that affect phenotypic variation. Furthermore, these data can be employed to elucidate human population migration and biological distance.

Ross (2004) examined patterns of migration in the Caribbean by analyzing three-dimensional facial shape variation among pre-contact Taíno groups from the Caribbean and pre-contact groups from South America and Florida. By comparing the craniofacial landmark data between these groups, this study suggests that there were at least two separate migration routes and two possible population sources for the peopling of the Caribbean. In addition to testing for evidence of Angolan biological contributions, the current study will employ similar techniques to examine the peopling of the contemporary New World, namely the African migration and biological diversity introduced by the Trans-Atlantic slave trade.

Craniometrics can also provide information regarding population history. For example, using craniofacial measurements, Schillaci and Stojanowski (2005) examined five prehistoric/protohistoric Tewa pueblos and found that at least one of the pueblo groups was matrilocal. This finding was contradictory to ethnographic data that suggests that the Tewa were bilocal or neolocal and contributes a new line of evidence for understanding population structure.

Increasingly, craniometric studies have shown that humans are far more diverse than once thought. For example, Ousley et al. (2009) used multivariate analyses of craniometric data to support Saurer's (1992) hypothesis that there are morphological differences between American whites and blacks. In addition, through the analysis of the Howells' craniometric dataset, they concluded that human variation exhibits strong geographical patterning both intra- and inter-regionally. Therefore, they identify significant differences among groups within continents. Ross (2004a) found significant variation among groups of European ancestry. She demonstrated that Bosnians and Croatians, who were thought to be relatively homogenous because of their common Slavic ancestry, exhibit distinct differences in cranial morphology. She concluded that this distinction was caused by the isolation of breeding groups produced by different religious affiliations. Ross et al. (2002) provided a systematic examination of craniometric variation among a broad spatial distribution of Latin American groups. Ross et al. (2002a) illustrate that pre-contact Caribbean and Latin American populations are far more heterogeneous than previously thought and supports a multiple population model for peopling of the New World; similar to what has been proposed by Keegan (2000) using archaeological data. They found morphological similarities between the

pre-contact Mexico and coastal Ecuador samples and found they were dissimilar to the Howells' Peruvian sample. This finding contradicts conclusions that South America was populated by a single migration from North America and suggests different populations peopled the New World**.**

These examples of research have implications for understanding the pattern of human variation both inter-regionally and intra-regionally. In addition, these results show that humans can be accurately classified into geographic origin using craniometrics despite overlap among groups. This kind of information has practical application in cases of mass disasters or genocide and provides us with a clearer picture of modern human biological variation. They contribute to the current study as heterogeneity among the post-contact Caribbean and Latin American groups is expected since several already heterogeneous groups (the Europeans, Amerindians, and Africans) were brought together. Furthermore, it is expected that specific biological contribution can be identified because of gene flow occurring within a single geographic region.

III. Ancestry, not "race"

As noted by Ousley and colleagues (2009), the frequently ambiguous use of the term "race" in the literature can be misleading. As such, it is necessary to define "race" and "ancestry" as to ward off confusion and promote proper usage of the terms. The concept of "race" is based on some kind of essence that makes one group of people different from another. This is often recognized as a phenotype (physical appearance), lineage ("purity of blood"), and/or culture (cultural traditions, religion) (Manning 2009). The concept of "race"

relies on the fundamental logic from the human psychology that categorizes people into "us" and "others." Thus, as stated by Manning (Manning 2009), "'race' exists not in nature but in the choices of individuals and groups." Therefore, the concept of "race" is culturally or socially constructed. Ancestry or the term "biological race" is more appropriate for discussing human biological variation where the division of groups reflects the frequency of heritable traits among members within a group (Ousley et al. 2009, Brues 1977).

Since the human species typically finds mates within their own social group (based on language, culture, and/or religion) or geographical location, they create breeding populations in which little contribution from genes outside of their group are incorporated. Through genetic drift, breeding populations become more biologically and morphologically distinct from other groups. As such, there is concordance between social races and skeletal biology, especially cranial morphology (Sauer 1992, Ousley et al. 2009).

While there are some who argue that craniometric analyses are still entrenched in the descriptive, typological approach of the past (Armelagos and Van Gerven 2003), biological studies conducted to investigate craniometric variation have been shown to be important and informative. The fact that physical anthropologists are "good" at identifying "race" is in fact that there is a concordance between social races and skeletal biology, especially cranial morphology (Sauer 1992, Ousley et al. 2009). While many physical anthropologists studying human variation have moved on from early studies of racial typology, many anthropologists and scholars from other disciplines have not. Therefore, without consistent use of terminology, research may become misguided or confusing to readers.

HISTORICAL BACKGROUND

I. The Trans-Atlantic Slave Trade

Portuguese voyagers began to visit the Atlantic coast of Africa during the fifteenth century. Through these early voyages, Africans were transported to the islands of the Atlantic; some went as free people, but many others in captivity. Portuguese mariners settled the islands of Madeira and the Azores in the early fifteenth century to grow wheat and continued to survey the Atlantic coast of Africa throughout the fifteenth century and by 1472, had discovered the uninhabited islands of Principe and São Tomé. By 1482, the Portuguese reached the mouth of the Congo River. Initially, obtaining gold and converting people to Christianity were the primary goals of the Portuguese explorers, but trade in other goods and appropriation of labor grew to be more important interests (Manning 2009). The Portuguese were the first to begin exporting slave labor from Africa. They imported slaves to Portugal and secondarily, the Atlantic islands (the Azores, the Cape Verde islands, and Madeira) for wheat production. The sixteenth century saw an increase in sugar production and a higher demand for slave labor in the Atlantic islands.

With the discovery of the New World by Christopher Columbus in 1492, and a realization of the monetary potential of plantation crops, precious metals, and missionization, the need for a new labor force was soon realized (Crosby 1972). During the sixteenth and early seventeenth centuries, the Portuguese developed a sugar industry in Brazil and the Caribbean which initially utilized indigenous labor. However, European diseases, forced labor demands, and warfare soon decimated the native populations (Skidmore and Smith

1992, Crosby 1972). Therefore, the conquest of the Americas followed by the Trans-Atlantic Slave Trade dramatically changed the population structure of the local indigenous groups.

Recognizing the financial potential, the Portuguese and Spanish began to import slaves from Africa. The first Africans to make the journey to the Americas came from the Iberian Peninsula rather than directly from Africa (Manning 2009). Near the beginning of the slave trade, the Spanish controlled much of the Caribbean and South America with their primary territories in the West Indies, Mexico, Central America, and northern South America. According to Rawley (1981), heterogeneity of African slave sources characterized the history of Spanish America.

Initially, the Spanish exploited indigenous populations as their main source of slave labor. They primarily obtained the Amerindian slaves through chiefs under their control. Early Portuguese settlers also recruited indigenous slave power and did so through raiding groups. There are many reports of successive waves of "old world" diseases introduced by the European and African immigrants that diminished the Amerindian populations (Manning 2009, Crosby 1972). According to Manning (2009), small pox was likely the most devastating disease introduced to the New World and was followed by the measles, typhus, and respiratory diseases. The indigenous populations of the Americas fell to one-fifth or even one-tenth of the original population present before 1500 (Manning 2009). While many Amerindian populations nearly became extinct because of brutality and disease, some bred with the European and African settlers. For example, many Taíno women became wives of the Spanish and African immigrants of the Bahamas and passed on the remnants of Taíno language and culture that persist in the Caribbean today.

Other European countries, inspired by the monetary potential, soon began to participate in the slave trade. During the next century, European exploration of the west coast of Africa expanded their geographical source of African slaves. During this early period of exploitation of slave labor from Africa, the Portuguese controlled many of the ports along the Atlantic coast of Africa focusing their attention on Senegambia, Upper Guinea, the Gold Coast, Benin, and Kongo. In 1575, the Portuguese seized the town of Luanda and began constructing the colony of Angola. At this time, African slaves were brought in increasing numbers to Portugal and then spread to other regions of Europe (Manning 2009). By 1600, the majority of captive African slaves were being sent to the Americas rather than the Atlantic islands (Manning 2009).

During the sixteenth and early seventeenth centuries, Upper Guinea (West Africa) was the main source of slaves destined for Spanish America. The source later shifted to West-Central Africa and from the early to mid-seventeenth centuries, Angola became the principal supplier of African slaves. According to Rawley (1981), the Spanish were also dependent upon other nations for slaves, including the Portuguese, Dutch, English, and French. The sources of slaves for these nations were not confined to one geographical area and the sources varied throughout the course of the slave trade. Estimates derived from historical documents suggest that out of roughly 13 million enslaved Africans, some of whom did not survive the journey across the Atlantic, approximately 8 million came from West Africa (Guinea, Sierra Leone, Windward and Gold Coasts), around 4 million from West-Central Africa (Cameroon down to Angola), with Southeast Africa (Mozambique/Madagascar) contributing approximately 1 million (Curtin 1969, Salas et al.

2004). Figures 1 and 2 provide an illustration of the various African slave ports and their destinations in the New World.

While ethnohistoric data can shed light on the origins of the African Diaspora, historical documentation is not always complete. Some countries, such as Portugal kept better documentation than others regarding the number of slaves exported and imported, ports of departure, and ports of arrival (Rawley 1981). Therefore, to understand the origin and direction of the African Diaspora, it requires the efforts of a variety of disciplines. Since the human cranium has a strong genetic basis, craniometric analyses can provide valuable information regarding genetic variation within and between human groups (Ackermann and Cheverud 2004, Marroig and Cheverud 2004, Roseman and Weaver 2004, Gonzalez-Jose et al. 2005, Sparks and Jantz 2002, Relethford 2004a) and can add valuable information to African Diaspora literature.

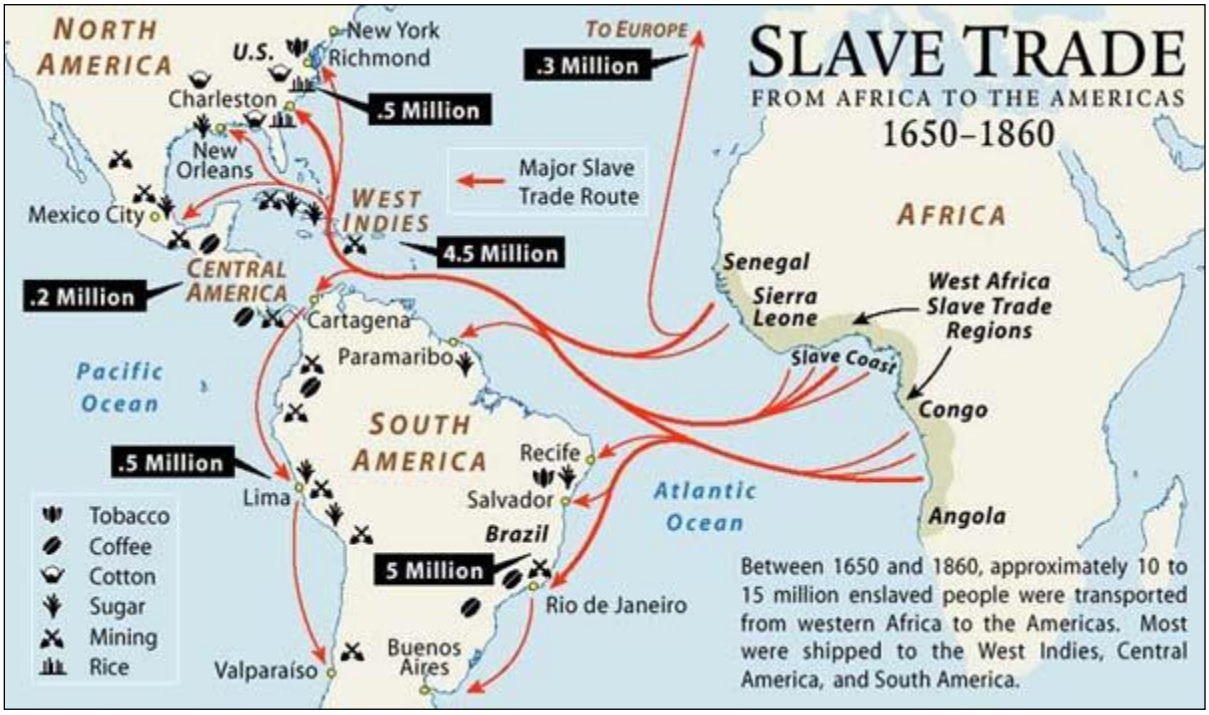

Figure 1. ***Slave Trade Route (Slavery in America, an educator's site made possible by New York Life, slaveryinamerica.org)***

Figure 2. ***Major Slave Ports in 1750 (Slavery in America, an educator's site made possible by New York Life, slaveryinamerica.org)***

II. The African Diaspora

The term "diaspora" is used to describe migrants who settle in distant lands and produce new generations (Manning 2009). It is in the interest of scholars to examine the influences of African origins in the New World, as well as other locations around the world. The ancestral origins of the slave trade are integral to African diaspora studies as they contributed to shaping black society in both Africa and the Americas.

According to Manning (2009), the study of the African diaspora acknowledges, but does not advocate, the concept of "race." Racial categorization is a culturally and socially constructed concept and often prejudicial. While the study of human variation through craniometric analysis was born out of creating "racial typologies," current research has shown that multivariate statistics can provide valuable information concerning biological distance, human migration, and gene flow among populations through space and time. The history of the African diaspora cannot be fully told without the concept of race since it is intrinsically tied to the social experience shared by descendants of African populations. However, the focus of this study is not on the social ramifications, cultural change, and adaptation of the African diaspora, but rather on the biological contributions. These biological contributions are tied to both geographical and sociocultural mechanisms and therefore, make craniometric analyses an appropriate means for understanding population history.

The Africans who were involuntarily forced to migrate to the New World had histories, collective identities, and recognizable cultures. These facets of their life actively contributed to the creation and continued adaptation of new cultural identifies in the New

World (Lovejoy and Trotman 2003). Current studies concerned with investigating the African diaspora attempt to formulate what it means to be "Black" during modern times and how Black identities can be understood (Manning 2009). Descendants from Africa experienced the New World differently depending on the people they encountered, where they were transported to, and who held colonial control. Africa is a large continent, home to the some of the most diverse languages and cultures, and as a result there was not only the coming together of Europeans and indigenous Americans, but also various African groups. Together they influenced the way in which the New World was constructed through language, culture, and biology.

Biological origins are important to understanding the past and present identity of people and may also shed light on biocultural adaptations, as well as provide insight to biomedicine. As such, craniometric analyses that elucidate on the origins of individuals may substantiate and provide context for archaeological, cultural, linguistic, biomedical, and nutritional evaluations. The next section will outline the materials used in this study, as well as the various methods employed to investigate and understand patterns of variation in the Caribbean and Latin America.

.

MATERIALS AND METHODS

I. Sample Information

Eleven groups totaling 559 crania were used in this study. Group names and sample sizes are listed in Table 1 and the geographical distribution of the groups is illustrated in Figure 3. Only adult crania were included in this study because the rapid growth changes that occur in juveniles may have potentially skewed the analyses and revealed more variation among and within populations than when just including adults alone. Males and females were pooled to incorporate all of the observed biological variation within the populations, as well as to increase sample sizes. According to Sardi et al. (2005), sex variation is negligible within each population in among-population comparisons.

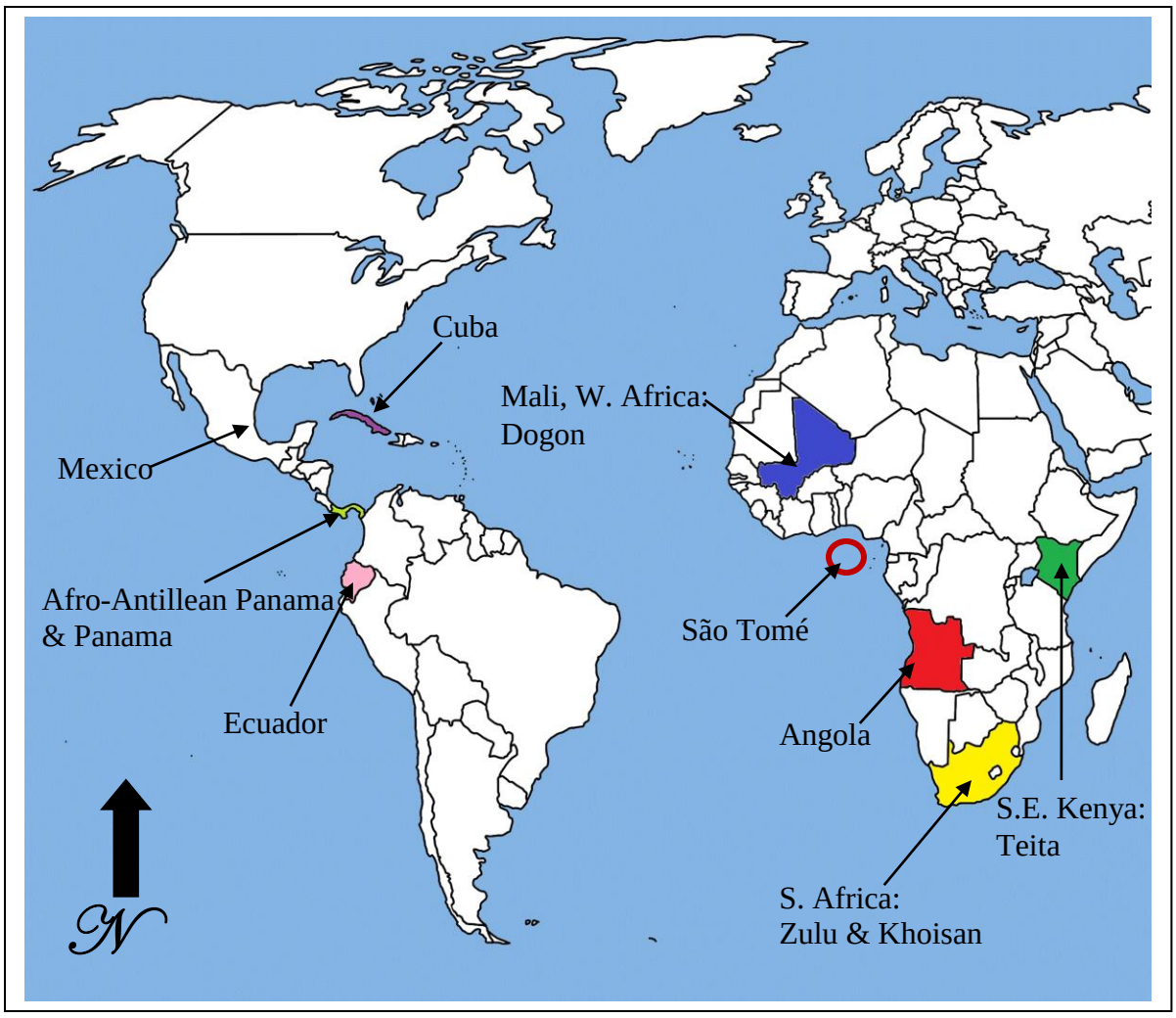

Figure 3. ***Sample geographical distribution*.**

Table 1. Group Names and Sample Sizes

Group	*N*	*Reference*	*Provenience*
Angola	68	Current Study	West Central Africa. 19th Century, Bocage Museum, Lisbon, Portugal
S.E. Kenya	83	Howells (1973)	Teita a Bantu speaking tribe
Mali, W. Africa	99	Howells (1973)	Dogon Tribe
South Africa	101	Howells (1973)	Zulu Tribe
South Africa	90	Howells (1973)	Khoisan Tribe (Bushman)
São Tomé	5	Current Study	West Central coast of Africa. Housed at the University of Coimbra, Portugal.
Modern Cuba	23	Ross et al. (2004)	19th Century cemetery collection from Museo de Montane, Havana, Cuba
Ecuador	51	Ubelaker (1994)	Historic, church Convento de San Francisco, Quito (A.D. 1540-A.D. 1940)
Mexico	21	Comas (1943) *in* Ross et al. (2002a)	Admixed Mexico
Panama	12	Ross	Contemporary, Morgue Judicial, Republic of Panama
Afro-Antillean Panama	6	Ross	Contemporary, Morgue Judicial, Republic of Panama

Unfortunately, some of the Caribbean and Latin American sample sizes are small as a result of poor preservation caused by the accelerated decay rates in tropical environments (Ross and Cunningham 2010). However, these are integral samples to understanding the scope of variation introduced by the arrival of Europeans and Africans in the New World, and were therefore included.

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 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), and individuals from São Tomé (n=5). All African data (excluding Angola and São Tomé) were collected by W.W. Howells (1973) and can be easily accessed online at http://konig.la.utk.edu/howells.htm (Howells 1996, 1973).

The Angolan sample is from the Silva Telles collection, and was recently acquired by the Bocage Museum in Lisbon, Portugal. The crania were collected from cemeteries in Luanda, Benguela, and Cabinda between 1897 and 1899 by Dr. Francisco Xavier da Silva Telles at the end of the Portuguese colonial reign in Angola (Meneses Tavares 2008) and the data on these skulls were collected by Dr. Ann Ross and me. The São Tomé sample was collected by me and is housed at the University of Coimbra in Coimbra, Portugal. The island of São Tomé is located off the west-central coast of Africa, west of Gabon. It was discovered

and populated by the Portuguese around AD 1470. The Portuguese used São Tomé and its neighboring island of Principe to cultivate sugar and during the process, imported large numbers of slaves from the mainland.

The nineteenth-century Cuban sample belongs to a cemetery collection from Museo de Montane, Havana, Cuba (Ross et al. 2004b). The materials from Ecuador are historic individuals from the church Convento de San Francisco cemetery (Ubelaker 1994). The Panamanian skeletal material includes both contemporary and Afro-Antillean individuals from the Atlantic/Caribbean coast. The Afro-Antillean individuals are black laborers from the British West Indies who came to Panama during the first half of the twentieth century. Lastly, a contemporary sample from Mexico was included. The Panamanian and Mexican data were collected and provided by Dr. Ann Ross.

II. Methods

Measurements

Metric data allows for a more objective analysis of population relationships, as such, standard cranial inter-landmark measurements (in mm) were utilized in this study. In addition, standard craniometric measurements are used so that it would be possible to include the Howells and Ecuadorian datasets for which 3D coordinate data were not available. The cranial landmarks and the standard craniometric measurements that were used in this study are presented in Tables 2 and 3 and Figures 4-6. Definitions for the craniometric measurements are also listed in Table 3. These measurements were reduced to seven according to their availability among the samples. The reduction of the measurements to just seven inter-landmark distances (ILDs) will not reduce the ability of statistical testing to provide information regarding biological distance. These seven ILDs are commonly used in craniometric analyses. These seven were also selected by Ross et al. (2002a) to investigate the craniometric variation in Latin America and the Caribbean. Multivariate and canonical statistical analyses were performed to describe the variance present in the dataset. Multivariate analyses are useful for demonstrating inter-group variation by comparing the means of multiple variables simultaneously.

Table 2. List of Landmarks

Landmark	Abv.	Associated Inter-Landmark Distances
1. Alare (paired)	al	NLB
2. Basion	ba	BBH
3. Bregma	b	BBH
4. Dacryon (paired)	d	OBB
5. Ectoconchion (paired)	ec	OBB
6. Eurion (paired)	eu	XCB
7. Superior Orbital Boarder	obhs	OBH
8. Inferior Orbital Boarder	obhi	OBH
9. Nasion	n	NLH
10. Inferior Nasal Boarder	ns	NLH
11. Glabella	g	GOL
12. Opisthocranion	op	GOL

Table 3. List of Craniometric Measurements (ILDs)

Abbreviation	Description	
GOL	Max. cranial length	distance between g – op in the midsagittal plane, measured in a straight line
BBH	Cranial height	distance between ba – b
XCB	Cranial breadth	distance between eu – eu, maximum width of skull perpendicular to midsagittal plane
NLH	Nasal height	distance between n – ns
NLB	Nasal breadth	distance from al – al, maximum breadth of nasal aperture
OBH	Orbital height	distance between the superior and inferior orbital margins
OBB	Orbital breadth	distance from d – ec, laterally sloping distance from dacryon to ectoconchion

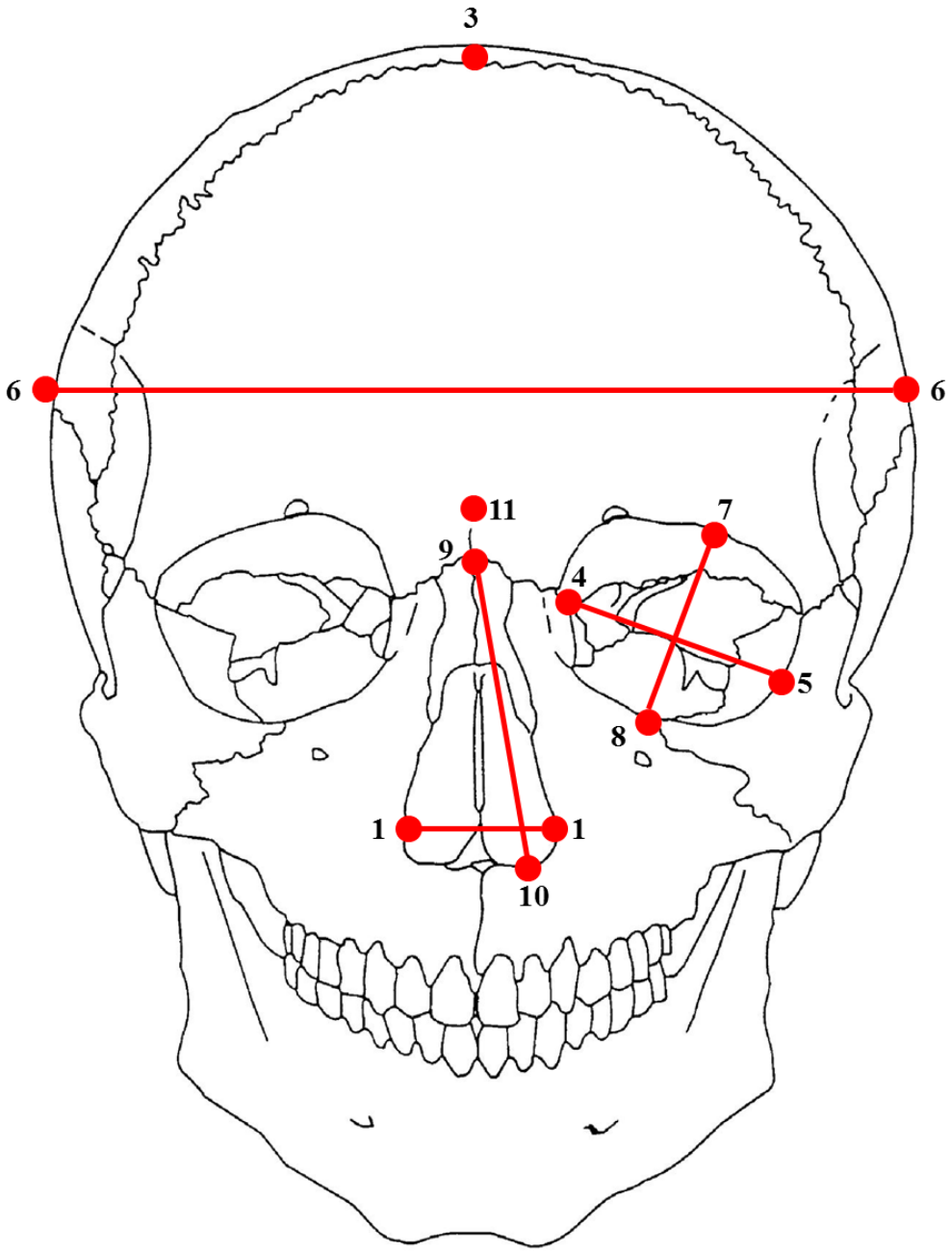

Figure 4. ***Anterior view of landmarks and inter-landmark distances (adapted from Buikstra and Ubelaker 1994 and Moore-Jansen et al. 1994).***

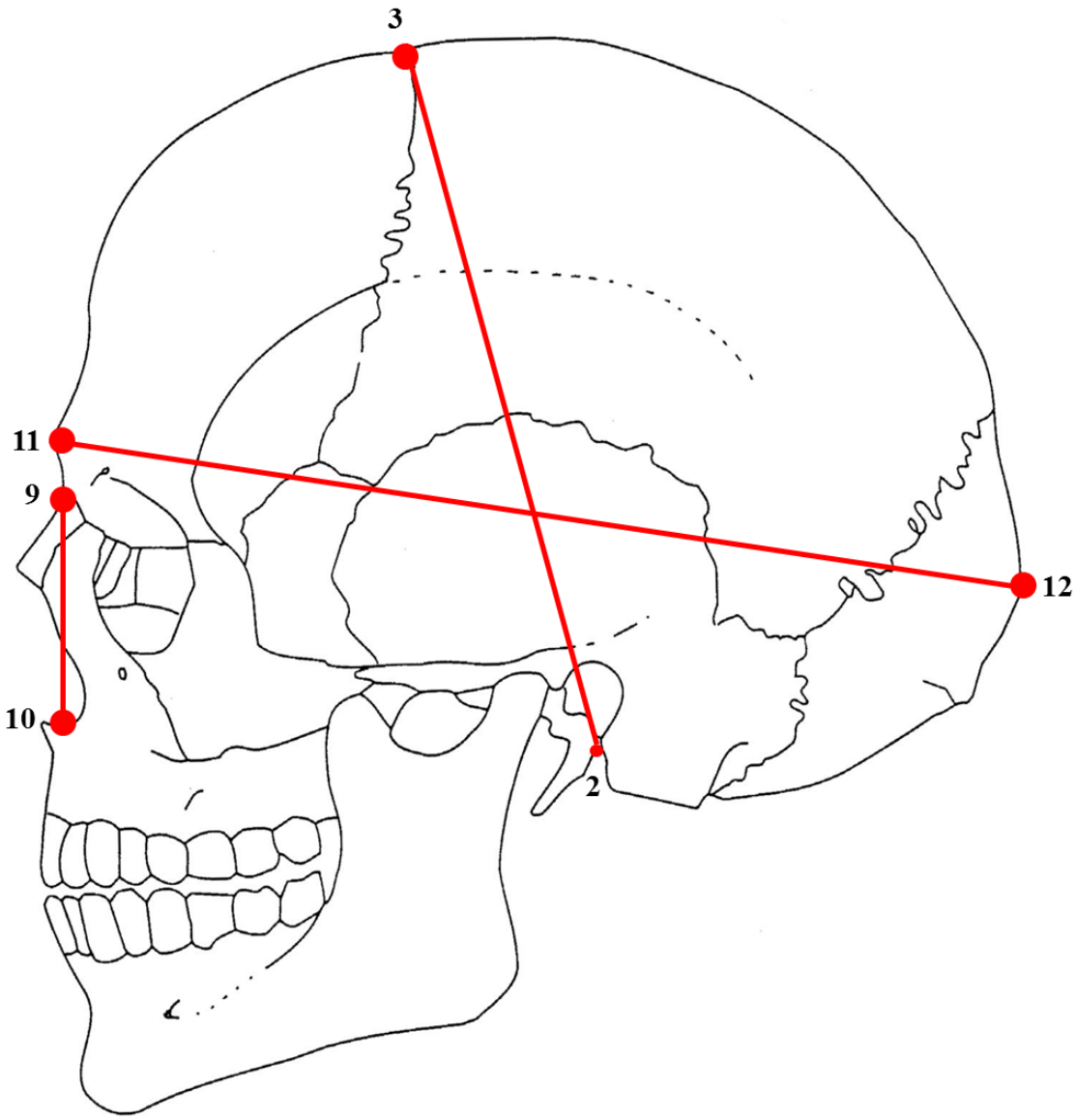

Figure 5. ***Lateral view of landmarks and inter-landmark distances (adapted from Buikstra and Ubelaker 1994 and Moore-Jansen et al. 1994).***

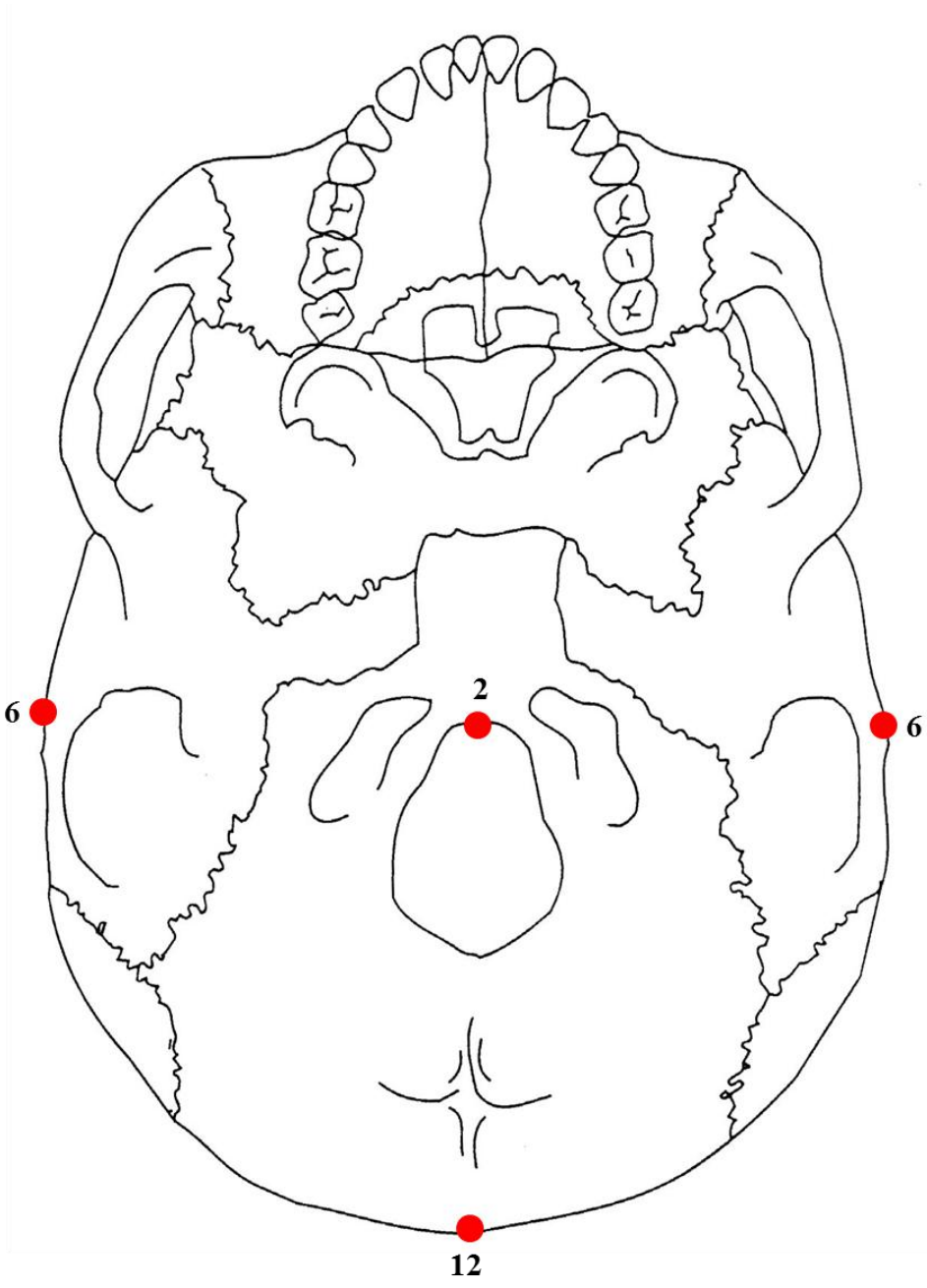

Figure 6. ***Inferior view of landmarks (adapted from Buikstra and Ubelaker 1994 and Moore-Jansen et al. 1994).***

Data Acquisition

The Angolan and São Tomé data were collected for this study. The Angolan data were collected by Dr. Ann Ross and me and measurements were taken using a Microscribe digitizer. Three dimensional landmarks were mechanically recorded using a Microscribe G2X digitizer (accurate to 0.23 mm). The procedure to collect the 3D craniometric landmark data consists of placing the tip of the Microscribe stylus on the landmark and recording the landmark by applying pressure to the attached foot pedal (Figure 7). This procedure collects the x, y, and z coordinates of the selected landmark and simultaneously collects the cranial inter-landmark distances that were used in this investigation. The program ThreeSkull, written by Steve Ousley (2004), aided in the collection of the x, y, and z coordinates and calculation of the inter-landmark distances. A suite of 75 standard, homologous cranial landmarks were recorded.

The São Tomé data were collected by me and were measured using the traditional 2D caliper-derived methods. Inter-landmark distances from the Howells' (1973) African 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 inter-landmark distances were simultaneously recorded.

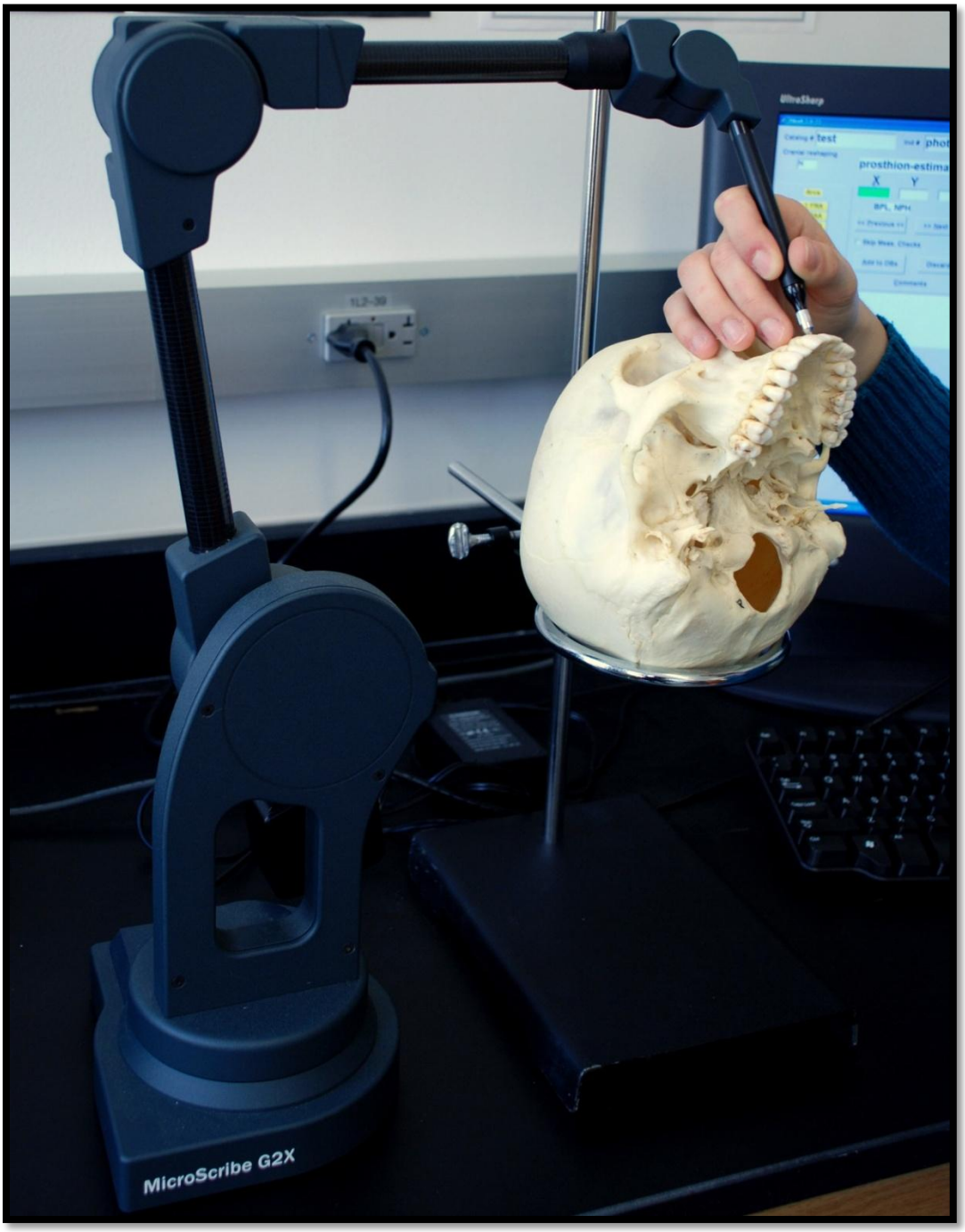

Figure 7. ***MicroScribe Digitizer***

Estimating Missing Variables

To maximize sample size and include the majority of the individuals from the original dataset, missing values were estimated using the statistical package NORM: Multiple imputations of incomplete multivariate data under a normal model (Schafer 1999). Multiple imputation (MI) is a simulation-based approach to the analysis of incomplete data. The missing part of the data is set is simulated $m > 1$ times, producing m equally plausible versions of the complete data (Schafer 1999). The multiple imputation procedure replaces each missing value with a set of plausible values. The statistical package NORM is an iterative simulation procedure and uses a type of Markov chain Monte Carlo technique to generate random draws, where the distribution of each draw depends on the previous draw (Schafer 1999).

When missing values were estimated, they did not exceed 20% of the sample. The most commonly and highest estimated variable was BBH. The greatest amount that BBH was estimated was 19% in the Ecuador sample. The total amount of estimated variables is listed in Table 4 along with their percentages. When pooling all of the samples, there were a total of 30 missing variables estimated, which makes up 5.4% (30/559) of the data.

Table 4. Percentage of variables estimated.

Variable	Angola	Cuba	Ecuador	Panama
GOL			1.96% (1/51)	16.6% (2/12)
BBH	1.5% (1/68)	4.3% (1/23)	19% (10/51)	16.6% (2/12)
XCB		4.3% (1/23)	1.96% (1/51)	8% (1/12)
NLH	1.5% (1/68)		5.88% (3/51)	
NLB			3.92% (2/51)	8% (1/12)
OBH	1.5% (1/68)		3.92% (2/51)	
OBB				

Statistical Methods

Statistical analyses were performed using Statistical Analysis Software (SAS) 9.14 (2001), unless otherwise stated. To accurately examine craniometric variation, it is necessary to account for size effects. Therefore, using the raw inter-landmark distance measurements (ILDs), size and shape variables were computed according to Mosimann and James (1979) and Darroch and Mosimann (1985). According to Mossiman and James (1979), *size* is defined as the geometric mean (GM) of all (*n*) cranial variables (ILDs) being considered. The GM of *n* variables is calculated as

$$\mathrm{GM}_Y = n\sqrt{\prod_{i=1}^{n} Y_{i,}}$$

In other words, SIZE = (GOL * BBH * XCB * NLH * NLB * OBH * OBB)** (1/7).

Once the geometric mean (GM) of all variables was computed, each variable was then divided by the GM to create shape variables (Y = X/SIZE). According to Falsetti et al. (1993), shape variables are simple ratios of the GM and are scale-free or dimensionless. These ratios measure the size of a particular region relative to the overall size of the cranium (Roseman and Weaver 2004). These variables do not necessarily remove absolute size from the analyses. However, this procedure provides a better evaluation of the "geometric similarity" among the populations being examined (Ross 2002a).

Next, a one-way analysis of variance (ANOVA) was performed on the size variable (GM) to test the null hypothesis (H_0) that the mean size is not significantly different among the groups. The alternative hypothesis (H_1) states that means are significantly different for any two of the 11 considered groups. If the H_0 is rejected, the *F value* (ratio of the sum of differences of central tendency divided by the average variance) should be greater than 5 and the *p-value* (probability of rejecting the null) should be $p < 0.05$.

To evaluate group similarities and differences, Mahalanobis D^2 were calculated. Mahalanobis D^2 is a function of the group means as well as the pooled variances and covariances that measures the degree of differentiation observed among the considered populations. The Mahalanobis D^2 values are Euclidean distances between two *N* dimensional points in space. Therefore, the smaller the Mahalanobis value between two groups, the more similar the two groups being compared are. Mahalanobis distances were also corrected for possible sampling bias using RMET, a computer program that performs population genetics analyses for metric data (Relethford 2004b).

Additionally, a canonical discriminant analysis was performed and canonical variates were derived from the newly transformed shape variables to examine interrelationships among the groups. Canonical variates are linear combinations of predictor variables that summarize between-population variation (Ross et al. 2002a). This procedure also provides the canonical correlations, the canonical structure, and the canonical coefficients. Also included are the eigenvalues, which indicate the percentage of total variation that each canonical component provides. Eigenvalues are the ratio of between-class variation to within-class variation for the canonical variable (SAS 2001). The first canonical component has the highest correlation with the groups, followed by the remaining in descending order.

Population Structure

To further investigate the amount of variation among the populations, a multivariate method by Relethford (1994:55) that estimates F_{ST} values from craniometric data was conducted. F_{ST} values were derived from the craniometric data using RMET and enabled comparisons to genetic markers. Craniometric data cannot be easily compared to allele frequency data unless genetic distance matrices are obtained. RMET, created by Relethford, is a computer program that performs population genetics analyses using metric data and is available at http://konig.la.utk.edu/relethsoft.html. The program provides an estimate for a kinship matrix, a distance matrix, an F_{ST} estimate, and eigenvalues and eigenvectors. Following Relethford (1994, 2002), minimum F_{ST} values ($h^2 = 1$) and middle-range values ($h^2 = 0.55$) were estimated.

RESULTS

I. Overall Population Means and Analysis of Variance (ANOVA)

Summary descriptive statistics (group means for raw variables) are presented in Table 5. The ANOVA for the size variable indicated a significant difference between at least two of the groups (R^2 = 0.31, *PR* > *F* 0.0001). Table 6 presents the within-class covariance matrix for each group.

Table 5. Summary descriptive statistics. Group means for raw variables.

Afro-Antillean Panama

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	6	177.00	6.66	166	183
BBH	6	131.00	2.10	129	134
XCB	6	131.83	3.87	126	135
NLH	6	50.33	3.78	43	53
NLB	6	26.50	3.51	23	32
OBH	6	34.50	1.87	32	37
OBB	6	39.83	2.93	36	43

Angola

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	68	176.99	6.47	164	194
BBH	68	129.24	5.08	118	139
XCB	68	128.19	5.63	115	142
NLH	68	47.10	3.28	33	55
NLB	68	26.53	2.22	22	32
OBH	68	34.57	2.11	29	39
OBB	68	39.44	1.51	36	43

Table 5 cont. **Summary descriptive statistics.**

Cuba

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	23	182.78	8.89	157	197
BBH	23	133.91	7.51	108	143
XCB	23	139.22	5.63	128	152
NLH	23	52.57	3.84	42	59
NLB	23	24.57	2.21	20	28
OBH	23	35.70	4.42	33	55
OBB	23	41.13	1.89	37	46

Dogon

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	99	173.57	6.98	157	194
BBH	99	130.01	4.95	118	152
XCB	99	134.65	5.19	121	148
NLH	99	46.91	2.66	41	54
NLB	99	28.04	1.68	25	32
OBH	99	33.24	1.86	29	37
OBB	99	38.81	1.80	35	43

Ecuador

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	51	173.25	9.09	157	188
BBH	51	130.43	8.00	117	168
XCB	51	142.84	5.45	130	153
NLH	51	50.61	3.81	42	58
NLB	51	24.67	1.60	22	30
OBH	51	34.92	1.92	31	39
OBB	51	40.10	2.54	32	46

Table 5 cont. **Summary descriptive statistics.**

Khoisan

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	68	176.99	6.47	164	194
BBH	68	129.24	5.08	118	139
XCB	68	128.19	5.63	115	142
NLH	68	47.10	3.28	33	55
NLB	68	26.53	2.22	22	32
OBH	68	34.57	2.11	29	39
OBB	68	39.44	1.51	36	43

Mexico

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	21	177.71	7.86	156	189
BBH	21	132.76	4.92	120	140
XCB	21	127.71	6.30	107	136
NLH	21	51.33	4.15	38	57
NLB	21	24.43	2.20	20	28
OBH	21	35.14	1.93	31	38
OBB	21	39.19	1.63	35	42

Panama

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	12	175.33	10.69	159	195
BBH	12	132.92	5.78	123	144
XCB	12	136.75	5.93	127	146
NLH	12	49.42	3.99	41	56
NLB	12	25.58	3.00	20	31
OBH	12	35.42	1.83	33	39
OBB	12	40.17	1.75	38	44

Table 5 cont. **Summary descriptive statistics.**

São Tomé

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	5	189.00	8.37	176	199
BBH	5	137.20	1.64	136	140
XCB	5	135.20	4.27	128	139
NLH	5	50.80	2.17	48	53
NLB	5	25.20	2.95	23	30
OBH	5	34.60	2.30	32	38
OBB	5	40.40	1.67	39	43

Teita

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	83	178.41	6.82	163	198
BBH	83	126.69	4.79	111	138
XCB	83	127.80	4.61	116	139
NLH	83	47.93	3.55	40	58
NLB	83	27.48	1.87	23	32
OBH	83	32.64	1.90	29	37
OBB	83	38.53	1.76	34	43

Zulu

Variable	*N*	*Mean*	*Std Dev*	*Minimum*	*Maximum*
GOL	101	182.32	6.29	171	196
BBH	101	131.43	6.14	119	146
XCB	101	133.02	5.19	120	149
NLH	101	48.77	2.90	41	57
NLB	101	28.35	1.88	25	33
OBH	101	33.36	1.94	28	39
OBB	101	39.87	1.78	35	45

Table 6. Within-class covariance matrix.

Afro-Antillean Panama				**DF = 5**			
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.00566	0.00029	0.00111	0.00127	-0.00185	-0.00005	0.00009
BBHs	0.00029	0.00458	0.00258	-0.00218	-0.00191	0.00246	-0.00034
XCBs	0.00111	0.00258	0.00432	-0.00044	-0.00208	0.00095	0.00014
NLHs	0.00127	-0.00218	-0.00044	0.00172	0.00026	-0.00105	-0.00012
NLBs	-0.00185	-0.00191	-0.00208	0.00026	0.00155	-0.00092	0.00012
OBHs	-0.00005	0.00246	0.00095	-0.00105	-0.00092	0.00184	-0.00089
OBBs	0.00009	-0.00034	0.00014	-0.00012	0.00012	-0.00089	0.00100

Angola				**DF = 67**			
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.00827	0.00102	0.00262	-0.00116	-0.00063	-0.00115	0.00035
BBHs	0.00102	0.00435	0.00123	-0.00083	-0.00058	-0.00026	-0.00001
XCBs	0.00262	0.00123	0.00551	-0.00078	-0.00096	-0.00047	0.00004
NLHs	-0.00116	-0.00083	-0.00078	0.00155	-0.00030	0.00005	-0.00021
NLBs	-0.00063	-0.00058	-0.00096	-0.00030	0.00081	-0.00020	-0.00011
OBHs	-0.00115	-0.00026	-0.00047	0.00005	-0.00020	0.00066	-0.00003
OBBs	0.00035	-0.00001	0.00004	-0.00021	-0.00011	-0.00003	0.00030

Table 6 cont. Within-class covariance matrix.

Dogon			**DF = 98**				
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.00578	0.00035	0.00086	-0.00073	-0.00017	-0.00055	-0.00015
BBHs	0.00035	0.00355	0.00070	-0.00060	-0.00023	-0.00022	-0.00026
XCBs	0.00086	0.00070	0.00454	-0.00065	-0.00030	-0.00032	-0.00037
NLHs	-0.00073	-0.00060	-0.00065	0.00092	-0.00013	0.00002	-0.00008
NLBs	-0.00017	-0.00023	-0.00030	-0.00013	0.00047	-0.00022	-0.00008
OBHs	-0.00055	-0.00022	-0.00032	0.00002	-0.00022	0.00051	-0.00003
OBBs	-0.00015	-0.00026	-0.00037	-0.00008	-0.00008	-0.00003	0.00043

Ecuador			**DF = 50**				
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.01233	0.00077	-0.00036	-0.00055	-0.00016	-0.00154	-0.00043
BBHs	0.00077	0.01173	0.00154	-0.00233	-0.00062	-0.00112	0.00015
XCBs	-0.00036	0.00154	0.00798	-0.00111	-0.00042	0.00012	-0.00115
NLHs	-0.00055	-0.00233	-0.00111	0.00203	-0.00010	0.00000	-0.00034
NLBs	-0.00016	-0.00062	-0.00042	-0.00010	0.00036	-0.00006	-0.00008
OBHs	-0.00154	-0.00112	0.00012	0.00000	-0.00006	0.00080	-0.00017
OBBs	-0.00043	0.00015	-0.00115	-0.00034	-0.00008	-0.00017	0.00095

Table 6 cont. Within-class covariance matrix.

Khoisan			**DF = 89**				
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.00766	0.00202	0.00275	-0.00084	-0.00050	-0.00114	-0.00025
BBHs	0.00202	0.00489	0.00143	-0.00038	-0.00073	-0.00057	-0.00031
XCBs	0.00275	0.00143	0.00682	-0.00112	-0.00096	-0.00065	0.00015
NLHs	-0.00084	-0.00038	-0.00112	0.00084	-0.00012	0.00016	-0.00012
NLBs	-0.00050	-0.00073	-0.00096	-0.00012	0.00084	-0.00031	-0.00009
OBHs	-0.00114	-0.00057	-0.00065	0.00016	-0.00031	0.00080	-0.00006
OBBs	-0.00025	-0.00031	0.00015	-0.00012	-0.00009	-0.00006	0.00041

Mexico			**DF = 20**				
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.00633	0.00145	0.00024	-0.00070	-0.00054	-0.00039	-0.00005
BBHs	0.00145	0.00622	-0.00058	-0.00115	-0.00103	0.00084	-0.00018
XCBs	0.00024	-0.00058	0.00442	0.00010	-0.00060	-0.00020	-0.00011
NLHs	-0.00070	-0.00115	0.00010	0.00191	-0.00036	-0.00010	-0.00035
NLBs	-0.00054	-0.00103	-0.00060	-0.00036	0.00075	-0.00041	0.00009
OBHs	-0.00039	0.00084	-0.00020	-0.00010	-0.00041	0.00067	-0.00007
OBBs	-0.00005	-0.00018	-0.00011	-0.00035	0.00009	-0.00007	0.00031

Table 6 cont. Within-class covariance matrix.

Panama			**DF = 11**				
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.02195	0.00522	0.00544	-0.00214	-0.00409	0.00018	-0.00011
BBHs	0.00522	0.00769	-0.00060	-0.00106	-0.00181	0.00060	-0.00026
XCBs	0.00544	-0.00060	0.00909	-0.00148	-0.00208	0.00027	0.00057
NLHs	-0.00214	-0.00106	-0.00148	0.00219	0.00003	0.00000	-0.00068
NLBs	-0.00409	-0.00181	-0.00208	0.00003	0.00158	-0.00046	0.00015
OBHs	0.00018	0.00060	0.00027	0.00000	-0.00046	0.00042	-0.00010
OBBs	-0.00011	-0.00026	0.00057	-0.00068	0.00015	-0.00010	0.00039

São Tomé			**DF = 4**				
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.02812	0.00557	-0.00045	-0.00161	-0.00321	-0.00229	0.00151
BBHs	0.00557	0.00554	0.00283	0.00031	-0.00223	-0.00039	0.00000
XCBs	-0.00045	0.00283	0.00455	-0.00020	-0.00138	0.00061	-0.00052
NLHs	-0.00161	0.00031	-0.00020	0.00058	-0.00004	-0.00028	0.00021
NLBs	-0.00321	-0.00223	-0.00138	-0.00004	0.00103	0.00027	-0.00013
OBHs	-0.00229	-0.00039	0.00061	-0.00028	0.00027	0.00063	-0.00050
OBBs	0.00151	0.00000	-0.00052	0.00021	-0.00013	-0.00050	0.00043

Table 6 cont. Within-class covariance matrix.

Teita			**DF = 82**				
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.00418	0.00108	0.00087	-0.00033	-0.00063	-0.00025	-0.00005
BBHs	0.00108	0.00430	0.00033	-0.00094	-0.00026	-0.00051	0.00009
XCBs	0.00087	0.00033	0.00399	-0.00087	-0.00023	-0.00030	-0.00009
NLHs	-0.00033	-0.00094	-0.00087	0.00155	-0.00007	-0.00008	-0.00046
NLBs	-0.00063	-0.00026	-0.00023	-0.00007	0.00058	-0.00030	-0.00012
OBHs	-0.00025	-0.00051	-0.00030	-0.00008	-0.00030	0.00068	-0.00003
OBBs	-0.00005	0.00009	-0.00009	-0.00046	-0.00012	-0.00003	0.00058

Zulu			**DF = 100**				
Variable	*GOLs*	*BBHs*	*XCBs*	*NLHs*	*NLBs*	*OBHs*	*OBBs*
GOLs	0.00526	0.00083	0.00127	-0.00077	-0.00030	-0.00070	0.00012
BBHs	0.00083	0.00454	0.00088	-0.00019	-0.00064	-0.00045	-0.00021
XCBs	0.00127	0.00088	0.00485	-0.00068	-0.00056	-0.00037	-0.00019
NLHs	-0.00077	-0.00019	-0.00068	0.00082	0.00002	0.00001	-0.00027
NLBs	-0.00030	-0.00064	-0.00056	0.00002	0.00053	-0.00018	-0.00012
OBHs	-0.00070	-0.00045	-0.00037	0.00001	-0.00018	0.00052	0.00002
OBBs	0.00012	-0.00021	-0.00019	-0.00027	-0.00012	0.00002	0.00046

II. Mahalanobis Squared Distances

Mahalanobis D^2 was used to measure the degree of differentiation among the group means and their pooled variances and covariances. This procedure reveals whether populations are significantly different from one another. The Mahalanobis squared distance results are displayed in Tables 7 and 8. Table 7 provides the Mahalanobis D^2 values. As the number between two groups approaches zero, the closer the group centroids are to one another. The *p-values* associated with the Mahalanobis D^2 values are displayed in Table 8. The *p-values* reveal which Mahalanobis D^2 values are statistically significant. Groups are significantly different when their corresponding *p-value* is <0.05. Therefore, the generalized squared distances reveals group relationships.

According to the generalized distances, nearly all African groups are significantly different from one another at the <0.05 level (most at the *p-value* = <.0001 level). This was expected as it has been shown that the amount of variation within a region (such as Africa) is greater than the amount of variation found among regions (such as Europe, Africa, and the Americas) (Relethford 1994). The Teita and Zulu are the only African groups that are not significantly different from one another (D^2 = 0.305, *p-value*=0.058). Interestingly, the Afro-Antillean Panamanian group is not significantly different from the Angolan or São Tomé samples (D^2= 2.12, *p-value*=0.119 and D^2=3.19, *p-value*=0.29). Additionally, the Afro-Antillean Panamanian sample is not significantly different from the Mexican, Panamanian, or the Zulu groups. Lastly, results reveal that São Tomé is not significantly different from Mexico (D^2=2.16, *p-value*=0.28).

Table 7. Mahalanobis D^2

From eth	*Angola*	*Khoisan*	*Dogon*	*Ecuador*	*Mexico*	*Panama*	*Afro-Antillean Panama*	*São Tomé*	*Teita*	*Zulu*	*Cuba*
Angola	0.000										
Khoisan	6.493	0.000									
Dogon	4.000	5.093	0.000								
Ecuador	13.865	13.965	9.407	0.000							
Mexico	5.622	17.477	12.337	12.436	0.000						
Panama	4.338	9.366	3.980	3.237	5.113	0.000					
Afro-Ant. Pan.	**2.120**	8.297	3.948	7.191	**2.768**	**1.529**	0.000				
São Tomé	4.392	10.592	10.211	12.264	**2.163**	5.439	**3.149**	0.000			
Teita	1.709	4.608	3.965	15.035	7.377	6.662	2.668	4.753	0.000		
Zulu	1.615	3.728	2.316	13.133	8.148	5.430	**2.395**	5.302	**0.305**	0.000	
Cuba	10.173	14.139	12.684	4.512	4.239	3.784	4.321	4.667	10.787	10.763	0.000

Table 8. Mahalanobis D^2 associated *p-values.*

From eth	*Angola*	*Khoisan*	*Dogon*	*Ecuador*	*Mexico*	*Panama*	*Afro-Antillean Panama*	*São Tomé*	*Teita*	*Zulu*	*Cuba*
Angola	1.000										
Khosian	<.0001	1.000									
Dogon	<.0001	<.0001	1.000								
Ecuador	<.0001	<.0001	<.0001	1.000							
Mexico	<.0001	<.0001	<.0001	<.0001	1.000						
Panama	<.0001	<.0001	<.0001	<.0001	<.0001	1.000					
Afro-Ant. Pan.	**0.119**	<.0001	0.003	<.0001	**0.080**	**0.535**	1.000				
São Tomé	0.006	<.0001	<.0001	<.0001	**0.282**	0.009	**0.293**	1.000			
Teita	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	0.041	0.003	1.000		
Zulu	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	**0.065**	0.001	**0.058**	1.000	
Cuba	<.0001	<.0001	<.0001	<.0001	<.0001	0.000	0.005	0.009	<.0001	<.0001	1.000

III. Canonical Discriminant Function

The four significant canonical variates are presented in Table 9. The eigenvalues indicate that 48% of the among-group variation is accounted for on CAN1, 30% on CAN2, 16% on CAN3, and 5% on CAN4. The total canonical structure and the correlation between the original variables and the canonical variates are presented in Table 10. The total canonical structure reveals that the variation on the first canonical axis separates the groups by nasal breadth (NLB) and the second axis separates the groups with respect to cranial breadth (XCB). The third axis is related to maximum cranial length (GOL), while the fourth canonical axis isolates the groups on orbital height (OBH). Both Figure 7 and Figure 8 are graphical representations of the class means on canonical variables and illustrate the variation among the groups.

Table 9. Significant Canonical Axes (Shape Variables)

No.	*Eigenvalue*	*Proportion*	*Canonical Correlation*	*Approx. F*	*df*	*PR > F*
1	***1.359***	***0.49***	***0.759***	***18.36***	***70***	***<0.0001***
2	***0.839***	***0.30***	***0.675***	***12.71***	***54***	***<0.0001***
3	***0.438***	***0.16***	***0.552***	***7.50***	***40***	***<0.0001***
4	***0.125***	***0.04***	***0.333***	***3.09***	***28***	***<0.0001***
5	0.021	0.01	0.145	1.14	18	0.3056
6	0.011	0.004	0.105	0.88	10	0.5467
7	0.005	0.002	0.071	0.69	4	0.6013

The significant canonical axes are italicized and highlighted in red.

Table 10. Total Canonical Structure

Variable	*CAN1*	*CAN2*	*CAN3*	*CAN4*
GOL	-0.501	-0.074	***0.709***	0.031
BBH	0.158	-0.270	-0.277	-0.129
XCB	0.430	***0.801***	0.126	-0.028
NLH	0.550	-0.505	0.006	0.565
NLB	***-0.770***	0.246	-0.332	0.337
OBH	0.411	-0.331	-0.125	***-0.618***
OBB	0.048	0.155	0.428	-0.477

The significant variables represented by each canonical axis are italicized and in red.

Figure 8 is a graphical representation of the first and second canonical axes and accounts for roughly 79% of the total among-group variation. The African groups have relatively moderate to wide nasal breadths, whereas the Latin American and Caribbean groups have relatively narrow nasal breadths (NLB) to varying degrees (Figure 8). All groups have varying degrees of cranial breadth (XCB); however, the Khoisan group displays the widest cranium and Mexico has the narrowest.

Figure 9 is a graphical representation of the third and fourth canonical axes. These axes account for approximately 20% of the total among-group variation. These canonical axes reveal that Cuba, São Tomé, and Khoisan groups have the longest vaults (GOL), while Dogon have the shortest vaults with the remaining groups falling in between in varying degrees (Figure 9). In addition, Figure 8 illustrates that the Zulu, Teita, Ecuador, and Afro-Antillean Panama have relatively short orbital height (OBH) and moderate cranial length (GOL) in comparison with the other groups.

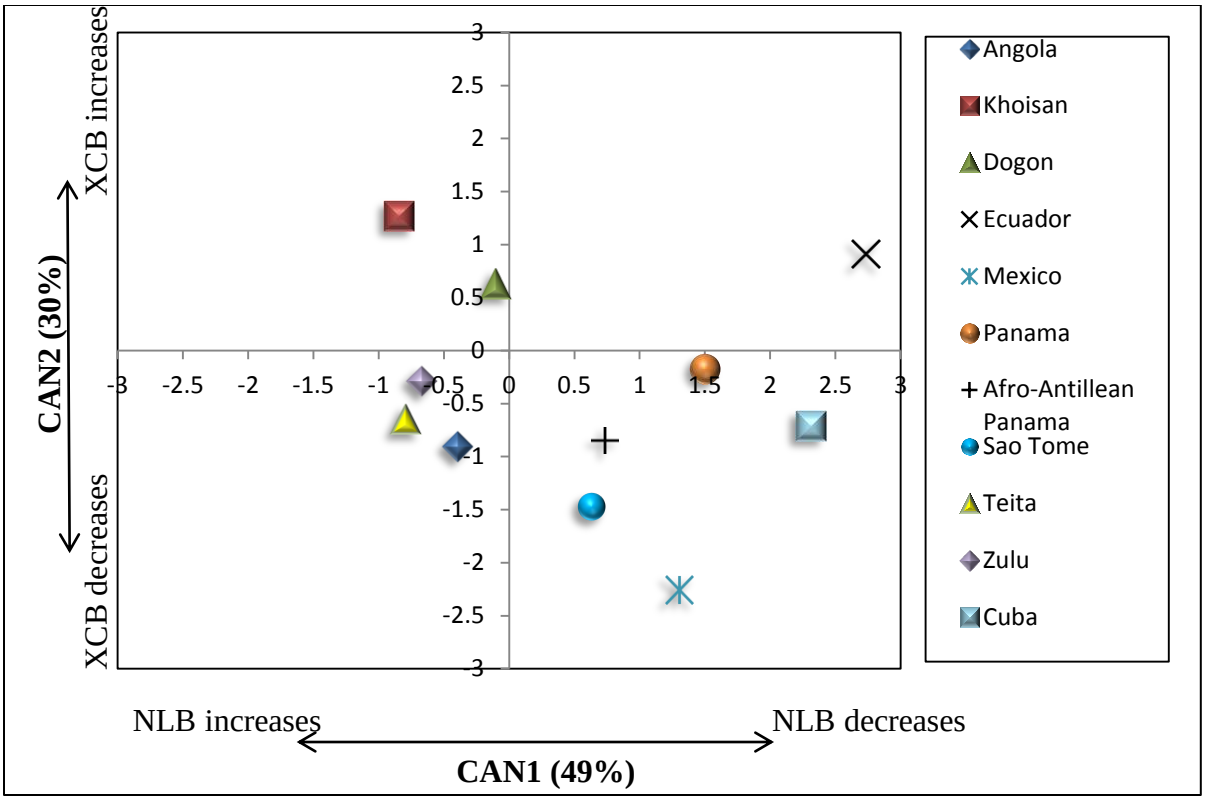

Figure 8. ***Class means on canonical variables (shape variables).***

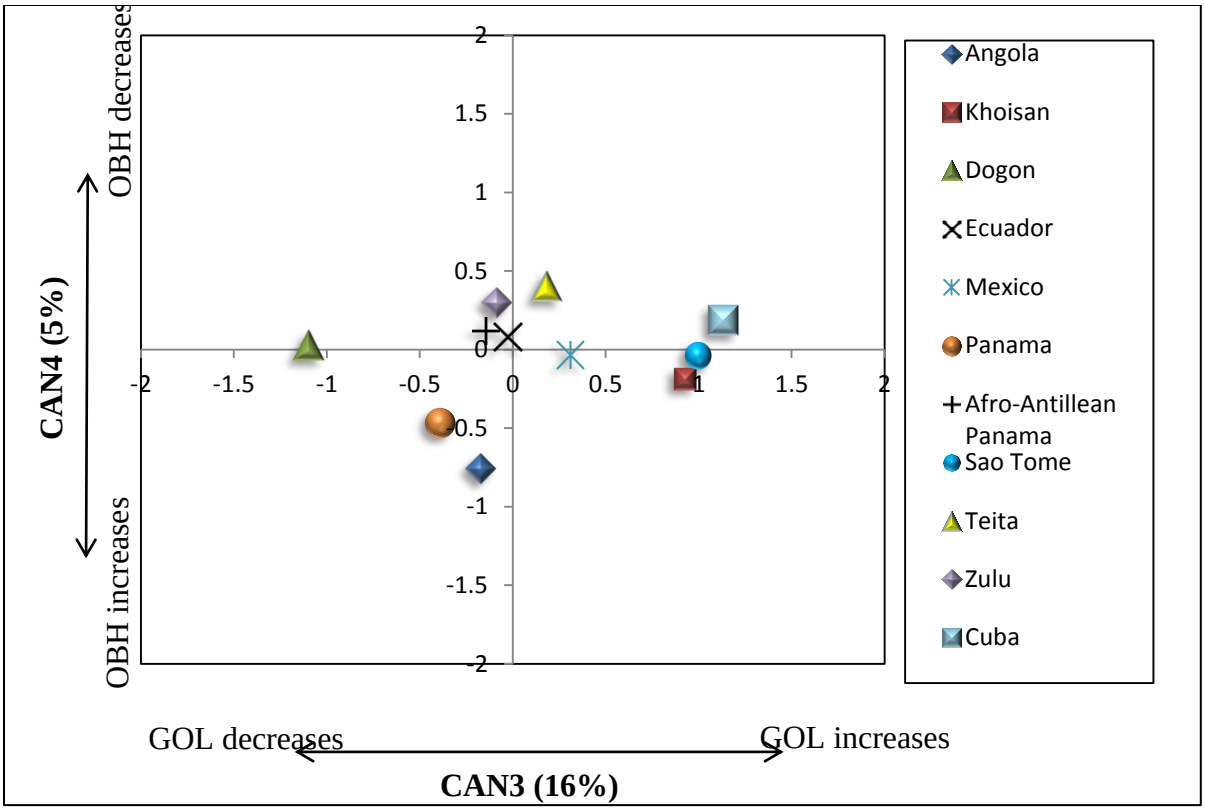

Figure 9. ***Class means on canonical variables (shape variables).***

VI. Population Structure

The unbiased minimum F_{ST}, which is used to measure the degree of differentiation among subpopulations, is 0.245 (S.E. = 0.011). These calculations were derived when assuming average heritability (0.55). Assuming complete heritability (1.0) for craniometric traits, the unbiased minimum F_{ST} is 0.146 (S.E. = 0.011). Both the average heritability and complete heritability results suggest that the groups are highly differentiated.

DISCUSSION

Previous studies have focused on broad geographical groups as being morphologically representative of all individuals within that broad area. However, modern day multivariate statistics has revealed a very different pattern of human variation and allows us to more narrowly identify human biological relationships. To date, there has not been a systematic examination of the craniometric variation present in the Caribbean and Latin America as it was influenced by the discovery of the New World and the introduction of forced slave labor. The purposes of this research was to use craniometric data to trace the geographical African origins of Caribbean and Latin American Blacks, investigate the patterns of variation evident in the Caribbean and Latin America, and investigate the biological Angolan (west-central Africa) contribution to the Caribbean and Latin America. The following discussion includes the major conclusions of each objective.

I. Biological Angolan and West-Central African Contribution

The results of this research found that the Angolan group is not significantly different from the Afro-Antillean Panamanian group (Figure 10). This indicates that these samples share similar morphology and therefore, express genetic similarity. This finding supports the hypothesis that there is evidence for an Angolan and/or west-central African influence in the Caribbean and Latin America. This was generally unexpected given the historical literature. It is unclear whether the Afro-Antillean Panamanian sample is representative of the African slaves transported to Panama during the trans-Atlantic slave trade since the Afro-Antillean

Panamanians most likely represent individuals from the British West Indies who came to Panama during the first half of the twentieth century. Either way, it is evident that there was an Angolan biological influence in the Caribbean and Latin America.

In addition, the results suggest that the morphology of the São Tomé sample is not significantly different from both the Mexican and the Afro-Antillean Panamanian samples (Figure 11). It is unclear at this time whether this finding supports the initial hypothesis that there is a west-central African contribution to the gene pools of the Caribbean and Latin America. As mentioned previously, São Tomé is an island found along the coast of west-central Africa. It was uninhabited until the Portuguese began cultivating sugar and importing slave labor from the mainland around 1470 AD. It is interesting to note that the results from this study indicate that São Tomé and Angola are significantly different from one another.

This finding was surprising since both São Tomé and Angola were controlled for long periods of time by the Portuguese and it might be assumed that the Portuguese imported individuals from Angola to São Tomé thus making them biologically similar. Therefore, it is uncertain what biological ancestral affinities are represented by São Tomé. This finding may be the result of a small sample size and would benefit from future analyses of a larger sample. In addition, it would be interesting to compare the Angolan and São Toméan samples to a Portuguese sample due to the continued contact between these groups and locations (Klein 1972) to see if there is a significant biological Portuguese contribution to São Tomé. Research may identify a larger Portuguese biological component in São Tomé since the Portuguese initially colonized the island.

Additionally, genetic data presented by Salas et al. (2004) report results for a principle components analysis of mtDNA. This analysis found that on the first principle component, São Tomé clustered with Caribbean, African American, and western African samples. The genetic research by Salas et al. (2004) may indicate that the biological ancestral affinity of São Tomé may represent a western African population.

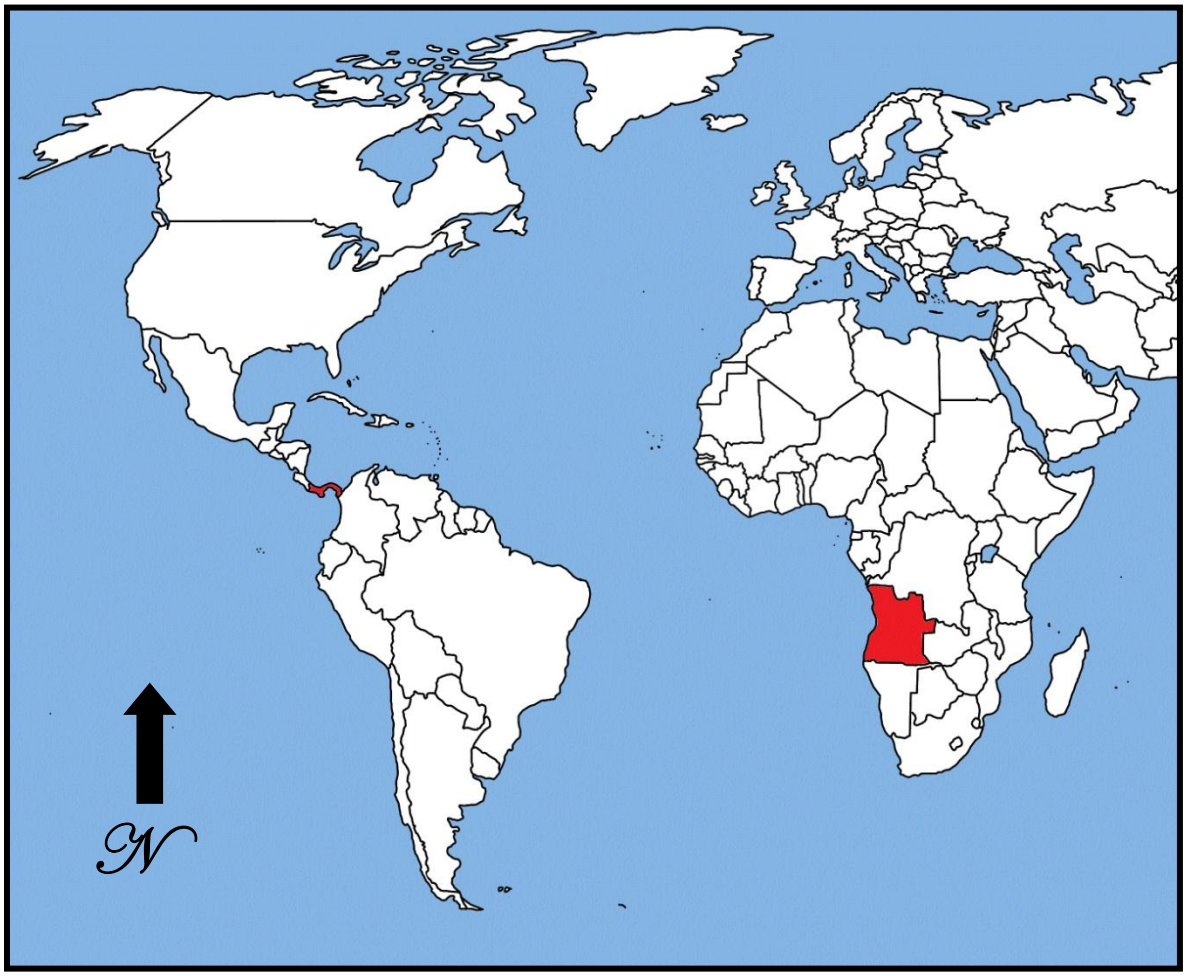

Figure 10. ***Angolan and Afro-Antillean Panamanian samples are not significantly different.***

Figure 11. ***São Toméan sample is not significantly different from the Mexican and Afro-Antillean Panamanian samples.***

II. Other Geographical African Origins and African Variation

The only western African sample included in this study was the Dogon tribe from West Mali. It is interesting to note that the results from this research did not show any biological contribution from the Dogon sample to samples in the Caribbean and Latin America (Figure 12). This finding is unique as it is well known that western Africa was one of the main suppliers of slaves during the trans-Atlantic slave trade (Curtin 1969). There were numerous western African groups that are known to have contributed to the slave population; however, these groups may not be represented within the scope of this study. Therefore, future research that expands the western African samples is warranted.

Another interesting statistical outcome was that the Zulu are not significantly different from Afro-Antillean Panamanians (Figure 13). This finding is intriguing because the Zulu are from southern Africa and southern African populations contributed relatively little to the slave trade in comparison to other groups (Curtin 1969). Additionally, results from this study have shown that the Zulu from southern Africa and the Teita from southeast Kenya (eastern Africa) are not significantly different from one another (Figure 14). A possible explanation for both of these findings is that the similarity between the Afro-Antillean Panamanians and the Zulu and the similarity between the Zulu and Teita are the result of Bantu migrations (Beleza et al. 2005, Phillipson 1993) and /or the acquisition of slaves by the western African populations from other regions of Africa.

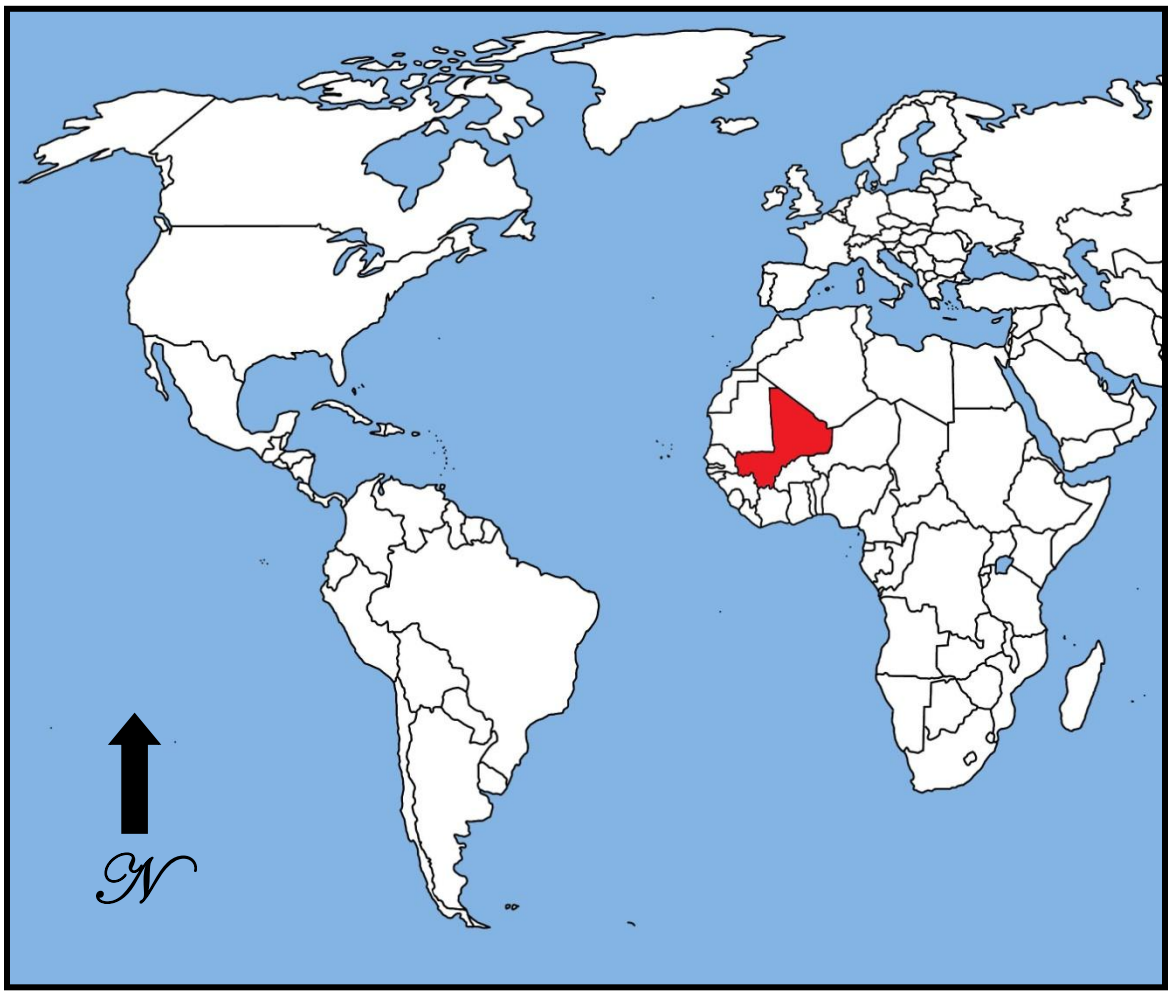

Figure 12. ***The Dogon sample from West Africa was significantly different from all other samples.***

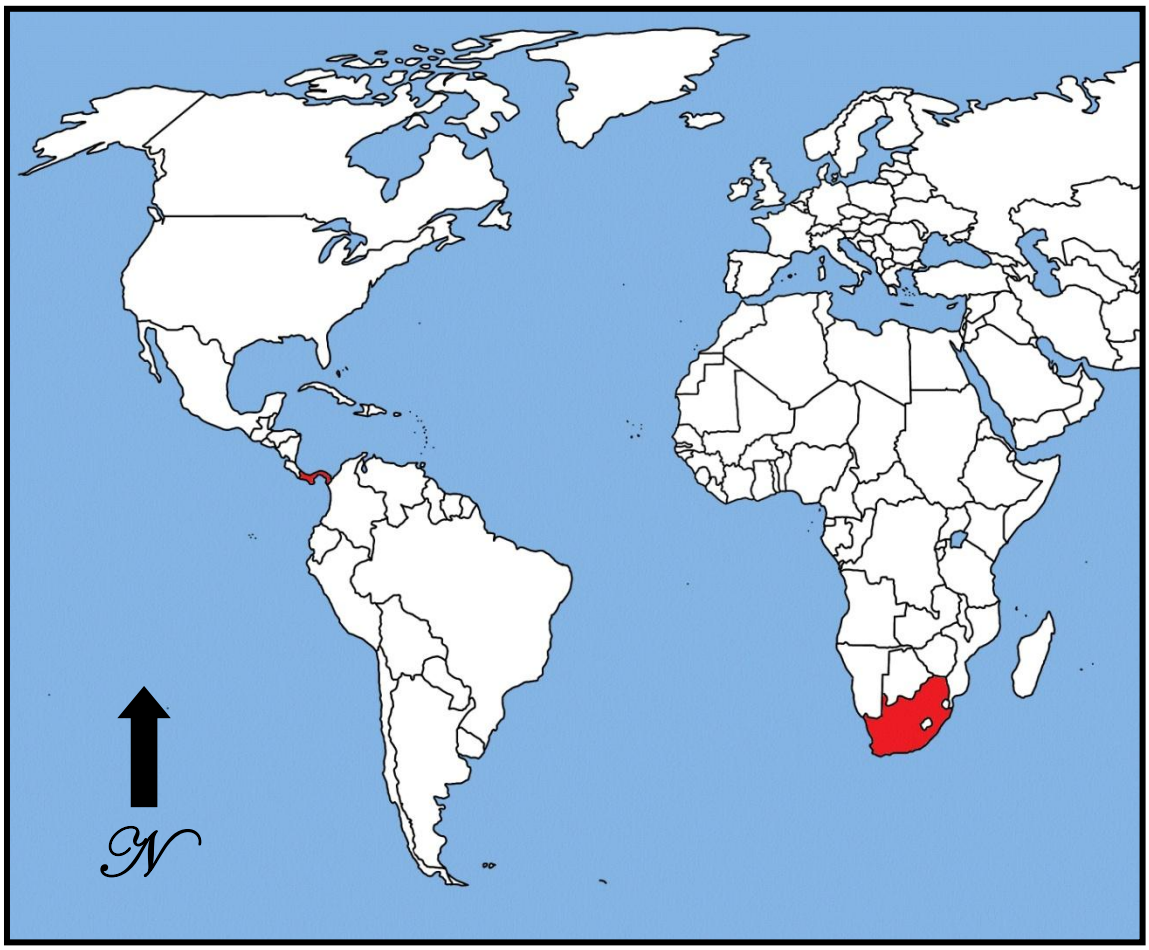

Figure 13. ***The Zulu (South Africa) sample is not significantly different from the Afro-Antillean Panamanian sample.***

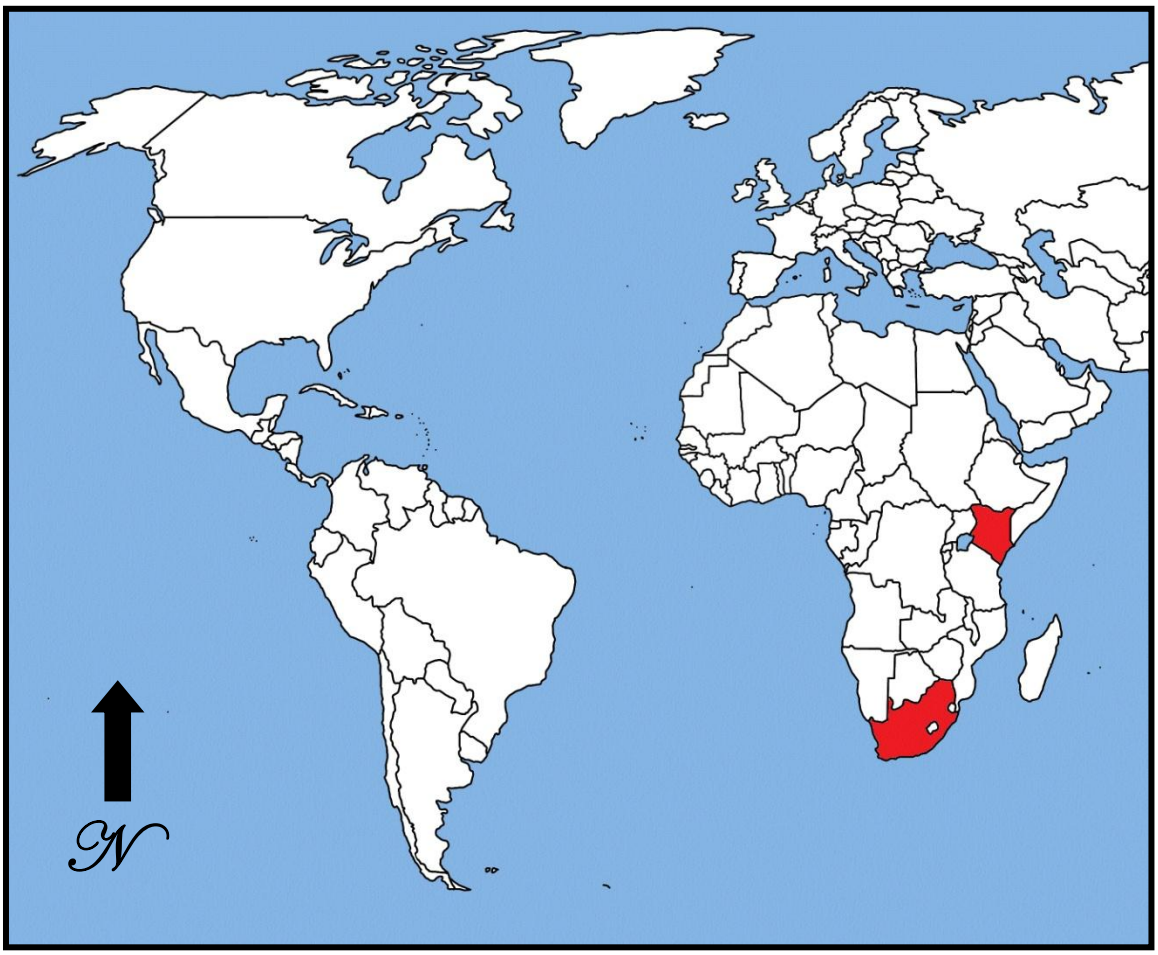

Figure 14. ***Zulu (South Africa) sample is not significantly different from the Teita (southeast Kenya) sample.***

Bantu migrations in Africa have been traced from a variety of evidence including genetic, linguistic, craniometric, and archaeological data (Ribot 2004, Cavalli-Sforza et al. 1994, Salas et al. 2002, Salas et al. 2004, Beleza et al. 2005). These migrations have been traced by and named after the diverse language group, *Bantu*. Tribes throughout Africa that speak a variant of the Bantu language group are considered related to one another. Several waves of migration have been identified and archaeological evidence suggests that the first Bantu dispersal began roughly 5,000 years ago around the present day boarder of Nigeria and Cameroon and then expanded southwards and easterly (Beleza et al. 2005, Phillipson 1993). The eastern Bantu migration formed a new expansion center by roughly 3,000 years ago and traveled southwards in two distinct expansion waves (Beleza et al. 2005, Newman 1995, Phillipson 1993). Figure 15 is an illustration of the suggested Bantu dispersals.

Both the Zulu (southern Africa) and the Teita (southeast Kenya) are Bantu speaking tribes and therefore, their similarity can be attributed to their shared migratory ancestral history through the Bantu migrations. The findings of this research also indicate that the Zulu and Afro-Panamanian samples were not significantly different. A principle components analysis of mtDNA conducted by Salas et al. (2004) show that both the southeastern Africans and Angolans sit tightly together in the west-central African cluster. The southeastern African samples used in the Salas et al. (2004) study were from Mozambique. Through mtDNA studies, Mozambique has been shown to have similar mtDNA sequences as groups to the north and can be attributed to the Bantu expansion (Pereira et al. 2001). Therefore, the finding that both the Zulu and the Angolan samples are not significantly different from one another can likely be attributed to the Bantu dispersion.

The Khoisan sample, which is also from southern Africa, was significantly different from all groups considered in this study. Although the Khoisan resides in southern Africa along with the Zulu, they are distinct from the Bantu groups and resided in the region prior to the migration of Bantu-speaking migrants (Pereira et al. 2001, Rightmire 1970). While constructing phylogenetic networks, Salas et al. (2002, 2004) excluded outliers from their principle components analysis if they had high levels of certain haplogroups. The Khoisan was one sample that was excluded because they had distinctly different haplogroup frequencies, thus indicating that they are biologically distinct and thereby, support the results of this study. In addition, through the analysis of mtDNA, Pereira et al. (2001) identify a southeastern African (Mozambique) slave contribution to the Americas that was higher than the southeastern African contribution to Europe. This is likely due to the location of Mozambique. Salas et al. (2004) using mtDNA found that the Brazilian and several of the Central American samples and Caribbean sample clustered with the southeastern Africans. The craniometric results from this research and the results from the genetic studies are consistent with and provide support for each other.

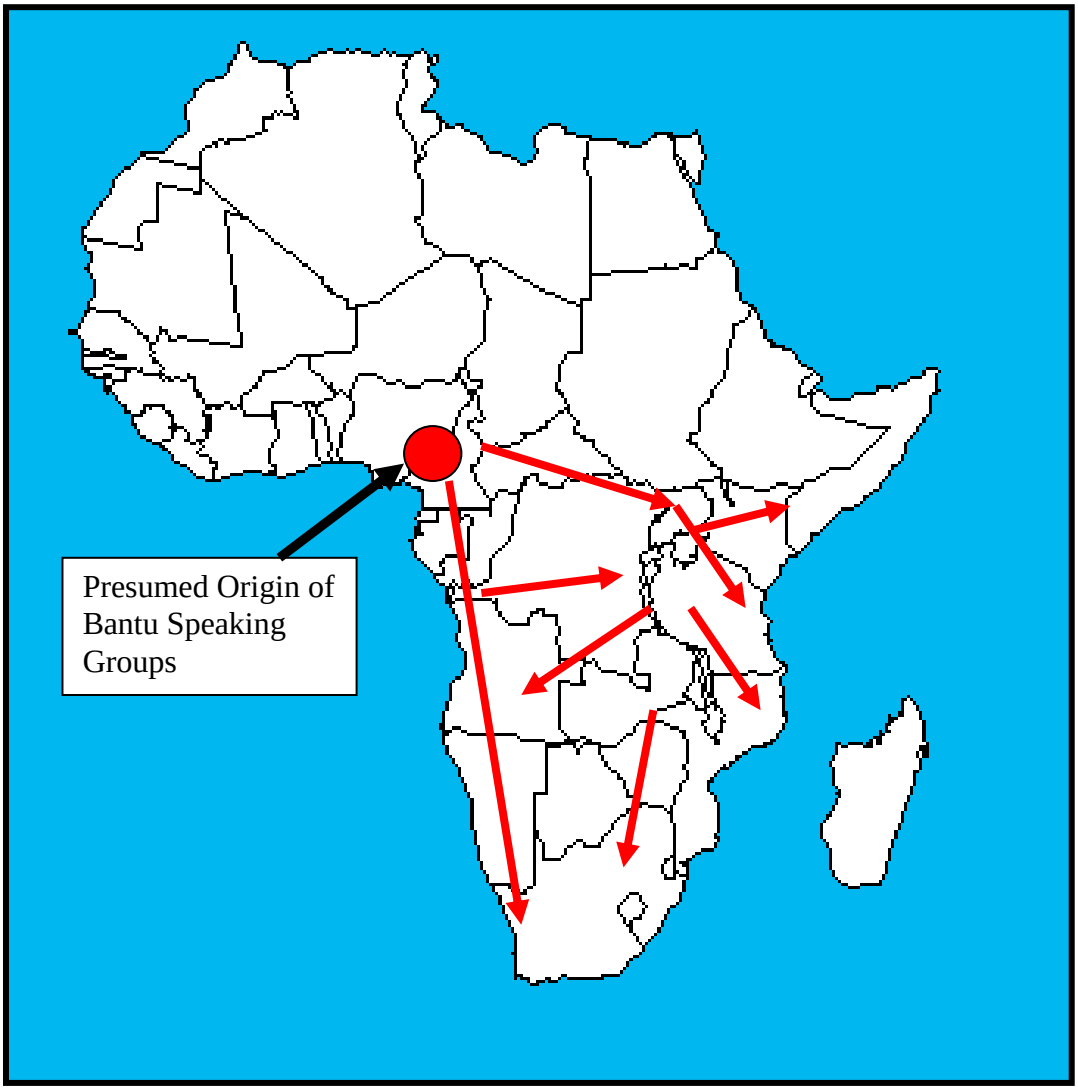

Figure 15. ***Routes of the Bantu Expansion (adapted from Beleza et al. 2005)***

III. Identified Patterns of Variation in the Caribbean and Latin America

Finally, results pertaining to the patterns of variation within the Caribbean and Latin America indicate that the Afro-Antillean Panamanian sample is not significantly different from both the Mexican and the contemporary Panamanian groups (Figure 16). This may suggest a similar indigenous and/or African biological relationship.

It was also found that the Mexican and Ecuadorian samples are significantly different from one another. This finding is noteworthy since Ross et al. (2002a) reported genetic morphological similarity between Mexico and coastal Ecuador. The Mexican sample used in this current research was historic and of admixed ancestry and the Mexican sample from Ross et al. (2002a) represents a pre-contact sample. This suggests that a significant biological change has occurred since the meeting of indigenous Americans, Europeans, and Africans as a result of European conquest and the slave trade. The introduction of heterogeneous Old World populations to the heterogeneous populations of the New World aided in transforming the biological composition of the region. Therefore, population aggregation would increase variability. Further research is required to understand local microevolutionary changes in underlying biological affinity between Mexico and Ecuador, as well as among the rest of the Caribbean and Latin America.

While this research has shown that African biological origins of the Caribbean and Latin American can be identified, it is unclear at this time if the results of this study were influenced by the genetic admixture from the Spanish and Portuguese colonists that controlled much of the Caribbean and Latin America. Research that investigates genetic markers of admixture have proposed that the African frequencies, particularly in countries

with low African frequencies, may derive from the Spanish and Portuguese colonists as these populations had several hundred years of African exposure during the Moorish stronghold on the Iberian Peninsula (Reuter 1934). In addition, the Spanish and the Portuguese were some of the earliest countries to export slave labor from Africa and therefore had several hundred years of potential gene flow to occur between them before traveling to the New World. Furthermore, Ubelaker and colleagues (2002) and Ross and co-workers (2002b) found an African affinity for a 17th Century Spanish sample, thus supporting these genetic studies using craniometric data. Therefore, it is likely that some of the African admixture present in the Caribbean and Latin America is the result of the African admixture already present in the Spanish and Portuguese populations. In addition, it is unclear whether the genetic morphological similarities found among countries and regions of the Caribbean and Latin America are the result of similar underlying African affinity or indigenous affinity. Therefore, a study including pre-contact and post-contact samples from the Caribbean and Latin America, Portuguese, Spanish, and various African populations, would aid in answering some of these questions and build upon the results reported here.

Figure 16. ***Afro-Antillean Panamanian sample is not significantly different from the contemporary Panamanian and Mexican samples.***

CONCLUSIONS AND FUTURE DIRECTIONS

The outcomes of this research support the hypothesis that there is an Angolan/west-central African genetic contribution to the Caribbean and Latin America as result of the slave trade. In addition, the results of this study illustrate that the specific geographical origins of the African Diaspora can be traced through craniometric analyses. This research not only contributes to an area of investigation in the Caribbean and Latin America that has not been fully visited before, it also provides a foundation from which future analyses can develop, improve upon the findings reported here, and provide a clearer picture of the various factors contributing to the biological variation.

Limitations

As with any analysis, there were various limitations to this study. These limitations include sample size, geographical group representation, and limited measurements (for some groups). Some of the sample sizes were small due to their preservation and taphonomic environments. However, the valuable information they provided is important to understanding biological variation and therefore, as long as it is understood that they may not be representative of the entire population, they can still be used. In addition, the study was limited to small geographical representations of Africa, the Caribbean, and Latin America. Therefore, the conclusions made by this study can only be applied to the various locations and groups used within the study. However, the conclusions yielded by the analyses of these groups are paramount to understanding human biological variation in the Caribbean and

Latin America as they were influenced by the slave trade and are valued since there has not been an investigation of this sort to date.

One of the limitations associated with traditional, two-dimensional craniometrics analysis is that the measurements or angles are ultimately based on the positions of the endpoints, or anatomical landmarks. The recorded measurements document incomplete information about the relative positions of these defining points (landmarks) in a three dimensional space (Bookstein 1991). For example, the information on biological variation may not be conveniently oriented between the distances of the caliper measurements that are taken from two landmarks in traditional craniometrics (Ross et al. 1999). Therefore, it may be difficult to relate the patterns of morphological variation in the real, physical space that they are meant to be described within (Ross and Kimmerle 2009).

Three dimensional craniometric data and geometric morphometrics are specifically useful because it allows for the x and y coordinates from traditional craniometrics to be analyzed spatially with respect to the z coordinate. While three dimensional geometric morphometric methods may provide more information regarding the spatial relationship of these points in space, standard craniometric analyses continue to prove useful and are still a valid method of investigating patterns of variation within and among populations. Many historically significant data sets for which it would take decades to re-analyze or that are no longer available such as those collected by W.W. Howells (1973) are still an important component of modern physical anthropological research. Therefore, geometric morphometrics will probably not rapidly replace traditional craniometrics. However, three dimensional landmark data collection and geometric morphometric analyses should be

recognized as the next step. Future data collection, when feasible, should attempt to collect the three dimensional landmark data using a program such as ThreeSkull (Ousley 2004) that simultaneously records the standard craniometric measurements so that both types of data are available for research.

Future Directions

Currently, a major problem within this field of study is the poor sampling coverage throughout Africa, the Caribbean, and Latin America and the lack of three dimensional data. Future research and data collection is needed to gain a complete understanding of the biological variation present in the Caribbean and Latin America, identify the specific geographical and cultural contributions of genetic variation, and understand microevolutionary trends. The results from this study encourage and support further sampling and analyses that include more African, New World indigenous, post-contact Caribbean, and Latin American populations, as well as Spanish and Portuguese samples. Therefore, this study provides the foundation for future examinations of the craniometric variation found within the Caribbean and Latin America.

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