BIOLOGICAL DISTANCE

AND THE AFRICAN AMERICAN DENTITION

DISSERTATION

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By

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ABSTRACT

Gene flow occurs whenever two human populations come in contact. African Americans are the result of gene flow between two biologically disparate groups: West Africans and Americans of European descent. This project utilized characteristics of dental morphology to trace genetic relationships among these three groups. Dental morphological traits are useful for this purpose because they are heritable, do not remodel during life (although they can be lost to wear or pathology), and can be compared equally among samples from past and present populations. The results of this research provide new knowledge about human microevolution in a biocultural setting. By analyzing observations from a variety of samples from African Americans, European Americans, West Africans, and western Europeans, conclusions were made on patterns of genetic change through time and space.

The specific hypothesis addressed is that since gene flow has been continuous among West Africans, African Americans, and European Americans in the American colonies and subsequently in the United States, the more recent a sample of African Americans observed, the more they tend toward the average, genetically, of West Africans and Europeans. Dental characteristics reflect this heritage and the pattern of temporally limited genetic similarities. In addition to testing this hypothesis, several predictions were made and tested regarding the historical patterns of admixture in African

Americans. These predictions involved whether gene flow has occurred at a constant rate, whether African Americans with greater admixture were more likely to take part in the Great Migration, and whether the dental morphology of the Gullah of South Carolina is especially like their West African ancestors.

The results of this research indicate that while admixture of European American genes into the African American gene pool has been continuous over the last 350 years, it has not occurred at a constant rate. Cultural trends and historical events such as the Civil War and the Jim Crow era affected the rate of admixture. A final product of the current research is a series of probability tables that can be used to determine the likely racial affiliation of an unknown individual. These tables are useful in historic archaeological and forensic settings.

Dedicated to my mother.

She said I could be the educated one.

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FIELD OF STUDY

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CHAPTER 1

INTRODUCTION

> The American Negro is an amalgam, and the application of the term 'Negro' to him is purely sociological. But the phrase 'American Negro' has real biological significance… (Herskovits, 1928a: 17).

Humans vary in generally predictable patterns based on the geography of their ancestry. The geographical aspect of our ancestry results in patterns of phenotypic variation. These patterns include expression of many of the characteristics used in the attribution of social race categories to individuals and populations. The research described herein addresses one issue in the overall discussion of race in America. This research was designed to provide information about the biological characteristics of the people in the United States designated as African American, and it is intended to provide information about the biological component of their socially designated race. The primary objective is to investigate the evidence for biological affinity between African Americans and the populations that contributed most to their gene pool, *i.e.* West Africans and Americans of Western European descent, using dental morphological characteristics as markers of ancestry. Using dental characteristics to trace gene flow, comparisons can be made among samples of populations who lived at various times in

the past. This is unlike most previous admixture studies that have used Mendelian genetic markers, and only make comparisons among modern peoples.

Genetically, African Americans are the products of gene flow between biologically disparate populations. The present project provides an example of evolution occurring in an historical, biocultural environment. The following hypothesis will be tested:

> Since gene flow has been continuous among West Africans, African Americans, and European Americans in the American colonies and subsequently in the United States, the more recent a sample of African Americans observed, the more they tend toward the average, genetically, of West Africans and Europeans. Dental characteristics reflect this heritage and the pattern of temporally limited genetic similarities.

Several sub-hypotheses also are addressed in this study. These involve the rate and pattern of admixture of European genes into the African American gene pool. For example, the information presented here is used to address questions such as, "Did events such as the Civil War and the Jim Crow era of the following century alter the rate of genetic exchange?" and "Did African Americans with greater amounts of European admixture migrate north at rates higher than chance would predict?"

While osteological characteristics of African Americans and dental traits of Africans have been studied (*i.e.* Gill and Rhine, 1990), no suite of dental characteristics specific to African Americans has been identified to date. In addition to addressing the

hypothesis and related questions, this research provides a description of the dentitions of African Americans and European Americans, which can be useful in forensic and archaeological identification. Finally, the results of this study may be important as a statistical demonstration of the relatedness of people often thought of as very different. In public debate, it is common for differences between racially based social groups to be emphasized. A quantification of admixture may also serve to point out the similarities shared among groups.

A model of African American admixture

One of the factors that makes the present study possible is the simplicity of the folk racial taxonomy used in the United States to describe persons of European heritage and persons of African heritage. Most other cultures that include these two groups, such as Caribbean or South American countries, utilize a classificatory system with many gradations between extremes (Davis, 1991). In the United States, however, the "one drop" rule has been the most common tool of folk taxonomy for at least the last 150 years. Described in Chapter two, the one drop rule is that any African ancestry, however remote, makes one African American.[1] While this folk taxonomy certainly does not reflect any real divisions in our species, it does affect social interactions, economic opportunities and mating patterns. Therefore, it is of real consequence, both culturally and biologically, to the people classified by it.

[1] Of course, this rule does not take into account African heritage for all *Homo sapiens*, or Africans of recent European heritage, such as the Boers.

Figure 1.1, below, is a schematic representation of the admixture and classification of Africans and African Americans in the United States over the last 400 years. While Africans were considered a distinct population at the beginning of slave importation to the U.S, as time passed their descendents were grouped regardless of whether their parentage was all African or mixed African and European. The addition of new genes from Africa was greatly slowed by the outlawing of slave importation in 1803 (although a small illegal trade continued for some time) and virtually ended by 1850 (Collins, 1904). Until shortly before the Civil War (1861-1865), there were few social constraints on European American men's sexual access to African American females. However, historical sources indicate that during the Civil War, Reconstruction, and Jim Crow era, changes in the Southern "white" culture's views of their relationships to their

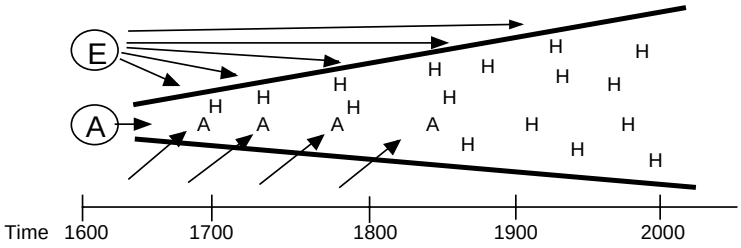

Figure 1.1. A model of continuous gene flow into the African American gene pool. "E" refers to Americans of European Ancestry, "A" to African immigrants to the U.S., and "H" to hybrids between E and A. Everyone between the two bars is considered African American. The thinner arrow indicates lower levels of gene flow after 1865.

former slaves caused new social sanctions to develop, somewhat limiting the sexual behavior of European American men (Williamson, 1980). These patterns are reflected in Figure 1.

In the United States, European Americans and African Americans are considered to be two distinct races. Whether the term used is African American, Afro-American, black, European, white, or one of any number of other names, people classify and are classified by their race every day. But what does this classification mean? Is it purely cultural, purely biological, or a combination of both factors? While a brief history of the meaning of races is presented in Chapter two, the following section of this chapter explains the definition of race used and the relevance of the concept to the present study.

A definition of race

Crews and Bindon (1991) suggest that any reasonable definition of ethnicity (and, by extrapolation, race) is acceptable, as long as it is clearly stated within the pertinent body of research. So, with suggestions from many people, I have developed a working definition.

Race is a natural and objective taxonomic unit based on the patterned variability observable among populations within a species. This variability intergrades among populations, and is potentially ephemeral. Race is a useful taxon as long as the subpopulations they represent can be discriminated at a rate higher than that predictable by chance alone. What this means is that, for example, three races exist if individuals can be attributed to their correct respective group with more than a 33% success rate. No reproductive isolation nor unique patterns of trait variability is included in this definition.

Natural classifications are those in which members of the taxa are recognizable by characteristics other than the ones on which the classification is based. Objective

classifications are those that are based on some compelling justification, external to nature, such as phylogeny. Different rational people working independently should be able to agree that an objective classification is the right way to classify the populations being studied (Ridley, 1991).

The taxon "race" is a construct of the human mind, as are all taxa. Corcos (1997, p. 12) states, "Species are real units in nature". He asserts that species are natural groupings of organisms, as opposed to races, which are artificial groupings with definitions that change through time. Species are commonly defined as a group of organisms that can interbreed to produce fertile offspring, and who are reproductively isolated from all other species (Mayr, 1951). While I would agree that it is generally easier to discern species than races, I would argue that taxonomic definitions of species are not always clear-cut (Wilson and Brown, 1952). The human declaration of species-level differences certainly does not affect the mating behavior of the organism being classified. Certainly, too, there has often been debate about an appropriate definition of a species. Race is part of a taxonomic system, a tool for organizing variation in which continuous temporal and spatial variation is divided into discontinuous categories. Classifications are constructs of the human mind. They are intended to reflect nature and are organized in order to address scientific problems. However, it must be recognized that our constructions do not limit natural variation, and there are exceptions to taxonomic rules.

Morphological traits follow a distribution based on the historic pattern of evolutionary forces acting upon them. The patterned anatomical variability of humans, as with other species, is the result of evolutionary forces acting in differing local

environments. Many characteristics show clinal distributions, gradual frequency change across geographic areas. This likely reflects selection to a gradual change in environment over a region. Alternatively, it may reflect gene flow, which tends to be gradually reduced over geographic space and/or limited by geographic barriers, such as mountains or oceans (Futuyma, 1986). There is no reason to expect that the clines for various traits should follow similar distributions, as different traits may be subject to different selective forces and may be affected differently by gene flow and random factors.

In considering patterns of variation seen in humans and other sexually reproducing animals, gene flow can be especially important (Futuyma, 1986). These patterns are observable at the subspecies level, which means that interbreeding is possible between individuals best described by different patterns. The patterns, and therefore the races, are ephemeral, and subject to change with each generation.

Innumerable articles have been written by authors seeking to define and delineate human variation in terms of race. Every author has a particular opinion about how this can best be accomplished, and many have their own agenda to pursue. Some authors, completely dismiss the idea that races exist (Corcos, 1997; Smedley, 1993). Some authors state that it is oversimplification to say that there is no such thing as race. Of course there is race, they say, but it is a purely social concept (Brace, 1964; Keita and Kittles, 1997; Paredes, 1997). Other authors describe something that is basically the same as race, but has a different name, such as "ethnic group" (Montagu, 1964a) or "polythetic sets of polytypic traits" (Clark, 1997). There are still other authors who say that biological races do exist, are definable, and can be useful tools for understanding human variation (Brues, 1977; LaVeist, 1996; Gill, 1998). Many include statements

about allele frequency variation and geographic separation. One of the more useful of the definitions provided by these authors is by Brues (1977, p. 1-2), "A division of a species which differs from other divisions by the frequency with which certain hereditary traits appear among its members," but even this definition is not very helpful in practice. How many traits must be different, and at how different a frequency? What kinds of traits are useful for describing a race? The definition is intentionally vague, to allow for as many different possible interpretations as needed.

Brues' (1977) definition can be a good beginning to the description of human variation in terms of race, but it is so vague that it leaves the reader wondering what the utility of such an ambiguous classification might be. Race can be useful concept for describing human variation if the definition the author is using is clearly explained and at least somewhat specific. Like Brues' (1977) writing, it should be clear in an author's work that he or she does not think of race in terms of typology or with any permanence. However, to aid in comparison with other researcher's work, it should also be clear how their definition relates to the research they are doing, and to the research of others.

Research-specific definitions are of limited utility. The most effective definition of race would be one that was universally accepted. In discussing the term "ethnicity, " Crews and Bindon (1991) state that any definition is acceptable, as long as it is plainly described in the text of a report of research results. Authors certainly should explain what they mean by terms such as "race" or "ethnicity. " But if many authors have unique definitions, the comparability of the results of their research is undermined. The best possible scenario is one in which a single, universal description of race can be agreed upon. This would not only improve comparisons among researchers; it might also lower

the level of acrimony associated with the topic. Often it seems that people who argue about the concept of race actually have very different concepts in mind. The definition developed and used for this project and described earlier is one that could be applied universally. Of course, after the extended history of disagreement about race and its applicability, there is no reason to think that this dissertation will bring about a new détente.

The utility of race as a descriptor for human variation

When is race useful? Despite historical errors of application that have served to support racism, there are several uses for a biological definition of race. Authors such as Brace (1964) would have us study biological variation variable by variable without recognition of patterning of characteristics. Such analysis adds little to the understanding of human variation overall, and ignores the possibility that suites of phenotypic variables may have adaptive significance together (Howells, 1973a). Without perception and description of patterns, human variation is unintelligible chaos.

Cooper (1984, p. 719) states, "All humans, in terms of their susceptibility to all but the rarest diseases, are genetically similar." I disagree with this statement, and offer malaria, salt-sensitive hypertension, phenyketonuria, breast cancer and cirrhosis of the liver as examples of diseases whose epidemiological patterning in part reflects patterns of human genetic variation (Reed, 1969). According to epidemiological researchers, African Americans are more susceptible to several diseases than West Africans or

European Americans, including some cancers, heart disease, stroke, and diabetes (Braithwaite and Taylor, 1992). Because of this variation in vulnerability to disease, the racial background of subjects, when clearly defined, can be an important part of medial research (Kiple, 1987; LaVeist, 1996). Unfortunately, while race is often used as a variable in epidemiological studies, it is rarely considered separately from other factors such as ethnicity and socioeconomic indicators and almost never defined (Herman, 1996). A better understanding of patterns of human variation and the evolutionary history and significance of those patterns could aid in predicting health risks and treatment outcomes.

When is race not useful? There are strict limits on the useful application of racial taxonomy. Race is not useful in describing all the members of a population equally. Except monozygotic siblings, no two individuals are genetically the same. It is not especially useful to spend time dividing the world's population into a specified number of races, following Coon, Garn and Birdsell (1950) and many others. More than 50 years ago, Ernst Mayr wrote, "Instead of expending energy on the describing and naming of trifling subspecies, …taxonomists might well devote more attention to the evaluation of trends in variation" (Mayr, 1951, quoted in Wilson and Brown, 1952). While Mayr was writing about the taxonomy of birds, the same could certainly be said for human classification. It is difficult to imagine a time when a researcher will be able to describe the totality of human variation without making sweeping generalizations. For now, a more general description of observed variation seems more fitting. The typological ideas of the anthropological past (often still present in the general population) are not in accordance with a modern understanding of evolution, genetics, and human variation.

The patterned variability seen in racial groups has been used as an excuse for social injustices. The word discriminate can have two meanings: to tell the difference between things, and to judge unfairly, based on the differences between things (Bennett, 1976). The social aspects of race are value-oriented, and based on the incorrect assumption that most or all behavioral traits are inherited simply. It is true that cultural traits are sometimes correlated with physical characteristics. This correlation does not imply causation. It is instead often the result of local cultural developments and assortative mating based on ethnicity (Brues, 1977). The biological concept of race should not have any bearing on social interactions or opportunities. When used appropriately, the application of race is purely taxonomic, and should clarify and simplify the understanding of human variation.

Research Design

Theoretical considerations

The results of the present study are interpreted under the assumption that dental traits are phenotypic characteristics that reflect genetic differences (Nichol, 1989; Scott and Turner, 1985). Differences in trait frequencies between samples are presumed to represent allele frequency variation between the populations. Evolutionary theory is used as the basis for conclusions regarding the manner in which gene flow changes a population's gene pool, which in turn is exhibited in a changed average phenotype. The assumption is made that variation in dental morphology reflects genetically influenced

variation (Scott and Turner, 1997). Several studies of heritability of dental traits support this assumption (Mizoguchi, 1977; Nichol, 1989; Townsend and Brown, 1978).

The framework of political economy (Roseberry, 1988) is used as a guide for the analysis of the social conditions that directed the historical patterns of gene flow that have occurred between European Americans and African Americans. Political economy is a way of interpreting cultural phenomena within the context of local, regional, and worldwide economic and cultural systems (Lewellen, 1992). The admixture that created African Americans existed because of political and economic power and inequality. My intent is to elucidate the microevolution of the African American population by addressing the social forces, both national and local, that shaped gene flow. Which populations had power over other populations is a matter of cultural historical particulars. As these conditions were not related to adaptations to the environment, the development of African Americans as a genetically distinguishable group was guided at least as much by these particulars of culture and history, agents of genetic drift, as by any forces of natural selection.

Measures of biological distance

Biological distance is the difference in mean trait expression between at least two samples (Howells, 1973b). The concept behind statistical measures of distance is that samples are composed of individuals who are in general more similar to each other than they are to individuals in other samples (Sokal and Rolf, 1981). By quantifying the average dissimilarity between individuals, a measure can be made of the difference

between the samples. A number given to reflect the distance between two groups has little meaning in and of itself, but is instead useful for comparing the relative distance between three or more groups (Everitt and Dunn, 1991). For example, a distance of 0.35 between groups A and B means nothing, unless it is known that the distance between groups A and C is 0.75. It can then be said that group A is more similar to group B than it is to group C. The intent is to generalize this quantification of distance between samples to the populations from which the samples were drawn.

The first methods developed for studying biological distance were ones that utilized continuous variables, such as cranial measurements. This should come as no surprise, as this kind of data was among the first to be systematically recorded by physical anthropologists (Blumenbach, 1865; Morton, 1839). In the recent past, however, most estimates of biological distance between samples have been based on discrete, or qualitative, traits, such as simple genetic markers (Relethford and Lees, 1982). These traits are useful for studying population variation, partly because there is no question of their applicability as markers of genetic variation. For example, if one's phenotype for the ABO blood group is O, the genotype being reflected is almost always $I^O I^O$ (Molnar, 2002). The sources of error in the knowledge of the genotype are those from typing or recording the data, or from rare genetic interactions, not from an inaccurate reflection of the genotype in the phenotype (Relethford and Lees, 1982).

The same cannot be said for traits with continuous or threshold phenotypic expression, such as characteristics of dental morphology. Most often the mode of inheritance and the heritability of these traits are not known, although studies to date support the contention that some portion of the expression of dental traits is heritable

(Corruccini et al., 1986; Hanihara, 1975; Harris, 1977; Lasker and Lee, 1957; Mizoguchi, 1977, 1985; Nichol, 1989; Townsend and Brown, 1978). There are difficulties in applying analyses of quantitative traits to questions of population relationships. Without knowing how accurately the phenotype being observed actually reflects the genotype, a researcher cannot know how accurately his or her analysis reflects the true genetic relationships of the groups under study. Most studies that rely on quantitative traits assume there are equal and additive effects of multiple genes in addition to environmental influence (Relethford and Lees, 1982).

The complexity of continuous traits is not a reason to avoid them. To the contrary, Chakraborty (1990) suggests that it may, in fact, be helpful in estimating population parameters such as biological distance. He states that an assessment based on a quantitative trait may be more accurate than one based on several discrete traits, due to the large chance of error inherent in their estimation.

An important question is whether biological distance analyses of discrete and continuous traits are really measuring the same thing. As stated by Chakraborty (1990, p.149),

> ... it is now universally accepted that the inheritance of quantitative differences depends on genes that are subject to the same laws of transmission and have the same general properties as the genes whose transmission and properties are exhibited in qualitative or classificatory differences.

When based on selectively neutral traits, biological distance is really a measure of the relative effects of genetic drift, which tends to make populations more different than each other, and gene flow, which tends to reduce the differences between groups

(Relethford and Lees, 1982). Some analyses (*i.e.*, Howells, 1973a; Morton and Lalouel, 1973) have found that discrete and continuous variables respond to drift and flow in similar manners (Relethford and Lees, 1982). Other reports disagree, stating that any particular quantitative trait will respond more slowly to both drift and flow. The assertion makes sense for the case of drift, because random changes to alleles at the multiple loci at affect phenotypic expression may be neutral and/or cancel each other out. However, it seems that there is little explanation for the supposed slowness of the effects of gene flow (Relethford and Lees, 1982). It is important to remember that some phenotypic traits have a large environmental component in their expression, so are likely to change quickly as the environment changes, even in the absence of genetic drift or gene flow (Cavalli-Sforza and Bodmer, 1971).

In addition to genetic drift and flow, natural selection may also make a contribution to biological distance between populations. The effects of selection are greatest when considering characteristics that make an important contribution to fitness, and when comparing groups that live in environments that have different selective pressures with respect to the characteristics under examination. Changes due to selection can be especially important when comparing changes in the genetic make-up of populations over time. Fortunately for the current study, characteristics of dental morphology have been shown to make very little, if any, contribution to individual fitness (Scott and Turner, 1997).

There is a large selection available to choose from when deciding which biological distance statistic to use in analyzing a particular data set. In general, the results of all the methods are similar to each other, and are highly correlated (Scott and

Turner, 1997). However, care should be taken to apply the method that most closely fits the data being analyzed, so as to introduce as few sources of error as possible. For the current analysis, both the mean measure of divergence (Greene and Suchey, 1976) and a pseudo-Mahalanobis' D^2 (Konigsberg, 1990) will be used to measure biological distances among the study samples. These statistics are described in Chapter four.

Forensic applications

Lasker and Lee (1957) authored the one of the first surveys in English of the use of dental characteristics to determine ancestry in a forensic setting. They noted that shovel-shaped incisors are most common in "Mongoloids" (persons of Asian descent), and that Carabelli's trait is most common in "Whites" (persons of European descent).[2] They did not identify any traits that were more common in persons of African ancestry. Shovel-shaped incisors and Carabelli's trait remain the most common, if not the only, dental traits used in forensic analyses (Burns, 1999; Krogman and Iscan, 1986).

Whether or not one feels that race is a useful construct in anthropology is beside the point when developing an individual's biological profile for law enforcement officials. These profiles are based on characteristics of the skeleton and teeth that correlate with geographical ancestry. In his 1992 paper entitled "Forensic anthropology and the concept of race: If races don't exist why are forensic anthropologists so good at identifying them?" Norman Sauer states:

[2] More recent analyses have brought this into question. See the discussion of Carabelli's trait in Chapter two.

> ... the successful assignment of race to a skeletal specimen is not a vindication of the race concept, but rather a prediction that an individual, while alive, was assigned to a particular socially constructed 'racial' category. A specimen may display features that point to African ancestry. In this country that person is likely to have been labeled Black regardless of whether or not such a race actually exists in nature. (Sauer, 1992: Abstract)

I would argue that it does not matter if "such a race actually exists in nature" since biological races are constantly in flux and are never clearly delineated. In the case of the United States, biological race co-varies with social race categories. It is the socially defined category that is real and on what we should be basing our research.

Toward this end, the data analyzed for the current research have been compiled to create tables that can be used in forensic applications. The traits that have the most different frequencies in the samples of modern African American and European Americans have been analyzed through logistic regression and Bayesian probability analysis to determine the probability of their co-occurrence in the general populations of these two groups. These probabilities have then been organized in tables according to the presence and absence of these traits. This kind of table will allow researchers to compare a dentition from a single individual of unknown origin to a large databank of trait observations quickly and easily. These probability tables are a new presentation of traits used for determination of racial affiliation. Generally, traits that are considered markers of race are simply listed, without mathematical information about the probability of their being seen in a single individual of any particular race (Burns, 1999; Gill and Rhine, 1990; Krogman and Iscan, 1986).

Predictions

At the onset of this project, several predictions were made concerning the results of the analysis. Inherent in the hypothesis is the prediction that, over time, more European admixture will be evident among African Americans. In other words, African Americans in the late time period, those born between 1920 and 1960, will have more in common with European Americans than do those in earlier groups (Davis, 1991; Williamson, 1980).

It is also predicted that this admixture did not occur at a constant rate. Social and historical trends and events affect patterns of gene flow among human beings. Because of changes on the part of the European American community in the perception of relations between the races, it is likely that much more admixture occurred during the period of slavery in America than occurred in the 100 years afterwards (Davis, 1991; Williamason, 1980). This decrease in the rate of admixture should be reflected as a greater amount of difference in average dental morphology between African Americans born between 1825 and 1910 versus those born between the years of 1650 and 1850, than in African Americans born between 1920 and 1960 versus those born between the years of 1825 and 1910.

In a similar vein, it is predicted that African Americans in northern samples will have more European admixture than those in southern samples, and that those in urban samples will be more admixed than those in rural samples. These predictions are based on historical indications that lighter-skinned African Americans, presumably people with

more European ancestry (and concomitant dental morphology), moved to the north and to cities in greater proportion than those with darker skin (Davis, 1991; Williamson, 1980).

A specific prediction deals with the Gullah, African Americans who live on the Outer Banks Islands of South Carolina and Georgia. While the sample of Gullah included in this study is from the late time period, it is predicted that they will show little European admixture, and be much like the West African sample. This prediction is derived from previous linguistic, cultural, anthropometric, and genetic studies that indicate a low level of admixture in the Gullah (Pollitzer, 1999; Rogers, 2000).

Finally, it is predicted that several characteristics of dental morphology will be identified that will be of utility when investigating ancestry in forensic and historical archaeological contexts. Of course, these traits will only be applicable to determining whether an individual would have been considered African American or European American.

CHAPTER 2

BACKGROUND

This chapter is divided into three sections. The first is a discussion of dental anthropology, focusing on the techniques and applications of the study of dental morphology. The broad geographical patterns of human variation described by previous researchers are discussed to the extent that they are relevant. The next section describes the evolutionary forces acting on patterns of human variation: mutation, natural selection, gene flow, and genetic drift. Last, there is a description of the biosocial history of African Americans, as it relates to their genetic make-up. This section is a review of the historical forces that defined who belongs to the socially defined group "African American". These forces determined whether sexual contact between individuals of different social groups was socially acceptable at various times in history, as well as who had opportunities for economic and social advancement in various regions of the nation. In addition, the methods of admixture studies and their findings for African Americans are described.

Dental anthropology

Dental anthropology is the study of humans and their nonhuman primate relatives from the evidence provided by their teeth (Hillson, 1996). Four basic characteristics of teeth are studied by dental anthropology: pathology, size, shape, and tooth morphology. Studies concerning dental pathology often focus on dental disease as an indicator of general health of a people (Brothwell, 1963; Hillson, 1979). The wear on teeth can be studied to learn about diet and tool use (Larsen, 1985; McKee and Molnar, 1988). Metric analyses can be used to study intrapopulation variation, interpopulation relationships, evolutionary changes, sexual dimorphism, and several other applications (Calcagno, 1989; Frayer, 1978). Like the present study, dental morphological studies generally focus on population variation, interpopulation relationships, and microevolution (Hanihara, 1967; Haeussler and Turner, 1992; Irish and Turner, 1990; Sofaer et al., 1972).

There are many advantages to using teeth in biological anthropological studies. Teeth are the hardest component of the skeletal system, and are the most likely part to be preserved in most taphonomic situations (Larsen and Kelley, 1991). Dental development and form are, in part, under genetic control, and are less affected by environmental factors than many other tissue systems (Larsen and Kelley, 1991; Scott and Turner, 1997). Also, information gathered from teeth can be compared equivalently across space and time, a benefit very difficult to replicate using DNA or blood groups studies (Scott and Turner, 1997; Irish, 1993).

Dental morphology studies

The study of dental morphology involves close observation of characteristics of tooth crowns and roots (Irish, 1993). The present study analyzes data from observations of morphological characteristics found on the crown surfaces of sample dentitions. Studies of dental morphology date to the first half of the 20th century, and include analysis of well-known traits such as shovel shaped incisors and Carabelli's trait, as well as many lesser known traits (Campbell, 1925; Weidenreich, 1937). Standardization of traits and techniques has continued to the present day, spearheaded by projects by Albert. A. Dahlberg and Christy. G. Turner II (Scott and Turner, 1985; Turner et al., 1991).

The inheritance of dental morphological traits

It is generally accepted that characteristics of dental crown morphology are under some genetic control (Hillson, 1996; Moorrees, 1962; Scott and Turner, 1997). In fact, much of the field of dental anthropology is based on this assumption. Despite this, little is actually known about the mode of inheritance or the heritability of dental crown traits. Historically, there have been two major trends of thought concerning this issue. Dental traits were first thought to be inherited in a simple, Mendelian way. Later research has indicated a quasicontinuous distribution of dental trait expression. This would indicate that these traits are inherited in a polygenic, threshold manner and are subject to a variety of genetic and environmental influences (Harris, 1977; Scott, 1973; Sofaer, 1970).

Today, most dental traits are viewed as quasicontinuous, or threshold, characteristics (Scott and Turner, 1997). Threshold traits are expressed in a discontinuous manner, but a continuous polygenic inheritance underlies that expression.

For a trait to be expressed, alleles for the trait must be present at a minimum number of loci (Falconer, 1981). Above that base number, the trait may show varied expression based on the number of alleles present at additional loci. Threshold traits can be discerned from traits with simple inheritance by two criteria (Grüneberg, 1952):

1) A positive correlation between incidence of a trait in a population and level of expression. Assuming a normal curve of expressivity, the more individuals that have a trait, the more that will show the trait at a high level. The dental traits of shoveling, maxillary canine tuberculum dentale, and Carabelli's trait have been shown to follow this pattern (Scott, 1973).

2) Frequency and expression of the trait will show environmental effects. Asymmetry in dental trait expression may indicate this (Scott and Turner, 1997).

To utilize data from continuous trait observations, an understanding of the concept of heritability (h^2) is helpful. Heritability is the proportion of phenotypic variance in a population that is attributable to genetic variation. It can be defined in broad (Hb^2) and narrow (Hn^2) senses. In the broad sense:

$$V_p = V_g + V_e, \quad Hb^2 = V_g / V_p$$

where V_p is the phenotypic variance, V_g is the variance due to differences in genotype, and V_e is the variance due to environmental influences (Crow, 1986).

In the narrow sense, the genetic variance is broken into its component parts, variance due to the additive effects of alleles (V_a), dominance effects (V_d), and epistasis, the interaction between genes (V_i). As an equation:

$$V_p = V_a + V_d + V_i + V_e, \qquad Hn^2 = V_a / V_p.$$

Heritability in the narrow sense is the equivalent of breeding value to developers of plant and animal commodities. It is a quantitative representation of the extent to which offspring resemble their parents, relative to the population mean. "Only the phenotypic values of individuals can be directly measured, but it is the breeding value that determines their influence on the next generation" (Falconer, 1981, p. 148).

Estimates of heritability are population, time, and environment specific (Crow, 1986). Heritability is only one of the components of phenotypic variance, so its value is dependent on all the other sources of variability. Population size and time effect heritability, because small populations, especially those that have been small for a long time, are more likely to have lower variation in genetic make-up (Falconer, 1981).

Heritability influences the degree of resemblance between relatives (Falconer, 1981). Members of a population of a species, on the average, are more related to each other than they are to members of other populations of the same species. Traits that reflect this greater degree of relationship, those that most accurately reflect the gene pool, are the ones that are best for studying the relationships between populations.

Crow (1986) describes a paradox in the fact that selection is always leading to homozygosity within a gene pool, yet quantitative traits are almost always highly variable. The author explains the apparent contradiction with the quadratic optimum

model, which assumes that fitness declines in proportion to the squared deviation from optimum phenotype. Environmental variability is inversely proportional to heritability, because fewer genetic forms are fit in many different kinds of environments (Falconer, 1981). If a wide range of phenotypes are all approximately equally optimal, deviations from average phenotype would have to be very large for fitness to decline.

What is the heritability of characteristics of dental morphology? Estimates vary according to which trait is being studied and from which population and time the sample being studied is drawn. For Carabelli's trait (described below) alone, estimates of heritability vary from 0.250 to 0.909 (Aoyagi, 1967; Skrinjaric et al., 1985). Mizoguchi (1977) estimated heritability of 14 dental characteristics, ranging from 0.47 to 0.95, and averaging 0.50, in a Japanese sample. Analyzing a sample of "American Whites" Scott and Potter (1984) found that heritability of seven dental characteristics ranged from 0.19 to 0.40, averaging 0.34. All of these estimates come from the study of trait expression in monozygotic and dizygotic twins, a method that some researchers have called into question (Christian et al., 1975; Corruccini et al., 1986; Kang et al. 1977). While exactly what portion of the expression of a dental characteristic is heritable cannot be known at this time, there is general agreement that some portion of that expression is determined by allelic variation. The present study relies on that determination, and the results reported here reflect the biological relationships among the samples under study to the degree that the dental traits observed reflect genetic variation.

Carabelli's trait and shovel-shaped incisors

Descriptions of studies of a few characteristics can provide a picture of the degree of knowledge and understanding about dental traits, their variation, and their mode of inheritance. Carabelli's trait, apparently first described in 1842 by von Carabelli (von Carabelli, 1842) may be the most studied of all dental morphological variables. The trait consists of a pit, Y-shaped fissure, bump, or cusp on the mesiolingual (tongue) side of the maxillary deciduous posterior premolars and permanent molars. It has been studied in many worldwide populations, past and present, including Australopithecines (Schwartz et al., 1998; Hawkey and Turner, 1998). In a recent survey, Correia and Pina (2002) surveyed 23 published reports of frequencies of first molar Carabelli's trait in populations ranging from Alaskan natives to Bantu speakers to American soldiers. They reported frequencies ranging from 13.5% (Portuguese) up to 85% (American Whites).

Several studies suggest a one gene, two allele mode of inheritance for this trait, and it is listed in Mendelian Inheritance in Man as a possibly following such a pattern (McKusick, 1994). However, the range of expression seen in this trait, from a pit to a large cusp (Turner et al., 1991), indicated that a one-gene, two-allele system cannot account for all variation. Partial penetrance has been proposed as an explanatory factor, as has the possibility that the trait actually includes more than one morphological phenomenon (Hillson, 1996). Many studies are now available that indicate a more complex mode of inheritance for this trait (Goose and Lee, 1971; Skrinjaric et al., 1985) as well as several other traits (Nichol, 1989; Tsai et al., 1996).

Shovel-shaped incisors are those with ridges on the mesial and distal margins of the lingual surfaces. Studies of shovel shaping date back to 1920, when Aleš Hrdlička

described the characteristic in the collections at the National Museum of Natural History, which represent populations worldwide (Hrdlička, 1920; Scott and Turner, 1997). Shoveling has usually been studied as a qualitative variable, but some researchers have studied it as a quantifiable metric trait by measuring the depth of the shoveling from the center of the lingual surface (Hanihara et al., 1975).

As a qualitative variable, frequencies of shovel shaped incisors range from 0.0% up to 91.9% in samples from a wide range of geographic areas (Scott and Turner, 1997). Western Eurasia, Africa, and Sahul-Pacific groups have the lowest frequencies, while the highest frequencies and greatest expression are generally found in Eastern Asian, Northern Asian, and Native American samples (Scott and Turner, 1997). In North America, the presence of shoveling is commonly used in making the determination that a skeleton is Native American. In the United States the treatment of the remains may therefore be subject to federal jurisdiction under the Native American Graves Protection and Repatriation Act (Myra Geisen, personal communication, 2002).

As with Carabelli's trait and all dental morphological characteristics, the mode of inheritance for shovel shaped incisors is unknown. Portin and Alvesalo (1974) analyzed the frequency of the trait in siblings and found that single and multiple locus inheritance were equally viable alternative hypotheses. Shoveling is one of the few morphological traits for which an adaptive significance has been considered. Its added mass and "I-beam" construction (Dahlberg, 1963; Scott and Turner, 1997) might add strength and stability when biting with the anterior teeth (Mizoguchi, 1985).

Geographical dental patterns

Scott and Turner (1997) present an immense database of dental observations and provide characterizations based on 16 crown and six root traits. The data come from the authors' own research as well as data gathered by many other researchers. The authors group humankind into five major geographical groups: Western Eurasia, Sub-Saharan Africa, Sino-American, Sunda-Pacific, and Sahul-Pacific. The specificity of the groups reflects to some degree the amount of research done in each part of the world. The Sino-American, Sunda-Pacific, and Sahul-Pacific groups are not relevant to the present research, and so are not described here. "Western Eurasia" combines Europe, North Africa, the Middle East, and the Indian subcontinent. The "Sub-Saharan Africa" description represents all aboriginal populations in Africa, south of the Sahara. The characterizations presented here are taken from Scott and Turner (1997).

Scott and Turner (1997) do not differentiate a regional description specific to Europe. Instead, they cluster their European samples with observations on groups from Western Eurasia and North Africa. They justify this grouping on linguistic, historical, and archaeological grounds. According to Scott and Turner (1997), the Western Eurasian dental pattern (not yet fully described enough to be considered a "complex") is one marked by the absence and/or scarcity of traits, rather than any wide variety of trait expression. Overall, the dentition could be characterized as simplified. Only two traits are present at rates higher than is seen in other regional populations: four-cusped mandibular first and second molars, and two-rooted mandibular canines. Carabelli's trait, long considered the hallmark of the European dentition, is also seen at high frequencies, but not higher than all other groups around the world. More than half of the 22 traits

discussed are seen at low frequencies in Western Eurasia: mesial canine ridge, winging, shoveling, double shoveling, odontomes, enamel extensions, deflecting wrinkle, mandibular molar cusps five, six, and seven, Tomes' root (Tomes, 1889), and three-rooted mandibular first molar (Cusp numbering here follows Hillson, 1996).

According to Scott and Turner (1997), the sub-Saharan African dental complex is characterized by the maintenance of the usual major cusps and the presence of the standard number of roots that generally are described for the human dentition. Crown traits that are especially high in sub-Saharan African samples are mesial canine ridge (Bushman canine), mandibular molar cusp seven, and Y-groove pattern on the mandibular second molar. These characteristics are considered distinctive of sub-Saharan African teeth (Irish, 1997). Many of the traits that are seen in low levels are the same as in Western Eurasia: winging, shoveling, double shoveling, odontomes, enamel extensions, and three-rooted mandibular first molars. In addition to these traits, three-cusped maxillary second molars, four-cusped mandibular first and second molars, interruption grooves, one-rooted mandibular second molars, and two rooted mandibular canines are also seen at low frequencies. Four-cusped lower first and second molars, three-cusped upper second molars, and lower canines with two roots are seen in high frequencies in Western Eurasia, and low frequencies in sub-Saharan Africa. Cusp seven, mesial canine ridge, and Tomes' root are seen in high frequencies in sub-Saharan Africa and in low frequencies in Western Eurasia (Irish, 1997; Scott and Turner, 1997).

The question of the relationship between Western Eurasians and sub-Saharans remains. The simplest and most accurate statement that can be made from the data available now is that these two regions are separable based on the frequencies of their

dental characteristics. While they may not be the most different groups in the world, they are different enough to make interpopulation comparisons a viable area of study.

The comparison of several traits can be used to examine the relationships between regional divisions of humans (Scott and Turner 1997). How closely Western Eurasians and sub-Saharans cluster, compared with populations from other regions, is influenced by the method used for analysis. By varying the clustering algorithm, ordination procedure, distance statistic, number of coordinates, and graphic display method, there are numerous methods that can be used for looking at population relationships. Which results are presented can depend on the intent of the author. For example, based on earlier research by Turner (1992), Scott and Turner (1997) present several phenetic trees indicating a relationship between sub-Saharan Africans and South East Asians that is closer than either has with any other regional population. This could be used to support the theory of a recent divergence between these two groups. Stringer et al. (1997), however, reports a cladistic analysis that would refute such a theory. The analysis includes nearly the same data as Scott and Turner (1997), but adds a sample of dentitions from the Krapina neanderthals as an outgroup. The results indicate 17,439 trees more parsimonious than the one suggested by Turner (1992).

Cladistic studies such as the two described above are limited by their inherent assumptions. Taxa analyzed through cladistics are supposed to include all the descendants of a single ancestor. The groups are assumed to be separate species, unable to interbreed (Hennig, 1979). As humans are a single species, able to interbreed, it would be impossible to say that the subspecies groups of humans being compared do not share a common ancestor. Also, cladistic analyses are based on shared, derived, homologous

traits, those that are shared between groups but derived when compared to other groups. This assumes that it is possible to tell which traits are homologous and therefore shared due to common descent and which are homoplastic and therefore shared due to convergent evolution (Wiley, 1981). Dollo's law, that complex structures, once lost, cannot redevelop, may make this a reasonable assumption when studying relationships between groups at higher taxonomic levels (Futuyma, 1986). However, for analyses such as Scott and Turner's (1997) and Stringer et al. (1997) that study relationships at low taxonomic levels, the application of the techniques of cladistic analysis may not be appropriate.

Why are there races?

Some interpopulational variation is the result of selection, change in the frequencies of some in populations due to differential reproductive success of individuals (Futuyma, 1986). Traits that most directly affect survivability and reproductive success are those most likely to be affected by selection. The most obvious (and probably most oft cited) example of this is clinal variation in skin color, reflecting proximity to the equator. Body proportions, facial features, and differences in frequencies of some blood group alleles, such as the sickle-cell allele and Duffy null allele, may also be examples of racial variation due to selection (Molnar, 2002). Selection produces lower trait expression variability within subpopulations. Greater variability is produced between populations for traits that are under different selection pressures in differing

environments. Variation between geographic populations will decrease in traits that are under selective pressure in a similar way across environments (Futuyma, 1986).

Other patterning seen in humans may be due to drift, changes in allele frequencies produced by random factors, such as population sampling error. The results of genetic drift accrue faster in small populations (Futuyma, 1986). Traits that have little bearing on survival or reproductive success are those most likely to be affected by drift. Characteristics of dental crown morphology are examples (Butler, 1982; Scott and Turner, 1997), as are many skeletal markers that have in the past been thought of as "discrete morphological traits". Drift produces reduced variability within populations, and greater variability between populations.

Gene flow, the exchange of alleles between populations, ameliorates diversification. There has always been allelic exchange between all extant groups of humans, as evidenced by the presence of only one worldwide species. Gene flow reduces variation between populations, but can increase intrapopulation variability. The variation in phenotypes seen around the world results from the balance that exists between forces that make geographically or culturally defined groups different, selection and drift, and gene flow, which maintains similarity.

The biosocial history of African Americans

Factors affecting admixture in African Americans

To study the biological history of African Americans, it is helpful to have an understanding of the history that influenced where and when gene flow occurred and to what social group the resulting people were assigned. The history of interbreeding of Africans, European Americans and African Americans in the United States, while brief in evolutionary terms, is nonetheless complex.

Scholars of African American history refer to the admixture of European genes into the African American gene pool as *miscegenation*. The term was coined in an election pamphlet titled "Miscegenation: The Theory of the Blending of the Races, Applied to the American White Man and Negro", published in 1863. The anonymous author explained that the term came from the Latin words *miscere* (to mix) and *genus* (race). The purpose of the pamphlet was to expound the societal benefits of miscegenation. If the races mixed, the best of both groups could be combined, and the problems inherent in a polytypic society would vanish (Kaplan, 1949).

There has always been contact between European and African populations (Rogers, 1970). The genetic exchange germane to the present study began in the seventeenth century with the advent of the African slave trade to North America (UNESCO, 1978). Anti-miscegenation laws are listed in colonial codes as early as the seventeenth century (Davis, 1991). However, census records show that the number of recognizably admixed people grew over time (Williamson, 1980). In 1850, the census

reported that 11.2% of the African American population was *mulatto*, meaning of mixed ancestry. By 1860, that number had increased to 13.2%. The determination of race was made by visual inspection of the census-taker, presumably based on skin pigmentation (David et al., 1976). It is interesting to note that while a note was made of the percentage of people of mixed ancestry, those people were counted as a sub-set of African Americans, not as a separate group.

Because of the continuous history of admixture, the answer to the question "Who is Black?" is one that has been constantly redefined. In recent history, this question has been answered with the "one drop" rule, meaning that one drop of African blood makes a person Black. The rule harkens back to a time prior to the genetic theory of heredity, when researchers thought characteristics were transmitted between generations through the blood (Klug and Cummings, 1991). Anthropologists refer to this rule as *hypodescent*, meaning that the hybrid of two groups with different social status will be ascribed to the group with the lower status (Davis, 1991). In some locales the "one drop" rule gained an early foothold. In other places, however, laws were on the books, sometimes until the 20th century, which defined a Black person as one with 1/4th, 1/8th, or even 1/16th Black ancestry. The use of terms such as *octoroon* and *quadroon* demonstrate that either Black or not Black was not always the case (Williamson, 1980).

The South can be divided into two portions. The Upper South got an early influx of slaves due to rice agriculture and was the first to settle on a biracial society. The Lower South, the area south of North Carolina, developed more slowly as a slavery-supported society, and did not abandon a graduated race system until the decades before the Civil War (Davis, 1991).

As the entire South accepted the "one drop" rule in society and later in law, Mulattoes and people of relatively unmixed African blood joined together in social struggle. Before the Civil War, a higher percentage of Mulattoes were free than of unmixed people (Williamson, 1980). These free Mulattoes often used their higher social standing to help slaves and former slaves after the Civil War. In other cases, Mulattoes saw the War as the end to a lifestyle to which they had become accustomed. Many of these people left the South, often heading west. After the War, African Americans of visibly mixed heritage were more likely than others to migrate from rural areas to urban center, and from the South to the North as part of the Great Migration (Davis, 1991; Williamson, 1980).

The years leading up to and including the Civil War, the period of reconstruction, and the beginning of Jim Crow laws are marked by a sea change in the relationships between African Americans and European Americans in the South. European Americans in the South envisioned living in a community where former slaves, whom they assumed to be their inferiors, were in a majority (Davis, 2002). While relations were never benign, the perceived threat to the dominant European American community that was posed by a free Black populous caused state governments to enact laws that more and more clearly delineated who was Black, who was White, and what behavior between the groups were legal (Davis, 1991; Davis, 2002).

The origins of the Jim Crow era can be traced back to the 1850s, but the period of its greatest impact is 1870-1950. The name comes from an African American character of mid-eighteenth century minstrel shows. The era is identified as a *de jure* codification of subordination of African Americans in all aspects of society. Laws were passed that

defined separation of the races in public places, disenfranchised African American men, and forbade interracial marriage (Woodward, 2002). Alabama outlawed relationships between Blacks and Whites that had the appearance of marriage in 1852. When the law was enacted, *Negroes* were defined in a separate section of the code, which identified the class as including "person[s] of mixed blood, descended, on the part of the father or mother, from Negro ancestors, to the third generation inclusive, though one ancestor of each generation may have been a White person" (Novkov, 2002). Eleven other Southern states passed laws against interracial marriage and miscegenation between 1870-1884 (Davis, 2002). *De facto* subordination was also a feature of the era, in the forms of lynching, employment discrimination, and a multitude of other ways. Prior to the Civil War, European American males had been relatively unrestrained by society in their sexual access to African Americans. After the war, however, laws and other social sanctions may have reduced the frequency of sexual relations between the races (Davis, 1991).

Studies of admixture

In order to study variation between populations trait frequencies should be quantified. Workman (1973) states, "... data on gene frequencies in a hybrid population and in the populations from which the hybrid population is known to be derived from can be used to estimate the proportions of the hybrid gene pool contributed by each parental population." There are four basic assumptions in most admixture studies (Reed, 1969):

1) The identities of ancestral populations are known. This assumption is met in the present study by a review of historical documents such as census data and documentation of collections.

2) There has been no change between the gene frequencies of ancestral populations and the modern populations representing them. This assumption relates to the use of genetic assays from blood samples. It is not relevant to the present research, as direct observations were made on representatives of the ancestral populations. This is a major benefit of using dental characteristics for this study.

3) Gene flow is the only factor influencing the genetic composition of the hybrid population. While it is a matter of debate whether dental traits have adaptive value, it is unlikely that their value would be great enough to have a significant selective effect in the period of time with which the current study is concerned.

4) Samples are unbiased and large enough. Samples were chosen from those available to limit as much as possible any bias inherent in the observed samples. Several large and several smaller collections were utilized for this study, in order to obtain a large sample size.

All traits are not equally useful for making comparisons among groups. Ideally, all traits would reflect the same amounts of admixture. Departures from this expectation come from the effects of drift and selection on allele frequencies. There are three things to look for in a trait for interpopulation analysis. First, interpretation will be simplified if

the trait is at relatively homogeneous levels within all three of the groups to be studied, the two parental groups and the hybrid. This helps lower the possibility of sampling error (Mascie-Taylor and Lasker, 1988). Finding traits that meet this requirement may mean looking at many characteristics to find a few appropriate for study. Second, traits that are most useful are those that have very different frequencies between the two parental populations (Reed, 1969). It is much easier to detect admixture in a hybrid if the ancestral populations have frequencies of an allele differing by 95% than by 5%. Third, characteristics should be chosen that are not under selection. One of the assumptions of admixture studies is that gene flow is the only source of change in the hybrid population. (Reed, 1969). This is because a trait under selection will not accurately reflect the proportions of genes coming from each parental population. Currently, there is no evidence that characteristics of dental morphology are subject to strong affects from natural, selection (Scott and Turner, 1997), and the amount of inter- and intra-population variation that observable in these characteristics indicates that many different phenotypes are fit. Studies of admixture also assume that trait frequencies observable in modern samples will precisely reflect the frequencies of the ancestral population at the time it donated alleles (Reed, 1969). If selection on the traits is present, it is unlikely that the modern frequency will be the same as in the past. Of course, traits can be examined that are observable on the remains of the parental population from the time of the admixture, such as dental or skeletal traits. The assumption, and therefore the chance to violate it, can be completely avoided.

The characteristics and samples used for population estimation must accurately reflect the allelic variation donated to the hybrid population. This requires knowledge of

the history of the populations in question. Due to historic population movements, it would not be accurate to make admixture estimates based on traits in modern-day Seminole Indians compared with those in skeletal remains found on the land they now inhabit. Samples from areas specific to the parental populations are better than general ones. It may be that taking samples from "sub-Saharan Africa" is inappropriate, when samples from "the Niger River basin" will more concisely reflect the population of interest. More accurate targeting of samples for analysis may help in locating traits with small intrapopulational variability, as local populations are generally more homogeneous than large, regional ones. It is important that this sampling strategy be equally applied to all the populations being studied. Of course, large samples from small areas may not be available. In this case, studies can be made based on a more general sample, as long as the possible consequences of this strategy are understood.

Studies of blood groups, mitochondrial DNA restriction fragment length polymorphisms (RFLP), and nuclear DNA RFLP's have suggested that sub-Saharan African populations are the most genetically diverse in the world (Irish, 1997). This information has been used to support the contention that Africa is the recent homeland for all human populations (Cann, 1988; Cavalli-Sforza et al., 1993). It may seem that all of this diversity will make admixture estimations impossible when looking at sub-Saharan African and non-African populations. In fact, if care is taken in the choice of characteristics studied and the samples drawn for comparison, estimates of admixture can be made with as much assurance as for any other regional population. For the present study, all but one sample from sub-Saharan Africa was drawn from West Africa, where the majority of the founding population for African Americans originated (UNESCO,

1978). The West African sample analyzed for the current project includes dentitions from Cameroon, Dahomey, Gabon, Liberia, Nigeria, and Senegal. Other dentitions listed by the curating facility as having originated in the "Gold Coast" were also included. These countries and the area known as the Gold Coast, are where the majority of Africans sold as slaves to the New World originated (Rogers, 2000; UNESCO, 1978; Wood, 1984). The remaining sub-Saharan sample, which is from South Africa, was recorded for this study for comparison with the West African samples and is not included in any statistical analyses of the biological affinities of African Americans.

The use of quantitative traits for admixture estimation may present another option for coping with the high variability in DNA observed in sub-Saharan Africa. The variation seen in simple traits does not seem to be indicated in some polygenically inherited traits, such as characters of dental crown morphology. Irish (1993, 1997) used dental morphology to describe the relationships between 28 samples that represent the entire continent of Africa. While the samples from North Africa cluster separately from those of sub-Saharan Africa, samples from both geographic areas group closely among themselves, suggesting great similarity.

One reason that the variation seen in traits such as blood groups may not be reflected on dental traits is their differing contributions to fitness (Irish, 1993; Scott and Turner, 1997). Blood antigens may provide immunity to diseases particular to a specific area with a concomitant specific population. Many different regional diseases would lead to many different alleles. On the other hand, dental crown characteristics have not been found to contribute to fitness (Scott and Turner, 1997), so that drift would be the main cause of variation in trait frequency. They are therefore likely to be much less variable

over a region than blood group alleles would be. Coupling this with their observability in non-living samples makes dental traits, and possibly other quantitative traits, appropriate for population comparisons, such as admixture studies.

A note about DNA

It may seem that DNA studies might better address the issue of admixture. However, there are several advantages of using dental traits as markers of genetic variation. Studying DNA in blood from modern representatives of the parental populations does not account for changes that may have occurred in the populations. Using DNA from historic bones or teeth is destructive, expensive, and cannot feasibly be performed on large samples. DNA analysis may also be limited by legal, curatorial, and community practices. Additionally, data from dental studies can easily be compared later to a particular specimen or sample, allowing interpretation with no expense or destruction.

Estimates of Native American admixture in African Americans

From the advent of the slave trade to the present day, Africans and African Americans have been in contact with Native Americans as well as European Americans. There is evidence that there has been significant introduction of African genes into some Native American tribes (Katz, 1986). The best studied example is of the Seminole, where mitochondrial and Y-chromosomal DNA indicates five percent African admixture (Huoponen et al., 2002). The question germane to the present study is how much Native American admixture is there in African Americans? Early serological studies indicated

little Native American admixture in African Americans (Glass, 1955; Roberts, 1955). More recent studies confirm this indication. Using mitochondrial DNA haplogroups Parra et al. (1998) tested 1,022 African Americans in ten regional samples. They found only two individuals with a haplotype associated with Native American ancestry (B). Chima et al. (2002) examined genotype frequencies of human polyomavirus JC, a harmless virus excreted in urine by 20% to 70% of adults. The genotype of the virus varies among human populations. Of the 78 African Americans tested, two had the strain of the virus associated with Native Americans (2.6%). While there is evidence of Native American admixture in African Americans, more gene flow between the two populations has gone the other way. The remainder of the present study will focus on European American contributions to the African American gene pool.

Estimates of European admixture in African Americans

Admixture estimates for African Americans vary, depending on characteristic studied and sample compositions (Reed, 1969). Usually authors are clear about the composition of the African American sample used. Sometimes they state the region in Africa from which that parental sample is derived. However, they are rarely clear about the composition of the European American sample. This makes it difficult to compare the various studies.

Some studies do address social ideas about race, admixture, and self-identification, but do not address the biological aspects of admixture. Herskovits (1928b) and Meier (1949) estimated admixture using self-reported ancestry. Using data compiled from several surveys, Herkovits (1928b) found that 71% of all African Americans

reported some European admixture. In a more limited survey, Meier (1949) found that 66% of African American students at Tougaloo College, Mississippi reported European ancestry.

Studies of blood group systems have sought to quantify admixture of non-African genes into the African American gene pool. In their estimation of admixture rates, Glass and Li (1953) used an average of the means of estimates of admixture based on the frequency of the Rh^0 allele in two New York City samples (Wiener et al., 1944; Levine, 1945). The frequency of the allele indicated a figure of 31.9% admixture for their computations, resulting in an estimate of 3.58% admixture per generation. Of course, a computation of a rate of admixture assumes the rate is constant over time. One of the predictions of the present study is that the rate of admixture in African Americans has fluctuated due to social and historical conditions.

Studies of the Duffy null allele (Fy^0) have shown it to reach estimated population frequencies of approximately 100% in Central African groups, while it is nearly absent in Western European samples. The Duffy null allele is present in about 70% of African Americans studied (Mourant, 1985). This percentage suggests that approximately 30% of Duffy alleles come from persons of non-Central African ancestry. However studies of the Duffy A allele (Fy^a) suggest admixture percentages between 21 and 26% (Mourant, 1985). Central and West African populations have 0% or next to 0% frequency of the Fy^a allele, while European populations reach frequencies of up to 90% (Reed, 1969).

Reed (1969) presents a table summarizing admixture studies. While the article was written 30 years ago, it still represents a useful digest of the available literature, as admixture estimations have more recently become less popular as a subject of research.

The table presents 13 estimates of admixture. The estimates range from five percent to over 30 percent, and include analyses based on R^0, R^1, R^2, r, M, AK^2, Jk^b, T, S, Gm^1, Gm^5, Fy^a, and Fy^b alleles. Variation in the estimates reflects lower levels of admixture in the southern United States than in the North and West. A mean estimate calculated from the results presented in the table would be 18.0%, which could serve as a reasonable estimate of European admixture in African Americans.

CHAPTER 3

MATERIAL

Anthroposcopic dental characteristics were examined in samples of several ancestral and chronological groups to obtain estimates of trait frequencies. In many cases, observations were made by examining dentitions. However, not all the collections available were of the original teeth. Some collections were of dental casts or photographs, because the people were alive at the time of original data collection, or because the original teeth have been reburied. See Chapter four, Methods, for a comparison of observations made in these media.

Samples were chosen to represent African Americans (AA) and their historical parental populations, namely European Americans (EA), Western Europeans (EU), and Sub-Saharan West Africans (WA). The founding populations are represented to the extent possible by samples from the time periods that the genetic contributions were made. For example, the earliest available African samples were studied to represent the population who contributed to African slave trade, which ended in the first decade of the 19th century (although it was impossible to find a large sample of West Africans that were definitely adults by 1810.) Also, collections of European Americans were chosen that included individuals who were adults by the time of the Civil War, when historians

predict the influx of European genes into the African American gene pool greatly diminished (Davis, 1991).

Sample descriptions are grouped by time period and geographical area, and are listed by the facility housing them. Table 3.1 at the end of this chapter summarizes the number of individuals per collection and group.

Sample descriptions

Early period American samples (born circa 1650-1850 EA n=33, AA n=35)

National Museum of Natural History

This sample includes individuals from several small collections originally analyzed by J. Lawrence Angel. Observations were made on teeth. The dentitions come from the following archaeological investigations (Angel, 1976; Kelley and Angel, 1987):

Calvert Street Baptist Church, Washington, D.C. (AA=7) circa 1807

Catoctin Furnace industrial slaves (AA=12) who died between 1790 and 1820

Clifts Plantation (EA=4, AA=6) who died between 1690 and 1770

Deep River Colonial Cemetery (EA=3, AA=2) who died between 1690 and 1770

Governor's Landing (EA=10, AA=1) who died between 1618 and 1820

Virginia Negroes (AA=7) who died around 1835.

Arizona State University

Observations were made on 16 individuals from a collection of 20 English soldiers from Fort William Henry, in Northern New York state. The men died between

1755-1757 in the French and Indian War (EA=16). The collection consists of teeth and photographs of teeth (Liston and Baker, 1996).

Middle period American samples (born circa 1825-1910 EA n=128, AA n=443)

Ohio State University

This sample comes from Freedman's Cemetery, a cemetery recognized to be the place of interment for African Americans in Dallas, Texas. Burials date from 1867 to 1907; however, the majority (75%) of the burials disinterred date between 1900 and 1907. The sample from which these dentitions was drawn is large: 1157 individuals. Due to its large size and the brief time period it represents, this sample is of particular interest. It can be used to compare with other samples of African Americans to test hypotheses about admixture across time and space. Individual dentitions were included in this study if there were a predominance of permanent teeth, and if the teeth were in a condition that reasonably permitted observation (AA=332). The remains have been reinterred. Observations were made from 5"x7" photographs of the teeth that were taken in a professional laboratory photographic setting with high quality equipment (Condon et al., 1998.)

University of Arkansas

This dental cast collection was made from remains excavated from Cedar Grove Cemetery, a rural African American cemetery in Arkansas. The period of the cemetery's use approximates that of Freedman's cemetery. This collection is of special interest, as it can be used in comparison to the Freedman's Cemetery sample to test the hypothesis that

admixture was lower in rural populations. For analysis, the casts (AA =15) were sent to Ohio State University by the Arkansas Archaeological Survey, the institution of ownership. They have been returned to AAS (Rose and Santeford, 1985.)

University of South Carolina

These materials were sent to Ohio State University for analysis. The materials sent belong to two collections, one of 36 African American slaves from around 1836 and one of 18 African American Union troops from Folly Island, South Carolina. Observations were made on teeth and photographs of teeth (Rathbun, 1987; Legg and Smith, 1989). The materials have been returned to USC (AA =7).

National Museum of Health and Medicine

Several collections of 19th century European American military skeletons are housed at the museum in Washington, D.C. Included in this analysis are five individuals from various battle sites (EA=2, AA=3) who died between 1866 and 1896. Also included is a collection of Civil War soldiers (EA=36, AA=1) who died 1861-1865, and soldiers from the Indian Territory battles who died in the 1870s and 1880s (EA=10.) (Sledzik and Moore-Jansen, 1991.) Observations were made on teeth.

New York State Museum

This museum houses two collections used in this study. The Oneida Poorhouse collection is from the 19th century almshouse in Oneida County New York (EA =21, AA=1). The individuals died between 1880 and 1894. The Wadsworth county

Almshouse sample is from the same time period and was also analyzed (EA =4, AA =2). These individuals died circa 1890-1900 (Phillips, 2001.) Observations were made on teeth.

The Cleveland Museum of Natural History

The Todd collection consists of 3,100 cadaver skeletons from mid-nineteenth century Cleveland, Ohio. Observations were made on 61 European American and 49 African American dentitions. The observations were made on those individuals who were born earliest, yet still had enough teeth to make analysis worthwhile. Their birth years ranged from 1880-1947. Since this collection roughly approximates Freedman's cemetery in time, it can be used in comparison to test the hypothesis that great admixture can be found in African Americans in northern cities than in the South. Observations were made on teeth (Jones-Kern and Latimer, 1996.)

National Museum of Natural History

The Terry collection is also made up of cadavers, but they were collected in late-nineteenth century St. Louis, Missouri (EA =5, AA =4). While the collection is very large, over 4,000 individuals, many of the dentitions are very worn or have been damaged during curation. The individuals observed for this study are amongst the oldest in the collection, and were born around 1860 (Hunt, n.d.)

Late period American samples born circa 1920-1960 (EA n =155, AA n =165)

University of Tennessee, Memphis, Health Science Center

This collection includes 300-400 casts of dentitions from modern European Americans and African Americans. The casts (EA =101, AA =100) were taken in association with orthodontic work being performed at the dental school. Most of the individuals were adolescents or young adults in the last two decades of the 20th century, and the casts are in excellent condition (Edward Harris, personal communication, 2002)

Case Western Reserve University

These casts are part of the large collection of the Bolton-Brush Longitudinal Growth Study. From this collection, observations were made on 54 European Americans born in Cleveland, Ohio the 1920s and 1930s (Behrents and Broadbent, 1984.)

Arizona State University

There is little documentation available for this collection, part of the larger ASU Anthropology dental cast collection. Observations were made on ten casts of modern African Americans from the University of Washington, who were cast as college students in the second half of the 20th century (Diane Hawkey, personal communication, 1999.)

Ohio State University

The dental cast collections at OSU include several hundred dental casts donated to the Anthropology department by Renee Menegaz-Bock. Only a small part of this

collection was analyzed for this project. Dentitions of Gullah people, African Americans from the outer banks of South Carolina, were cast in the 1950s as part of a larger study of their ancestry and biology. This analysis includes observations on the casts of 55 dentitions of people born in the 1920s though 1940s (Menegaz-Bock, 1968).

West African samples (born circa 1800-1900 WA n=184)

The American Museum of Natural History

The Von Luschan collection consists of skulls purchased by a German anatomist from worldwide sources, then sold to the AMNH. From among the West African skulls, 131 dentitions were suitable for analysis, although several allowed only maxillary observations. Individuals identified as being from Cameroon, Dahomey, Gabon, Liberia, Nigeria, and Senegal were included, as well as other individuals without specific national origin, such as those listed as having originated in the "Gold Coast." The individuals were born throughout the 19th century. Observations have been made on the dental morphology of these collections by a previous researcher (Irish, 1993.)

British Museum of Natural History

An African Explorer in Gabon acquired the Du Chaillu skull collection for the Museum around 1864. From this collection, 41 dentitions were in a condition that allowed observation (WA =41) (Bennington and Pearson, 1912).

National Museum of Natural History

These dentitions come not from a single collection, but from West African skulls that were acquired piecemeal by the museum. They are mostly from Gabon and include three from the British Museum's Du Chaillu collection that are on permanent loan to NMNH (WA=13) (Bennington and Pearson, 1912).

South African sample (born circa 1940, SA n=35)

Arizona State University

Observations were made on dental casts of 35 modern Bantu-speaking people cast in the late 1960s by Donald H. Morris. The individuals were ages 12-17 at the time of casting. These casts were included in the original data collection to test the hypothesis that dental characteristic patterns are essentially the same in West Africa and South Africa (Haeussler et al., 1989).

Western European samples (born 3rd , 18th, and 19th centuries AD EU n=139)

American Museum of Natural History

As part of the Von Luschan collection from the 1800's and 1900's, the AMNH houses a collection of 400 European skulls. From this collection, 70 dentitions were analyzed from western European countries, including France, Germany, Switzerland, Sweden and Norway (Morant, 1924.)

British Natural History Museum

The Poundbury skeletal collection is from a third century Roman Britain cemetery. The bones and teeth are in excellent condition due to the lime content of the soil in which they were buried. However, many of the teeth are heavily worn. From the larger collection, 69 dentitions were in a condition appropriate for morphological observations (Farwell and Molleson, 1993.)

Several additional facilities were contacted to see if they had collections that would be applicable for this analysis. These include the Harvard Peabody Museum, the Yale Peabody Museum, The Field Museum in Chicago, and Howard University in Washington D.C. The collections at these institutions were either inappropriate or unavailable for this study.

Institute	Collection	Code	Early American		Middle American		Late American		African		European	Total
			EA	AA	EA	AA	EA	AA	West	South		
AAS	Cedar Grove	CEGRO				15						15
AMNH	Western European	EUROP									70	70
	West African	WAFRI							131			131
ASU	Fort William Henry	FWHEN	16									16
	South African	BANTU								35		35
	University of Washington	UOFWA						10				10
BMNH	Du Chaillu	WAFRI							41			41
	Poundbury	POUND									69	69
CWRU	Bolton-Brush	BOLBR					54					54
CMNH	Hamann-Todd	HAMTD			61	49						110
NMHM	19th Century	19CEN			2	3						5
	Civil War	CIVIL			36	1						37
	Indian Territory	INTER			10							10
NMNH	Calvert Street	CALST		7								7
	Catoctin Furnace	CATFU		12								12
	Clifts Plantation	CLIFT	4	6								10
	Deep River Colonial Cemetery	DEEPR	3	2								5
	Governor's Landing	GOLAN	10	1								11
	Terry	TERRY			5	4						9
	Virginia Negroes	VANEG		7								7
	West African	WAFRI							13			13

Continued.

Table 3.1. Summary of collections and groups.

Institute	Collection	Code	Early American		Middle American		Late American		African		European	Total
			EA	AA	EA	AA	EA	AA	West	South		
NYSM	Oneida Poorhouse	OPOOR			21	1						22
	Wadsworth Almshouse	WADSW			4	2						6
OSU	Freedman's Cemetery	FREED				332						332
	Gullah	GULLA						55				55
USC	South Carolina	SOCAR				7						7
UTMHC	Dental Collection	UTDEN					101	100				201
Total			33	35	139	414	155	165	185	35	139	1300

Table 3.1 (Continued)

CHAPTER 4

METHODS

This chapter describes the methods used for data collection and analysis for this project. The methods employed in making the observations are described first. A description of the statistical techniques used concludes the chapter.

Morphological observations

Observations were made of 29 dental characteristics, each observation made on all the teeth for which that observation is applicable. Both sides were scored when present. At maximum, 136 observations could be made per dentition. Table 4.1 lists the traits and the teeth for which they were observed. Also listed in Table 4.1 are the codes used in this study for each observation. In addition to these observations, a record was made of the collection, location, age, sex, time period and ancestry of each individual's dentition. A total of 1,300 dentitions were observed for this study. Only occlusal, buccal, or lingual surface traits were observed. The decision to leave out root traits was based on the fact that in most cases they would be unobservable, since the data came

Trait	Teeth scored	Code
Winging	UI1	WING
Midline diastema	UI1	DIAS
Shoveling	UI1	UI1SS
	UI2	UI2SS
	UC	UCSS
	LI1	LI1SS
	LI2	LI2SS
Curvature of labial surface	UI1	UI1LC
Double shoveling	UI1	UI1DS
	UI2	UI2DS
Peg shape	UI2	UI2PS
	UM3	UM3PS
Interruption groove	UI1	UI1IG
	UI2	UI2IG
Congenital absence	UI2	UI2CA
	UM3	UM3CA
	LI1	LI1CA
	LM3	LM3CA
Tuberculum dentale	UI1	UI1TD
	UI2	UI2TD
	UC	UCTD
Canine mesial ridge	UC	UCMR
Canine distal accessory ridge	UC	UCDR
	LC	LCDR
Premolar mesial and distal accessory cusps	UPA	UP3MD
	UPP	UP4MD
Tri-cusped premolars	UPA	UP3TC
	UPP	UP4TC
Disto-sagittal ridge	UPA	UP3DS
Metacone	UM1	UM1MC
	UM2	UM2MC
	UM3	UM3MC
	UM3	UM3C5
Carabelli's trait	UM1	UM1CB
	UM2	UM2CB
Hypocone	UM1	UM1HC
	UM2	UM2HC
	UM3	UM3HC

Continued.

Table 4.1. Dental traits used, with trait codes.

Table 4.1 Continued.

Trait	Teeth scored	Code
Maxillary molar cusp 5 (Hypocone)	UM1	UM1C5
	UM2	UM2C5
	UM3	UM3CB
Parastyle	UM1	UM1PR
	UM2	UM2PR
	UM3	UM3PR
Lower premolar cusp variation	LPA	LP3LC
	LPP	LP4LC
Anterior fovea	LM1	LM1AF
Groove pattern	LM1	LM1GP
	LM2	LM2GP
	LM3	LM3GP
Cusp number	LM1	LM1CN
	LM2	LM2CN
	LM3	LM3CN
Deflecting wrinkle	LM1	LM1DW
Trigonid crest	LM1	LM1MT
	LM2	LM2MT
	LM3	LM3MT
Protostylid	LM1	LM1PS
	LM2	LM2PS
	LM3	LM3PS
Mandibular molar cusp 5 (Hypoconulid)	LM1	LM1C5
	LM2	LM2C5
	LM3	LM3C5
Mandibular molar cusp 6 (Entoconulid)	LM1	LM1C6
	LM2	LM2C6
	LM3	LM3C6
Mandibular molar cusp 7 (Metaconulid)	LM1	LM1C7
	LM2	LM2C7
	LM3	LM3C7

from casts, photographs, and museum skeletal collections, where if the teeth were in the alveolar bone, they would often not be able to be removed. In the case of photographic collections, only occlusal variable could be observed. Other factors that limited observations of traits included preservation, cast quality, and dental wear.

Traits were observed on any adult tooth in a condition permitting observation. Teeth with wear, caries, or calculus were observed to the extent that traits were not obscured. Permanent teeth in mixed dentitions were included to allow for a larger sample. Both left and right sides were scored; the higher or more complex of the two scores represents the maximum expression of the trait in the individual. This is a commonly used method of gathering the most observations per each individual (Scott and Turner, 1997).

All but two dental traits were scored according to the ASU Dental Anthropology System, described by Turner et al. (1991). This paper is a compendium of descriptions of dental traits, some originally described by its authors, as well as many other traits originally described by other researchers. The two traits scored differently than described by Turner et al. (1991) are midline diastema and trigonid crest. Midline diastema, a gap of at least 1 mm between the two maxillary central incisors, is not included in the ASU system, but was recommended as a possible distinguishing characteristic for Africans and their descendants (Joel Irish, personal communication, 1998). Also, while some researchers use the ASU system's distal trigonid crest, others instead recognize a mesial and/or middle trigonid crest. For this analysis, it was found to be simplest to use a single observation that included distal, middle, or mesial crests, which I referred to as "trigonid crest."

In most cases the scores have the same meaning as in the ASU system. However, there are three traits, metacone , hypocone, and cusp seven size, where the ASU system includes a half grade, such as 3.5. During the development of the system, this grade was added to better represent the range of variation that has been found. It does not really

indicate a half step in size change, rather a more complete description of the size variation that actually exists between the scores of three and four. For ease of computation, these half grades were elevated to full grade. In the case of metacone size, the choice of scores would not be 0, 1, 2, 3, 3.5, 4, 5, but 0, 1, 2, 3, 4, 5, 6 instead. Also, in the case of groove pattern, the ASU system categories are Y, +, and X. Here, these are scored as 1, 2, and 3, respectively.

Not all the traits for which observations were made were included in the full statistical analysis. A few traits, such as maxillary premolar disto-sagittal ridge were left out because they occurred in too infrequently in any sample to be of use. The trait "cusp number" was removed because it was a repetition of the information in available in the traits "cusp 5," "cusp 6," and "cusp 7."

Statistical Methods

Intra-observer error

To estimate intra-observer error, I scored a sample of 50 dental casts from the Dayton Museum of Natural History on two separate occasions. At least a week passed between the two scorings. Each dentition was scored for 19 of the characteristics included in this study. The results of these tests are presented in Table 4.2. In the table, "% same category $\pm$ 1" is the frequency that both observations were within one grade of each other, "uncertain" indicates observations that were only made once, "MGD" and "NGD" are the mean and net grade differences, and "SE" refers to the standard error. The mean grade difference for each trait ranges from 0.04 to 1.52. This means that, on

average, the difference between the two scoring events went from less than one-half of a grade to about a grade-and-one-half. A difference of more than one grade was seen in only two characteristics, lower anterior and posterior premolar lingual cusp variation. As this intra-observer study occurred before the research for this project began, it is likely that the error seen in these traits was due to observer inexperience, as these are the two traits with the most complex variation in expression.

Trait	% same category ±1	uncertain	MGD	SE MGD	NGD	SE NGD
WING	98	100	0.160	0.061	0.080	0.064
UI1SS	98	96	0.480	0.079	0.060	0.105
UI2SS	94	100	0.580	0.088	0.040	0.123
UI1DS	100	100	0.100	0.043	0.060	0.044
UI2IG	98	72	0.070	0.000	-0.070	0.067
UI1TD	98	88	0.260	0.091	-0.170	0.096
UM2HC	96	94	0.392	0.022	0.250	0.025
UM2C5	100	82	0.040	0.041	0.040	0.041
UM2CB	94	94	0.450	0.128	0.240	0.147
LI2SS	100	100	0.060	0.034	-0.060	0.034
LP3LC	60*	92	1.520	0.221	0.430	0.31
LP4LC	76*	90	1.170	0.250	-0.440	0.303
LM1MT	100	80	0.040	0.040	0.040	0.040
LM1DW	82	82	0.170	0.078	0.000	0.086
LM1PS	98	96	0.150	0.062	0.120	0.066
LM1C6	98	88	0.120	0.0620	0.070	0.063
LM2GP	90	84	0.850	0.143	-0.080	0.222
LM1C7	100	92	0.090	0.043	0.000	0.047
LM2CN	100	82	0.100	0.065	-0.100	0.065

N=50 (examined twice)

Table 4.2. Intra-observer error rates for selected traits.

Comparing data from observations on different materials

To address the question of the comparability of traits scored from photographs and teeth, a preliminary study of photographs of teeth that were also scored as teeth was conducted to determine if the difference between the two forms of observation was statistically significant. Dentitions from the Hamann-Todd collection were scored, then photographed. A month later, observations were made on the photographs, and the results of the two observations were compared for agreement. The results of this test are presented in Table 4.3. Overall, fewer characteristics are observable from photographs. However, when observations were made on both the dentition and the photograph, the variation between the observation was no greater than that found in observing the same material twice. Previous studies have shown little error in comparing observations from dental casts to those made directly on dentitions (Christy G. Turner II, personal communication, 1999.)

Combining observations

Previous studies have shown that the asymmetry found in scoring antimeres is generally small for dental characteristics (Harris and Bailit, 1980; Scott, 1980; Mizoguchi, 1988) and generally fluctuating (Scott and Turner, 1997). Fluctuating asymmetry is random variation (Van Valen, 1962), so that the use of either the right or left antimere, or a mixture of the two, should yield the same result. The point of comparing the right and left sides is to see if it is possible to combine the sides to make more observable data points. A G^2 statistic (Sokal and Rohlf, 1981) was employed to test the relationship of right and left observations in samples with more than 20 individuals.

When samples were large enough, males and females were tested separately. A $G^2 < 3.44$ means right and left observations are not related, so either can be used. If there is a $G^2 \geq 3.44$, right and left observations are related (Mardia et al., 1979), but this can be either

Trait	% same category +1	uncertain	MGD	SE MGD	NGD	SE NGD
WING	100	100.0	0.000	0.000	0.000	0.000
DIAS	100	73.3	0.000	0.000	0.000	0.000
UI1SS	100	73.3	0.200	0.200	0.200	0.200
UI2SS	100	73.3	0.400	0.163	0.000	0.211
UCSS	100	46.7	0.333	0.333	-0.333	0.333
UI1LC	86.7	93.3	0.556	0.176	-0.556	0.176
UI1DS	100	66.7	0.333	0.111	0.000	0.111
UI2PS	100	94.0	0.000	0.000	0.000	0.000
UI2IG	100	73.3	0.000	0.000	0.000	0.000
UI1TD	93.3	64.9	0.667	0.422	-0.667	0.422
UP3MD	93.3	80.0	0.714	0.359	-0.429	0.564
UM2MC	100	93.3	0.300	0.331	-0.300	0.331
UM2HC	100	93.3	0.333	0.167	0.111	0.2
UM2C5	93.3	93.4	0.714	0.286	-0.429	0.369
UM3CA	100	73.3	0.166	0.167	-0.166	0.167
LI2SS	100	86.7	0.100	0.100	-0.100	0.100
LP3LC	93.3	73.4	1.250	0.372	0.750	0.479
LP4LC	100	80.0	0.778	0.401	0.333	0.471
LM1AF	80	93.3	1.667	0.401	1.667	0.654
LM1MT	100	93.3	0.000	0.000	0.000	0.000
LM2GP	100	73.3	0.000	0.000	0.000	0.000
LM1C7	100	93.3	0.667	0.599	-0.667	0.599
LM2CN	93.3	66.7	0.286	0.286	-0.286	0.286
LM2C5	100	73.3	0.500	0.500	-0.500	0.500
LM3CA	100	80.0	0.000	0.000	0.000	0.000

N=15 (examined twice)

Table 4.3. Comparison of observations made on photographs and teeth for selected traits.

a positive or negative relationship. This relationship is indicated by the statistic phi (Thomas, 1976). If phi is positive, that the relationship between right and left is positive, so essentially are equal, and either can be used. It is only if the probability is less than 0.05 and phi is negative that right and left are negatively correlated and one cannot be substituted for another. These data have no such relationships. With no statistically significant directional asymmetry the right and left scores for each individual were combined, with the greatest trait expression being used for analysis.

A similar comparison was performed to see if it was reasonable to combine scores of males and females. Previous research has shown that there is little sexual dimorphism in the frequencies of dental morphological characteristics (Hanihara, 1992; Irish, 1993; Scott, 1980; Scott and Turner, 1997). Trait frequencies for males and females in the five largest samples were compared using the same methods applied in comparing right and left scores, above. Frequencies show the likelihood that males and females are similar enough to be included in the same group. While there were exceptions they were few enough to be accounted for by chance. Tables of right versus left and male versus female comparisons are provided in Appendices B and C, respectively.

Choosing breakpoints

For purposes of statistical analysis, arbitrary "threshold levels" have been used for many of the characteristics to account for their quasicontinuous nature. To determine the threshold breakpoints for this analysis, the weighted averages of score for each characteristic was compared among the African American, European American, and West African samples, to see how to best divide the scores to emphasize differences

between the three groups. Special emphasis was placed on most clearly delineating African Americans from European Americans. I then compared those breakpoints with those used by other authors. Observations were dichotomized with guidance from Haeussler et al. (1989), Irish (1993), Irish and Turner (1990), Scott and Turner (1997), and Turner (1987). Differences between the breakpoints initially suggested by the current data and breakpoints used by the other authors were found for UI2SS, UI1DS, UI2DS, UM1CB, LCDR, and LP4LC. The breakpoint for UI2SS was changed to match Haeussler et al. (1989). UI1DS was thrown out because there was no variation among the group frequencies. UI2DS was maintained with a breakpoint of one because it differentiated West Africans from African Americans at that score. UM1CB was changed to agree with other authors, except Scott and Turner (1997). LCDR was changed to match Irish and Turner (1990). LP4LC was maintained at a breakpoint of three because it better differentiated West Africans and African Americans at that score than at two, which was used by the other authors. Breakpoints are listed in Table 4.4. Numbers listed in the presence and absence columns refer to the possible scores in the ASU system, with each column listing the qualifying range of expression. In all but one of the traits, higher numbers represent greater or more complex expression of the trait. The exception to this rule is winging, where only a score of "1" represents bilateral winging, and higher scores indicate counter- or unilateral winging.

Maxilla	Absent	Present
TRAIT		
WING	0, 2-4	1
DIAS	0	1
UI1SS	0-2	3-7
UI2SS	0	1-7
UCSS	0-1	2-7
UI1LC	0-1	2-4
UI1DS	0	1-6
UI2DS	0	1-6
UI2PS	0	1
UM3PS	0	1
UI1IG	0	1-4
UI2IG	0	1-4
UI2CA	0	1
UM3CA	0	1
UI1TD	0-1	2-6
UI2TD	0-1	2-6
UCTD	0-1	2-6
UCMR	0	1-3
UCDR	0-1	2-5
UP3MD	0	1
UP4MD	0	1
UP3TC	0	1
UP4TC	0	1
UP3DS	0	1
UM1MC	0-4	5-6
UM2MC	0-4	5-6
UM3MC	0-4	5-6
UM1HC	0-4	5-6
UM2HC	0-1	2-6
UM3HC	0-1	2-6
UM1C5	0	1-5
UM2C5	0	1-5
UM3C5	0	1-5
UM1CB	0	1-7
UM2CB	0	1-7
UM3CB	0	1-7
UM1PR	0	1-6
UM2PR	0	1-6
UM3PR	0	1-6

Mandible	Absent	Present
TRAIT		
LI1SS	0	1-7
LI2SS	0	1-7
LI1CA	0	1
LM3CA	0	1
LCDR	0	1-5
LP3LC	0-3	4-9
LP4LC	0-2	3-9
LM1AF	0-1	2-4
LM1GP	0, 2-3	1
LM2GP	0, 2-3	1
LM3GP	0, 2-3	1
LM1CN	4-5	6
LM2CN	4	5-6
LM3CN	3	4-6
LM1DW	0	1-3
LM1MT	0	1
LM2MT	0	1
LM3MT	0	1
LM1PS	0	1-7
LM2PS	0	1-7
LM3PS	0	1-7
LM1C5	0	1-5
LM2C5	0	1-5
LM3C5	0	1-5
LM1C6	0	1-5
LM2C6	0	1-5
LM3C6	0	1-5
LM1C7	0	1-4
LM2C7	0	1-4
LM3C7	0	1-4

Table 4.4. Presence-absence breakpoints used for the current study.

Measures of Biological Affinity

The application of statistics that estimate biological distance (or affinity) is required in order to test the hypothesis and predictions described in Chapter one. Statistics of this kind measure the similarity of expression of characteristics in different samples, to quantify average differences between those samples. The characteristics can be metric (continuous) or nonmetric (categorical or ordinal), and the studies can be univariate or multivariate. The data collected for the present research are multivariate and categorical. For the present study, small distances between groups indicate that the groups are more similar in their dental morphology than groups separated by large distances. The assumption is made that similarities and differences in overall patterns of dental morphology indicate degrees of relatedness between the groups being compared.

Mean measure of divergence and Pseudo-Mahalanobis' D^2 are the most appropriate biological distance statistics for addressing the hypothesis and predictions. Most studies of biological distance that rely on data from dental morphology use the mean measure of divergence as the primary, if not sole, biological distance statistic. The purpose of using pseudo-Mahalanobis' D^2 as well as the mean measure of divergence in the current analysis is to compare the results of the two statistics. While both are applicable to the kind of data available in dental morphological studies, the statistics differ in whether they are applicable to correlated or uncorrelated characteristics. The two statistical applications were compared to see if they would yield similar results.

Mean Measure of Divergence

The MMD statistic was developed by C. A. B. Smith, and was first used to look at changes due to inbreeding in mice (Grewal, 1962; Berry et al., 1967). Berry and Berry (1967) first applied it to the study of biological affinities or distance in humans. The MMD estimates biological distance between pairs of samples based on the degree of phenetic similarity (Irish 1997). The statistic assumes the statistical independence of traits. Small distances indicate that groups are phenetically similar, from which it can be inferred that they share genes and are related.

Like D^2, it is useful if trait expression varies between groups, when frequencies are between 0.50% and 0.95% (de Souza and Houghton, 1977). Some major benefits of its use are its ability to work with incomplete data and its applicability to samples as small as ten to 20 observations. MMD is defined as:

$$\frac{\sum(\theta_1 - \theta_2)^2 - (1/(n_1 + ½) + 1/(n_2 + ½))}{c}$$

where θ equals

$$\sin^{-1}\left(\frac{r}{n+1}\right)^{1/2} + \sin^{-1}\left(\frac{r+1}{n+1}\right)^{1/2}$$

(Freeman and Tukey, 1950)

and is the arc sin ($\sin^{-1}$) transformations of the observed frequencies in the two samples being compared. The variance of $\theta_1 - \theta_2$ is approximated by $(1/(n_1 + ½) + 1/(n_2 + ½))$. The sample sizes are n_1 and n_2, and c is the number of characters employed (Green and Suchey, 1976; Sjøvold, 1977).

Pseudo-Mahalanobis' D^2

The Pseudo-Mahalanobis' D^2 is defined as the sum of squares of differences between corresponding mean values of two sets of measurements, weighted by the variance/covariance matrix (Burnaby, 1966):

$$D^2 = (\chi_{ik} - \chi_{jk})' \Sigma (\chi_{ik} - \chi_{jk})$$

where χ_{ik} is the trait frequency for sample i for trait k, and χ_{jk} is the same for sample j. The middle term (Σ) is the pooled covariance matrix of Z scores for the tetrachoric correlations between the k traits (Brown, 1977; Manly, 1994), which adjust for correlations between characteristics being used (Konigsburg, 1990; Mizoguchi, 1977) and the threshold nature of dental morphological traits (Scott and Turner, 1997). As with MMD results, small distance results indicate that groups are phenetically similar, from which it can be inferred that they share genes and are related. The results of MMD and pseudo-D^2 are presenting in tabular form as well as in graphic representations of their first two or three vectors of principal coordinates, a form of multidimensional scaling. The amount of variation accounted for by each vector is provided (Mardia et al., 1979).

Other statistical techniques

The biological distance statistics described above quantify differences between samples. The statistics described in the present section depend on the biological distance results, and were used for two purposes. Procrustes transformation was used to compare the results of MMD and pseudo-D^2 statistics to see if they produce similar results. Logistic regression and Bayesian prediction were used to determine the probability of

group membership of an individual. Group membership determination was possible because the biological distance results indicated that there are differences between the late time period African Americans and European Americans.

Procrustes' transformation

Different biological distance analyses, such as the mean measure of divergence and Pseudo-Mahalnobis' D^2, do not necessarily result in statistics that are comparable. They results may not be of the same scale, or may not be representable graphically on the same axes. The purpose of Procrustes' transformation is to rotate and scale two sets of coordinates so as to achieve the best fit between them (Gower, 1971; 1975). For the present study, the coordinates come from principal coordinates analysis of four distance matrices, and show the first two axes of each matrix. The better the fit between two sets of coordinates, the smaller the summed deviations should be. Gower (1971) refers to the statistic as R^2 (for residual), but it can also be found as S^2 (for sum of squares) (Goodall, 1991) and M^2 (for minimum) (Jackson, 1995). R^2 is defined as:

$$R^2 = \sum \Delta^2(P_i P_i^*)$$

where P_i and P_i^* represent the corresponding points in two different matrices of coordinates. The R^2 statistic is the sum of squared differences after rotation and scaling. The smaller the R^2, the smaller the difference between the two sets of coordinates. For this study, a small R^2 will indicate good agreement between the MMD and pseudo-D^2 statistics.

Logistic regression

Logistic regression is similar to regular multiple regression except that the dependent variable is of a presence or absence nature, rather than continuous (NCSS, 1999). It can be used to predict group affiliation based on two or more variables. Probability is defined as:

$$\text{Prob}\ (Y|y_1) = 1/1 + \exp(1(\beta_0 + \beta_1 X_1 + \beta_2 X_2 + \ldots + \beta_p X_p))$$

and

$$\text{Prob}\ (Y|y_2) = 1 - \text{Prob}\ (Y=y_1)$$

where Y is the dependent variable, in this case social race category, and β is the vector that corresponds with each dental characteristic in the analysis (Everitt and Dunn, 1991; Hoffman and Duncan, 1988).

Bayesian probability

Bayesian, or inverse probability, is a means of calculating the probability that an event will occur in future observations, based on the number of times it has not occurred in previous observations (Bernardo and Smith, 1994). Bayesian probability is appropriate for categorical data (Lucy et al., 1995). However, unlike logistic regression it is best applied to predictions within the sample groups, rather than in the populations from which the samples are drawn. Logistic regression cannot be used when the frequency of observation for any trait combination is zero. For this reason, in addition to

probabilities based on logistic regression, Bayesian probabilities were computed for each trait combination in the forensic probability tables. The statistic is defined as:

$$P(i) = \frac{n(I_1, A_i)}{n(A_i)} \cdot \frac{n(I_2, A_i)}{n(A_i)} \cdots \frac{n(I_n, A_i)}{n(A_i)} \cdot \frac{n(A_i)}{N}$$

where $P(i)$ is the assignment of a particular ancestry to an individual, and $n(I_1, A_i)$ is the number of individuals in which the particular trait under consideration is present. The repetition of this variable in the equation is dependent on the number of traits being compared at the same time (Lucy et al., 1995).

The data collected for this project can be utilized for forensic determination of social race by applying logistic regression and/or Bayesian probaility. A subsample of African American and European American dentitions was tested to find the traits that showed the most divergence between the two groups. Only the late groups were included, those born in the 20th century. For the forensically applicable portion of the current research, the Gullah were excluded for the African American sample, because their dental morphology was found to be quite different from other contemporaneous African Americans. Using these data in a multinomial logistic regression yields probabilities of affinity of an unknown individual from the populations from which the samples were drawn. Bayesian probabilities are only strictly to be applied to within-sample prediction, so are not as robust when applied to individuals known to be from the populations in question, but not of the original study materials. These probabilities, based on comparisons of two, three, and four traits, have been arranged in tables in Appendix D. A set of observations from an individual dentition can be compared to the

tables to determine the probability that the observed characteristics would be found in either of the two groups.

After completion of the tables, a test was made of the accuracy of prediction of ancestry possible using these tables. Observations of the presence or absence of the eight traits included in the analysis were made for ten individuals known to be from the populations from which the samples were drawn, but not included in the samples themselves. When the observations were made, Their actual social race affiliation was not known. These observations were then compared with the tables, and a determination of probable ancestry was made.

CHAPTER 5

RESULTS

This chapter presents the results of the analyses performed as described in Chapter four. The first section is a description of the frequencies for the dental traits under study. This is followed by results and interpretations of the statistics that measure biological affinity, namely mean measure of divergence and pseudo-Mahalanobis' D^2. Some of the results for these two statistics were compared through the use of Procrustes transformation. The final section describes probability tables based on this research that can be used in forensic situations to determine the socially ascribed race of an unknown individual.

Trait frequencies

Prior to further statistical analyses, it is valuable to examine the trait frequencies for of all the morphological characteristics scored in the various samples. Several factors that affect analysis of these data are apparent. First, the material that the observations came from affects what observations could be made. Second, several traits were observed at such low frequency among all of the samples that their inclusion in further

analysis would be pointless. Last, the variation in trait frequencies gave a good indication of which traits would be best for forensic application.

Limitations on observations

Observations were made on photographs, dental casts, and teeth themselves. The material of each sample affected what observations could be made. No observations of incisor winging or midline diastema could be made for the Freedman's cemetery collection, the single largest sample used in this project. This is because observations were made on photographs of the teeth, taken in a photographic laboratory on site of the excavation. At the Freedman's Cemetery site, teeth were in an excellent state of preservation, but almost all of the alveolar bone had deteriorated. Teeth were not kept in the bone for analysis; rather, they were arranged on two Lucite and clay plaques, one for each arch. Winging and midline diastema are descriptions of how the teeth are positioned in the alveolar bone, so no observation of them could be made due to the poor bone preservation at that site.

As mentioned in Chapter four, any observation based on photographic material were missing most of the data for non-occlusal characteristics. This includes observations of Carabelli's trait and parastyle. Observations were limited in the Freedman's Cemetery sample, as well as in some individuals in the Fort William Henry and South Carolina collections.

Materials other than photographs also place limitations on which characteristics are observable. Dental casts often were missing data on third molars, either because the casting material did not go far enough back into the mouth or because the individual had

had these teeth removed. Casting may also prevent a clear observation of an interruption groove. In order to be counted as "present," the groove must extend from the enamel onto the root. If soft tissue was present during the casting, as it was in all cast samples except Cedar Grove, the root is not visible.

Even observations made directly on teeth are limited by the condition of those teeth. Samples from early time periods, such as Poundbury, had many observations obscured by attrition, while dental restorations prevented observations of traits in more recent samples. In the collections of West African material, the historical acquisition of skulls without mandibles limited the number of individuals in the collection that were acceptable for data collection. Despite these several limitations on data collection, many thousands of observations were made.

Low frequency traits

Several traits were found to be absent or at such low frequencies in all of the samples as to be of negligible help in studying relationships among the samples. These traits include maxillary first incisor double-shoveling, tri-cusped anterior and posterior maxillary premolars, disto-sagittal ridge of the maxillary anterior premolar (also known as Uto-Aztecan premolar), and congenital absence of the mandibular first incisor. Based on previous research (Scott and Turner, 1997), these traits were expected to be rare or absent form the samples analyzed for the current research. For some of these traits, their presence, even at low frequencies, would not have been predicted. They were included only because they are a standard part of collection for the ASU dental scoring system.

It should be noted that in the following discussion of trait frequencies, right and left observations were combined. For each individual, a single observation was counted for each trait on each tooth on which it was observed. An individual with both right and left teeth present would only contribute one observation, the higher expression of the two possible, to the individual count used in determining trait frequency.

Double shoveling of the maxillary incisors is most commonly seen in Asian and Asian-derived groups, such as Native Americans (Scott and Turner, 1997). Prior to the current research, no data existed on the frequency of the trait in Europeans. Haeussler et al. (1989) indicated low frequencies of the characteristic in San and Bantu speakers (2.0% and 0.0%, respectively). Out of the 923 observations made, six maxillary first incisors (0.65%) had double shoveling. Three of these were in African Americans and three were in European Americans.

According to Turner et al. (1991) tri-cusped maxillary premolars are rare worldwide, observable in about 1/8,000 teeth, so it is not surprising that they are rare in the samples studied here. In fact, what is surprising is that two tri-cusped anterior and three tri-cusped posterior maxillary premolars were seen at all. Observations were made on 1,135 anterior maxillary premolars and 1,142 posterior maxillary premolars, giving a rate of 0.2% overall for both teeth. This is quite a large frequency, given Turner et al.'s (1991) estimate of .013% occurrence. Four of the tri-cusped premolars were seen in African and African American samples, of which 1,507 observations were made, for a frequency of 0.27%. One such tooth was seen in European and European American dentitions, of which 770 premolars were observed, for a frequency of 0.13%.

Disto-sagittal ridge is a synonym for Morris' Uto-Aztecan Premolar (Morris et al., 1978). The trait was originally named for the linguistic group of the people it was found in, and in which it was thought to be a recent mutation (Hillson, 1996). More recent studies (Johnston and Sciulli, 1996) indicate that the characteristic is not limited to Uto-Aztecan speakers, but is instead a rare but widespread variant in many Native American populations.

Two premolars with disto-sagittal ridge were observed in this study, both in African Americans. Since 557 observations were made for this trait in African Americans, the trait occurs in 0.36% of the sample. The occurrence of this trait in African Americans may simply be due to mutation, or it may reflect Native American admixture.

In the present study, observations were made of congenital absence, or agenesis, of third molars, lateral maxillary incisors, and central mandibular incisors. Congenital absence is one of the harder characteristics to differentially diagnose, as it can be confused with teeth that are either unerupted or lost antemortem (Turner et al., 1991). In general, third molar agenesis is much more common than incisor agenesis (Brothwell et al., 1963). Only three mandibular central incisors were determined to be congenitally absent, out of 1,152 teeth for which the observation could be made. One of these was in an African American, for which there are 581 observations, giving a frequency of 0.17% The other two congenitally absent mandibuar central incisors were seen in 280 observations in European Americans, for a frequency of 0.71%

The fact that the traits described above occur in samples of both African and European derived populations at similarly low frequencies indicates the relative similarity

of these two groups when compared with other populations worldwide. Both shoveling and disto-sagittal ridge are associated with Asians and Asian derived populations. It appears that, at least in these features, African and European derived groups share more in common that either does with other major world populations.

Traits of forensic utility

The frequencies of all the characteristics were compared between groups, in order to determine which traits would be most helpful in a forensic analysis. Traits were ranked according to the difference in their frequencies in African American samples, as compared to European samples (AA percent present minus EA percent present). Eight traits were found to have a difference of 20% or greater: maxillary canine tuberculum dentale, mandibular anterior premolar lingual cusp variation, mandibular posterior premolar cusp variation, mandibular first molar deflecting wrinkle, mandibular first molar trigonid crest, mandibular second molar cusp five, mandibular third molar cusp five, and mandibular first molar cusp seven. It is interesting to note that of the 29 traits examined for this project, only eight were found at different enough frequencies to warrant inclusion in an analysis for predicting ancestry in an unknown individual. The statistical analysis and resulting tables of these eight traits are described in the section on forensic analysis, later in this chapter.

Measures of biological affinity

Determining which traits were useful for each analysis

As described above, some traits were left out of the analyses because they occurred at frequencies that were too low to be of use in comparing samples. Other traits were excluded from the analyses of biological distance because their frequencies were either too high (>95%) or too low (<5%) in some, but not all, groups. These traits were still open for consideration for their forensic utility, as their frequencies might be different in late period African Americans and European Americans. Third molar traits were also excluded, as they had fewer observations than the same characteristics on first and second molars. The traits excluded for these reasons are listed in Table 5.1.

After eliminating the above named traits, it was still necessary to determine which characteristics would be best studied with the different analytical tools to be used. Traits that are correlated are not usable in mean measure of divergence analyses, but are usable in pseudo-Mahalanobis' D^2 analyses. For this project, both of these statistics were used, so that a wider range of the traits observed could be analyzed.

In order to decide which traits would meet the assumptions of each statistic, it was necessary to determine the correlations of each trait, when compared with each other trait. This was done using a likelihood ratio chi-square statistic (Sokal and Rohlf, 1981). For MMD, one trait was chosen out of each group of intercorrelated characteristics. For example, UI1SS, UI2SS, and UCSS are all correlated with each other. UCSS was chosen for inclusion in the MMD analysis because, of the three intercorrelated traits, it has the

most observations. The characteristics included in the MMD analyses are listed in Table 5.2.

WING	UI1IG	UM3C5	LM3CA	LM3C5
UI1SS	UCMR	UM3CB	LM1GP	LM2C6
UI2PS	UM3MC	UM1PR	LM3GP	LM2C6
UIM3PS	UM2HC	UM2PR	LM3PS	LM3C6
UI1IG	UM3HC	UM3PR	LM1C5	LM3C7

Table 5.1. Traits excluded from biological distance analyses due to lack of variation or lack of observations.

DIAS	UCTD	UM2C5	LM1AF	LM1C6
UCSS	UCDR	UM2CB	LM2GP	LM2C7
UI1LC	UP3MD	LI2SS	LM1DW	
UI2DS	UP4MD	LCDR	LM1MT	
UI2IG	UM2MC	LP3LC	LM2PS	
UM3CA	UM1HC	LP4LC	LM2C5	

Table 5.2. Traits used in MMD analyses.

The larger the number of variables included in carrying out pseudo-Mahalanobis' D^2 analyses the greater the complexity. For this reason, maxillary and mandibular characteristics were considered separately when using this statistic. Also, because the information must be reformulated each time a new group is added or deleted from the analysis, fewer analyses were run of the D^2 statistic. The characteristics used in these

analyses were found to be correlated using the likelihood ratio chi-square (Sokal and Rohlf, 1981). Several characteristics were removed from the analysis of mandibular characteristics, as their correlations with other traits were too small, causing the matrix to be singular and therefore impossible to invert. The final list of traits used in the analyses are listed below in Table 5.3.

Traits used in analysis of maxillary teeth				
UI2SS	UI2TD	UP3MD	UM2MC	UM2C5
UCSS	UCTD	UP4MD	UM1HC	UM1CB
UI1LC	UCDR	UM1MC	UM1C5	UM2CB
Traits used in analysis of mandibular teeth				
LI1SS	LP4LC	LM1PS	LM2C5	
LI2SS	LM2MT	LM2PS	LM1C6	

Table 5.3. Traits used in maxillary and mandibular pseudo-Mahalanobis' D^2 analyses.

Mean measure of divergence

The MMD was used to analyze relationships between groupings of the samples at various levels of relationship. One analysis was made of the relationships between the four groups African Americans, European Americans, Europeans, and West Africans. Another analysis consisted of comparisons of the six groups Late, Middle, and Early African Americans and European Americans. Several additional analyses concern the relationships between specific samples, such as Freedman's Cemetery and Hamann-Todd African Americans. MMD results indicated that some groups could be combined and

others could not. Comparisons were made between groups, going from large geographic or time samples to smaller, more specific comparisons.

Europeans

The European samples consist of Poundbury, a third century Roman London collection (Farwell and Molleson, 1993), and a wide-ranging western European collection gathered in the nineteenth century (Morant, 1924). One might expect differences between these two collections due to the time and space differences between them. It is fair to question whether these samples can be rightfully grouped together. However, the MMD result for these two groups is only 0.0016, a negligible difference. Whether an MMD is statistically significant is determined by the total chi-square (χ^2), the sum of the chi-squares for each of the variables (Sjøvold, 1977). The total chi-square for this comparison is 29.35, below 38.885, the 0.05 significance level for 26 degrees of freedom (Mardia et al., 1979). The groups were combined for further analyses, and from here on the term Europeans refers to the combined western European and Poundbury samples.

Africans

Three African samples were collected for this study, two West African samples and one collection of South African Bantu speakers. The West African groups were collected in the 19th century; the South African collection dates from the 1960s. The two West African samples were combined and compared to the South African group. The West African versus South African MMD result is 0.2048, much larger than between the European samples that were combined. The total chi-square, 64.63, is statistically

significant. These groups were not combined, and the sample of South African Bantu speakers was excluded from further analyses.

African Americans

The Gullah people are the least admixed of all African American populations (Pollitzer, 1999). For this reason their sample was compared to the other African American and West African groups, to see if their inclusion in with other African American samples was warranted. The results are presented in Table 5.4.

	West Africans	Early African Americans	Middle African Americans	Late African Americans
Gullah MMD	0.4361	0.3781	0.0830	0.3291
total χ^2	329.91*	183.24*	180.73*	400.30*

Table 5.4. MMD results for Gullah and other African derived groups.

Statistically significant differences at the $p<0.05$ level are denoted in table 5.4 with an asterisk, as they are in other tables that present results of significance tests. There are statistically significant differences between the Gullah and each of the other groups to which it is compared. It is interesting to note that the groups that are most different phenotypically are the West Africans, whom the Gullah are thought to be descended from with little admixture, and the late African Americans, who are their contemporaries. These results are counter to the prediction made that the Gullah sample would have a close affiliation with the West African sample. Despite these results, the Gullah are

certainly socially considered to be African American. Therefore, in analyses that group all the African Americans, the Gullah were included. In other situations, where subsets of African Americans were compared with each other or other groups, the Gullah were omitted.

Between group comparisons

Table 5.5 lists the MMD values for comparisons of the highest level ancestral groups studied here. For this table, as for all the following MMD tables, the MMD is listed first in each cell. The number in parentheses is the total chi-square for each pairwise comparison. All of the total chi-square values are statistically different from zero.

	European American	West African	African American
European	0.0454 (103.53)*	0.3573 (465.52)*	0.2417 (538.73)*
European American		0.4017 (735.37)*	0.2701 (1131.03)*
West African			0.0774 (219.37)*

Table 5.5. MMD results for highest level ancestral groups.

As expected, Europeans and European Americans are more similar to each other than either is to West Africans or African Americans. Also as expected, West Africans are more similar to African Americans than to either of the other groups. The first two principal coordinates of these relationships are shown in Figure 5.1. The amount of variation accounted for by each dimension is noted at each axis. The graph shows the

relatively close relationship between the European (EU) and European American (EA) samples, but shows a relatively distant relationship between the West African (WA) sample and African Americans (AA). European admixture in the African American gene pool may explain the distance between African Americans and their West African ancestral group.

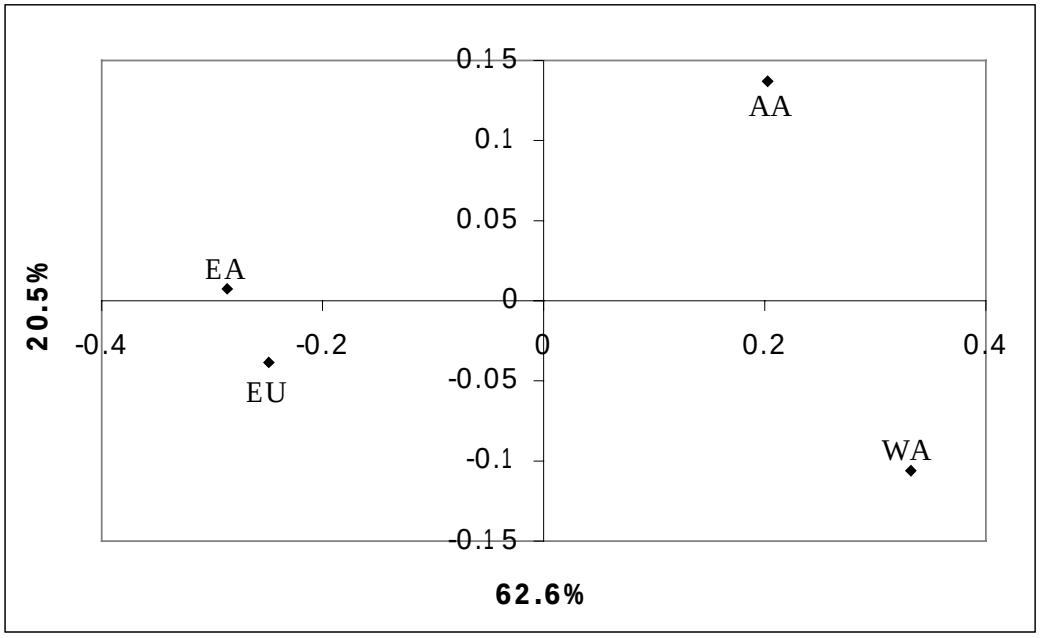

Figure 5.1. First two principal coordinates of MMD results for West Africans, Europeans, African Americans, and European Americans.

The next level of analysis performed was to compare samples representing ancestral populations, Europeans and West Africans, with time-separated samples of their descendant groups, European Americans and African Americans, respectively. Table 5.6 shows the MMD values for Europeans and their American counterparts. Figure 5.2 shows the relationships between these groups as indicated by the principal coordinates.

	Early European Americans	Middle European Americans	Late European Americans
Europeans	0.0688 (74.48)*	0.0635 (93.84)*	0.0975 (151.05)*
Early European Americans		-0.0179 (21.06)	0.1972 (144.58) *
Middle European Americans			0.1790 (205.13)*

Table 5.6. MMD results for Europeans and European derived American time groups.

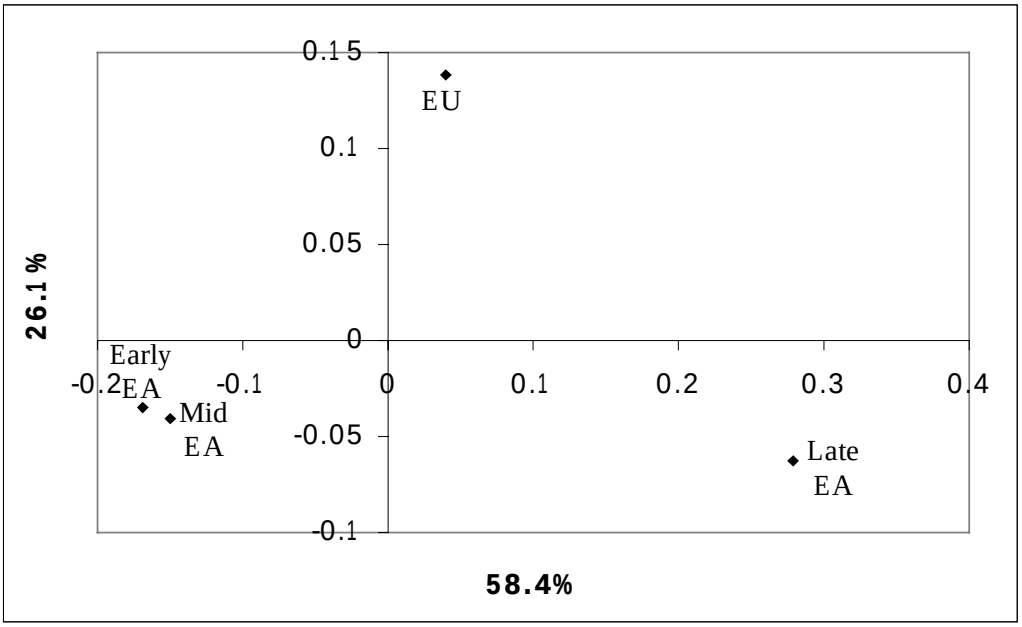

Figure 5.2. First two principal coordinates for MMD results for European and European derived samples.

Discussion

The MMDs comparing all time-separated groups of European Americans to their European counterparts are statistically significant. It might have been expected that the Early European American group would not differ from the European sample, as they are

supposed to represent their recent descendents. The fact that the Early European sample is statistically different from the European sample may indicate that the Early European American sample does not well represent the actual population of European Americans in the early time period. In fact, the Early European American sample is the smallest of all the time period samples, whether European American or African American (n=33). The MMD between Early and Middle European Americans, however, is negative, indicating that these groups are the same. The total chi-square is not significant, which either confirms this conclusion, or leads to the false conclusion of rejecting the accurate hypothesis that Early and Middle European Americans are different groups. Like the table, the graph indicates the close relationship between early and middle time periods of European Americans. However, if these two groups are similar because they are descended from Western Europeans, unlike the later European Americans, the graph would be expected to show a closer relationship between the early/late dyad and the Europeans themselves.

The lack of change between Early and Middle European Americans, as indicted by table 5.6 may imply that the subset of areas of Europe that immigrants came from did not change very much between the two time periods (1650-1850 and 1825-1910). It could also be interpreted to represent a lack of new immigration for Western Europe during the 19th century, so that middle period European Americans are simply the descendants of the early European Americans. However, historical sources conflict with this second explanation (Jones, 1992).

The observation that late European Americans are different from their early or middle counterparts in this analysis probably indicates a change in the area of Europe that

immigrants came from in the 20th century. It is generally known that the end of the 19th and beginning of 20th centuries saw an influx of Eastern and Southern Europeans to the United States (Jones, 1992). It could be that this shift is reflected in the dental morphology of the groups. A study of Eastern and Southern European dentitions would be necessary for supporting evidence of a change in the geographic origins of European immigrants.

The relatively distant relationship between the early and middle European American pair and the European sample, as seen in Figure 5.2, may indicate that while the early and middle European Americans are essentially the same group, neither represents a random sample of the original western European population. This problem could exist historically, meaning that the western European migrants were not a representative sample of western Europeans. Or, it may instead exist in the sampling strategy involved in this project, meaning that the samples of European Americans used do not accurately reflect the ancestry of the European American population. It may also be that the early and middle European American samples are representative of both European Americans and their ancestral population, but that the sample of western Europeans inaccurately reflects the population from which it was drawn. A final possible explanation is that dental morphology does not accurately reflect the relationships between these groups, no matter the samples used for the current project.

Table 5.7 shows the MMD relationships between West Africans and their American counterparts. There is a statistically significant difference between the West African sample and the Early African Americans. Like the difference between the

European and Early European Americans, this difference many be due sampling error, as the early African American sample is quite small (n=35). The principal coordinates for the MMDs listed above are shown in Figure 5.3.

	Early African American	Middle African American	Late African American
WA	.0491 (51.97)*	.0830 (209.03)*	.1635 (239.62)*
Early African American		.1570 (108.93)*	.1875 (117.16)*
Middle African American			.0830 (180.73)*

Table 5.7. MMD results for Africans and African derived American time groups.

Figure 5.3. First two principal coordinates for MMD results for African and African derived samples.

Discussion

In examining Table 5.7, the MMD for West Africans has doubled compared to early and middle African Americans, and doubles again when compared to middle and late groups. This seems to indicate a progressive change in African Americans away from the West African pattern. However, within the African American samples, the difference between the middle and late time periods is about half that of the early to middle times. This may reflect differences in the origin and/or amount of new, non-African Americans genes coming in to the African American gene pool during these time periods. Figure 5.3 does not show any close relationships among the four groups included. However, the point representing the late African Americans is slightly more distant from all the other groups than any of them are to each other.

In order to look at changes over time in the African American dentition, MMDs were calculated among early, middle, and late groups of European and African Americans. Table 5.8 presents the results, along with MMDs for these groups with the samples of their ancestral populations, namely Europeans and West Africans. These relationships are shown in Figure 5.4, the principal coordinates of Europeans, West Africans, and early, middle, and late European and African Americans. Unlike the other figures in this chapter, Figure 5.4 is drawn in three dimensions, as two dimensions do not explain enough of the variation present to be useful.

Discussion

All of the total chi-square results in Table 5.8 are statistically significant, with the exception of the relationship between early and middle time period European Americans, as discussed earlier. Assuming that the characteristics under study herein are selectively neutral, statistically significant differences between time-separated samples but within ancestral groups result from either genetic drift or gene flow. Gene flow can come either from new immigration from the ancestral regions, or admixture between the groups. The admixture component of this change makes an especially important contribution in African Americans.

	Early EA	Mid EA	Late EA	WA	Early AA	Mid AA	Late AA
EU	.0688	.0635	.0975	.3573	.3608	.2210	.3548
	(74.48)*	(93.84)*	(151.05)*	(465.52)*	(187.21)*	(464.02)*	(472.92)*
Early		-0.0179	.1972	.3267	.3069	.3060	.4415
EA		(21.06)	(144.58)*	(210.34)*	(119.69)*	(249.54)*	(283.32)*
Mid			.1790	.3587	.3642	.3047	.4560
EA			(205.13)*	(355.77)*	(160.20)*	(448.80)*	(436.13)*
Late				.4950	.4900	.3033	.2951
EA				(776.93)*	(264.61)*	(821.55)*	(479.97)*
WA					.0491	.0830	.1635
					(51.97)*	(209.03)*	(239.62)*
Early						.1570	.1875
AA						(108.93)*	(117.16)*
Mid							.0830
AA							(180.73)*

Table 5.8. MMD results for Europeans, Africans, and American groups.

Among statistically significantly different relationships, the closest are between West Africans and early African Americans (MMD 0.0491), Europeans and middle European Americans (MMD 0.0635), and Europeans and early European Americans (MMD 0.0688). This indicates the similarities that should be expected between ancestral groups and their recent descendents.

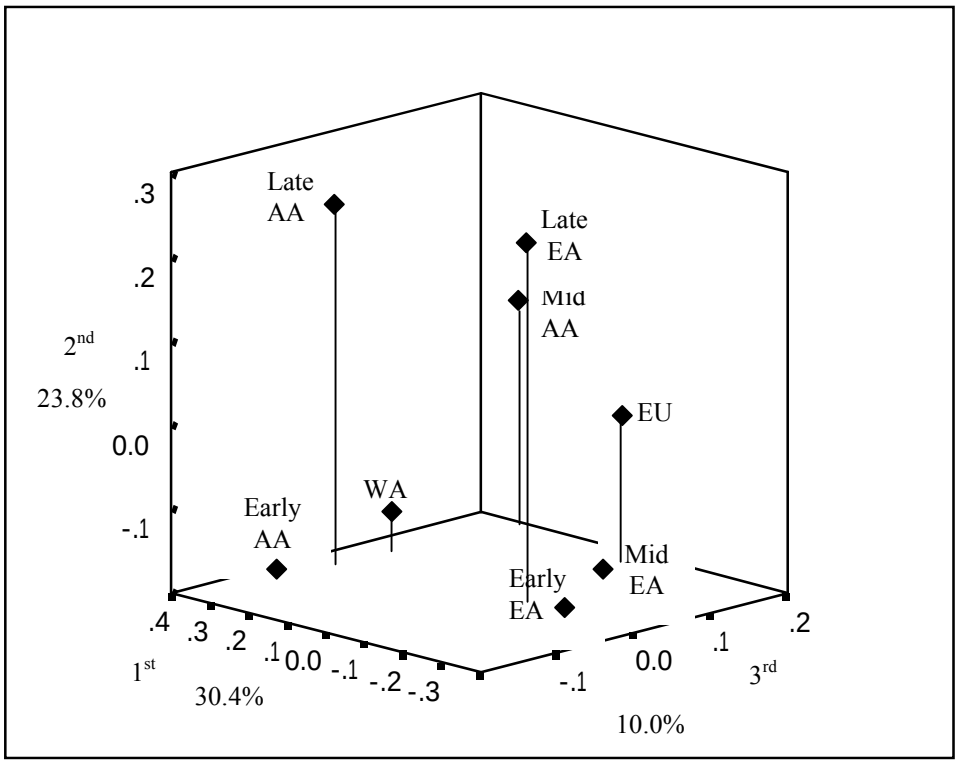

Figure 5.4. First three principal coordinates for MMD results for Europeans, West Africans, and their descendant American groups, by time.

By far, the greatest differences between groups are seen between late European Americans and West Africans (MMD 0.4950) and early African Americans (MMD 0.4900). While it cannot be tested for statistical significance, it is interesting to note that

these results are larger than the MMD for the European versus West African comparison (*i.e.*, MMD 0.3573). It might have been suspected that the two ancestral groups would have been the most different among the comparisons. Perhaps the observation that the greatest difference from West Africans is not with the Europeans but with the most recent sample of European Americans reinforces the hypothesis that new, non-western European genes make a significant contribution to the late European American gene pool.

Comparing European Americans with their African American time period counterparts, it can be seen that, over time, the distances between the groups diminishes. The European American/African American MMDs are 0.3069, 0.3047, 0.2951 for early, middle, and late time periods, respectively. While the change indicated is slight, it is also progressive over time. While no test exists to see if this change is statically significant, the results do support the main hypothesis of this research, that over time African Americans become closer to the average of their ancestral groups, western Europeans and West Africans.

Figure 5.4 indicates the differences between European and European derived groups, to the right of the X-axis, from West Africans and their descendents, African Americans, to the left. These differences are clear across all time periods. As expected based on Table 8, early and middle European Americans cluster, as do West Africans and early African Americans. Differences over time are shown in the same way for the two ancestral groups. Early samples are located near the bottom of the graph, middle time period samples are higher, and late samples are at the top of the graph. The graphic representation of these data does not make clear what is changing in the average phenotypic expression of these groups, only that the same kinds of changes are occurring

in both groups. The MMD supports the primary hypothesis that dental morphology reflects a trend over time for African Americans to develop more similarity to European Americans.

In order to test predictions about the relationship of admixture to urban and northern movement during the African American Great Migration, MMDs were made comparing urban and rural groups in the south, as well as southern and northern urban groups. The large Freedman's Cemetery sample represents the urban South. The rural South is represented by Cedar Grove, a small sample from rural Arkansas. The urban North is represented by the African Americans of the Hamann-Todd collection, a mid-sized sample from Cleveland, Ohio. These three groups are roughly contemporaneous, and are included in the middle time period African American sample. These three subsets of the middle African Americans were compared with the middle time period European Americans. Table 5.9 presents the MMDs for these groups. All of the associated chi-square values are statistically significant. Figure 5.5 presents the principal coordinates for the MMD's in Table 5.9.

	Freedman's Cemetery	Cedar Grove	Hamann-Todd African American
Middle European American	0.3283 (512.86)*	0.2906 (103.66)*	0.3753 (222.82)*
Freedman's		0.0456 (60.06)*	0.2886 (150.83)*
Cedar Grove			0.6516 (170.99)*

Table 5.9. Comparisons among subsets of middle African Americans and middle European Americans.

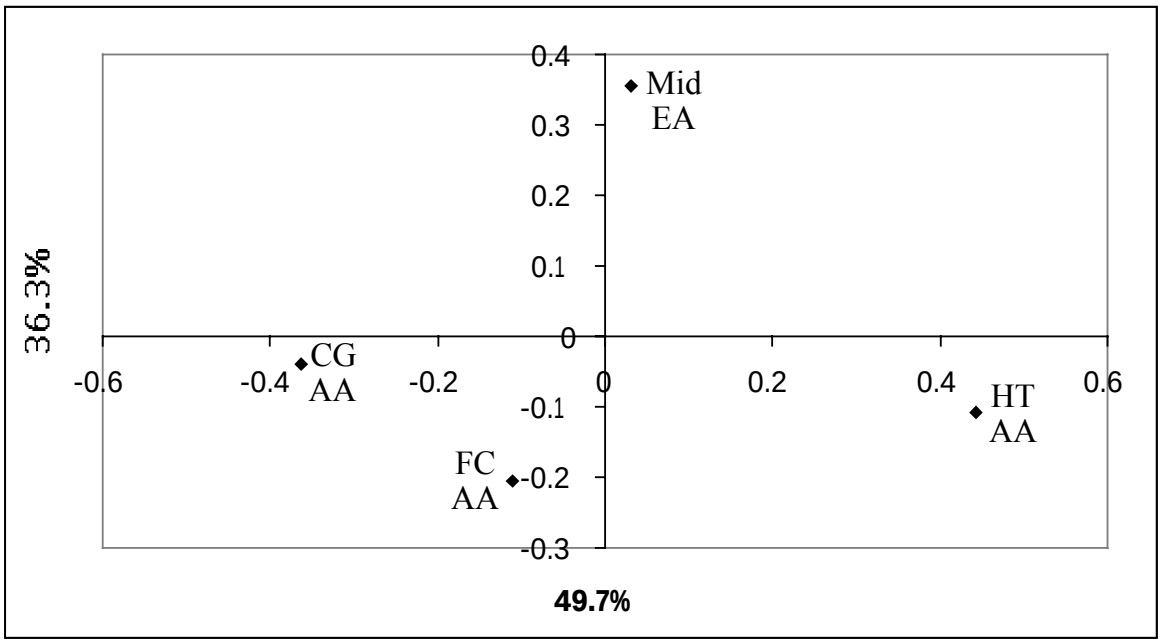

Figure 5.5. First two principal coordinates for MMD results for middle European Americans and selected middle African American collections.

Discussion

Among the African American samples compared here, the closest relationship is between Freedman's Cemetery and Cedar Grove. This is not surprising, as the two cemeteries are in the same geographical region, and share many similarities in mortuary practices and coffin design (Condon et al., 1998; Rose, 1985). The most distant relationship between the three African American samples is between Cedar Grove, which is Southern and rural, and Hamann-Todd, which is Northern and urban. These relationships provide evidence in support of the predictions made about admixture being greatest in northern cities, less in southern cities, and least in the rural South. However, when these groups are contrasted with European Americans of the same time period, the reverse is indicated. The MMD comparisons with middle time period European

Americans increase in distance from Cedar Grove, to Hamann-Todd, to Freedman's Cemetery. This suggests that greater admixture is found in rural southern African Americans than either of their urban counterparts. It may be that greater admixture was occurring in the South, and that the results of admixed people moving to cities and to the North cannot be seen in middle time period collections. It may also be that lighter-skinned African Americans were more likely to migrate north more than darker skinned people, but that dental morphology does not correlate with skin color. One support for this possibility is the relatively low MMD between European Americans and African Americans in the Hamann-Todd collection (MMD 0.2886). These two groups were as related as the individuals buried at Freedman's Cemetery were to the African Americans in the Hamann-Todd collection. Figure 5.5 shows the close relationship between Freedman's Cemetery and Cedar Grove. The figure also suggests the relative dissimilarity between the European Americans and any of the African American samples.

Pseudo-Mahalanobis' D^2

Due to the nature of computing tetrachoric correlations for each trait-by-trait comparison, and the fact that each time a new group is compared new matrices must be created for all samples, fewer results were produced using the Pseudo-Mahalanobis' D^2 than using the mean measure of divergence. Results for the pseudo-D^2 analyses are summarized in Tables 5.10 (maxillary traits) and 5.11 (mandibular traits). When using this statistic, there is no equivalent of the chi-square for MMD, so no test of significance is available. The information in these tables is graphically presented in Figure 5.7, which shows the principal coordinates of the relationships for both maxillary and mandibular D^2

analyses. The percentages at the sides of the figure are the amount of variation explained by each dimension. The variation explained for the maxillary and mandibular data are different.

	Late European American	Middle African American	Middle European American	Early African American	Early European American
Late African American	4.175	7.692	7.775	6.676	17.243
Late European American		4.472	4.563	10.015	10.769
Middle African American			3.184	7.982	8.698
Middle European American				8.303	6.499
Early African American					10.295

Table 5.10. Pseudo-D^2 distances for maxillary traits.

	Late European American	Middle African American	Middle European American	Early African American	Early European American
Late African American	0.507	0.094	0.471	0.122	0.488
Late European American		0.525	0.119	0.601	0.148
Middle African American			0.401	0.122	0.374
Middle European American				0.449	0.000
Early African American					0.410

Table 5.11. Pseudo-D^2 distances for mandibular traits.

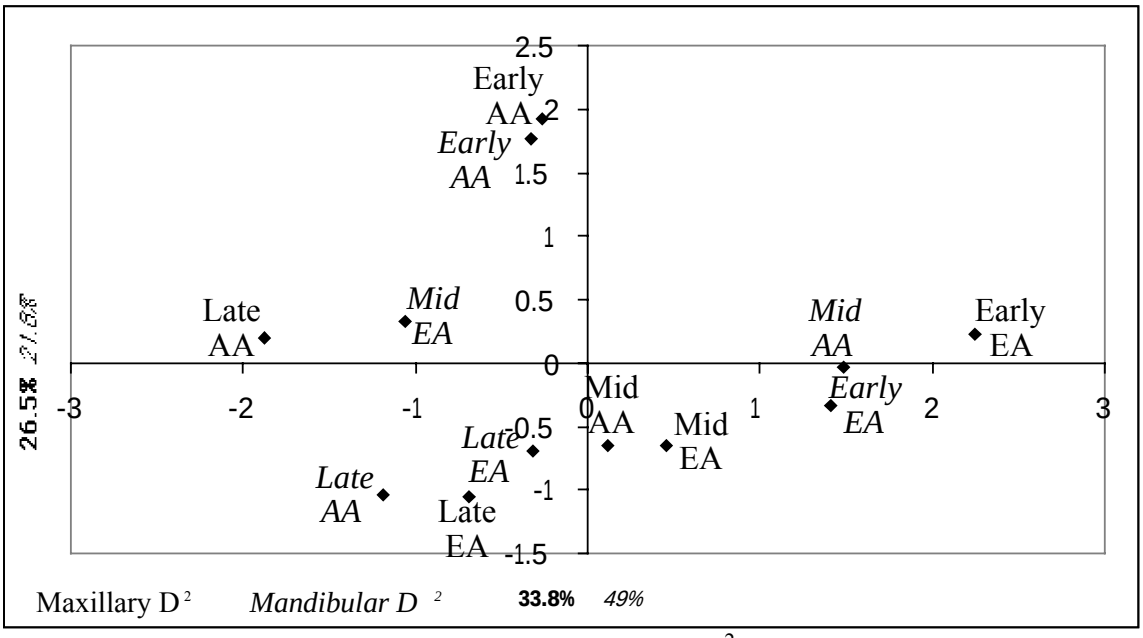

Figure 5.6. First two principal coordinates for pseudo-D^2 analyses.

Discussion

Tables 5.10 and 5.11 show the relationships between European Americans and African Americans for early, middle, and late temporal periods. The results for the maxillary traits indicate that the time differences between groups make a greater contribution to variation than do differences in ancestry. Late and middle African Americans and European Americans cluster most closely, with early African Americans and European Americans being distant from each other and all other groups. The results based on the mandibular trait pseudo-D^2s are more difficult to characterize. As was seen with the MMD analysis, early and middle European American samples are essentially the same group. However, there is a large difference between early and middle African Americans, and a relatively small difference between middle and late African Americans.

While this agrees with the prediction based on change in the African American gene pool slowing down after the Civil War (Davis, 1991), it does not explain the observed similarity of early European Americans and middle African Americans, the smallest distance in the matrix (Figure 5.7). For both maxillary and mandibular traits, the early African Americans are comparatively different from all other groups. However, the early European Americans and middle and late European and African Americans show no discernable pattern.

Procrustes analysis

In order to compare the results from MMD and pseudo-D^2 analyses, a Procrustes transformation was performed on the principal coordinates. The MMDs were recalculated as separate sets of results for maxillary and mandibular traits, in order to be comparable to the pseudo-D^2 computations. These results are given in Tables 5.12 (maxillary traits) and 5.13 (mandibular traits). Figure 5.8 shows the principal coordinates for the information presented in these tables.

Discussion

Tables 5.12 and 5.13 show the similarity between early and middle period European Americans. However, the maxillary traits indicate an unexpected relationship between early European and African Americans. No other result of the current research supports the idea that these groups are not separable. Considering the small sample sizes of the early period American groups, the lack of statistically significant difference is more likely an artifact of small sample size than from any true relationship. Figure 5.8

shows several trends over time, although the meaning of those trends is not evident. For the maxillary data, the African American samples clearly trend left over time. The picture is not as clear for European Americans, based on maxillary traits. The trend of African Americans over time, based on mandibular traits, is in a direction toward the top of the graph, as it is for European Americans.

	Late European American	Middle African American	Middle European American	Early African American	Early European American
Late African American	0.113 (112.94)*	0.074 (83.12)*	0.443 (213.15)*	0.244 (81.39)*	0.402 (142.64)*
Late European American		0.113 (182.50)*	0.231 (143.36)*	0.395 (122.18)*	0.239 (99.27)*
Middle African American			0.222 (182.15)*	0.187 (71.10)*	0.247 (126.86)*
Middle European American				0.292 (66.88)*	0.000 (11.48)
Early African American					0.218 (0.22)

Table 5.12. MMD results based on maxillary traits.

	Late European American	Middle African American	Middle European American	Early African American	Early European American
Late African American	0.507 (367.03)*	0.094 (97.62)*	0.471 (222.98)*	0.122 (35.77)	0.488 (140.86)*
Late European American		0.525 (639.05)*	0.119 (61.77)*	0.601 (142.43)*	0.148 (45.31)*
Middle African American			0.401 (266.32)*	0.122 (37.83)*	0.374 (127.67)*
Middle European American				0.449 (93.32)*	0.000 (9.58)
Early African American					0.441 (70.4)*

Table 5.13. MMD results based on mandibular traits.

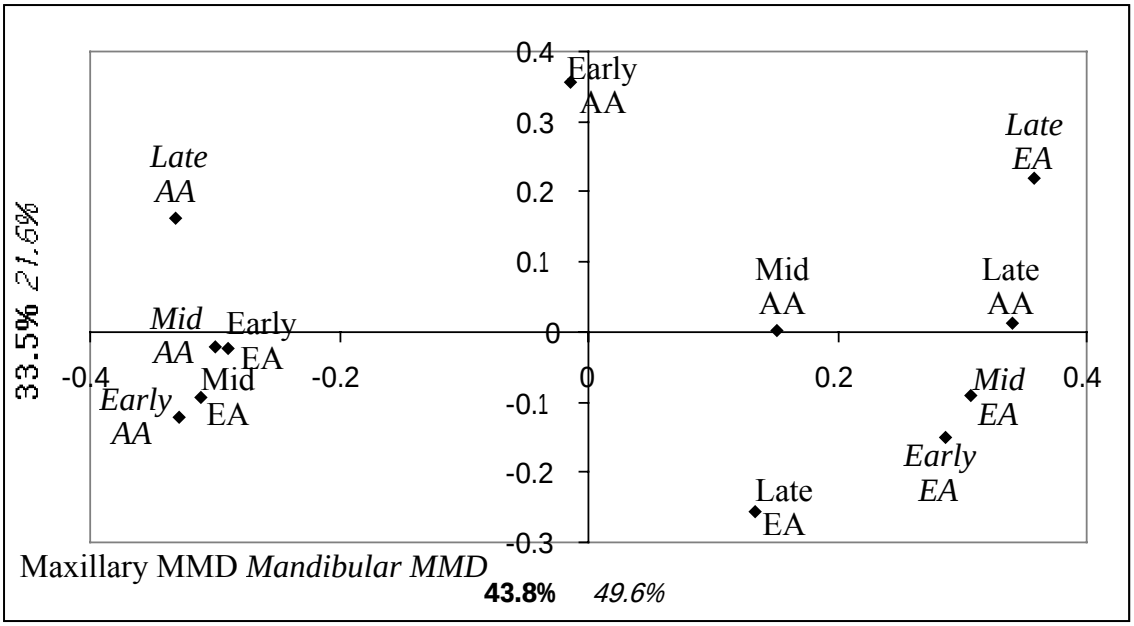

Figure 5.7. First two principal coordinates for MMD analyses, maxillary and mandibular traits considered separately.

It is inappropriate to compare Figure 5.7, that is based on MMD data, to Figure 5.6, based on pseudo-D^2 data. They are of differing scales and rotations. Instead, for comparison, Figures 5.9 and 5.10 show the relationships between the six samples after rotation and scaling of the principal coordinates for MMD and pseudo-D^2, respectively. The coordinates for maxillary MMD results act as a baseline for both tables. Each of the other groups has been redrawn to its best fit, meaning the one that yields the smallest residual.

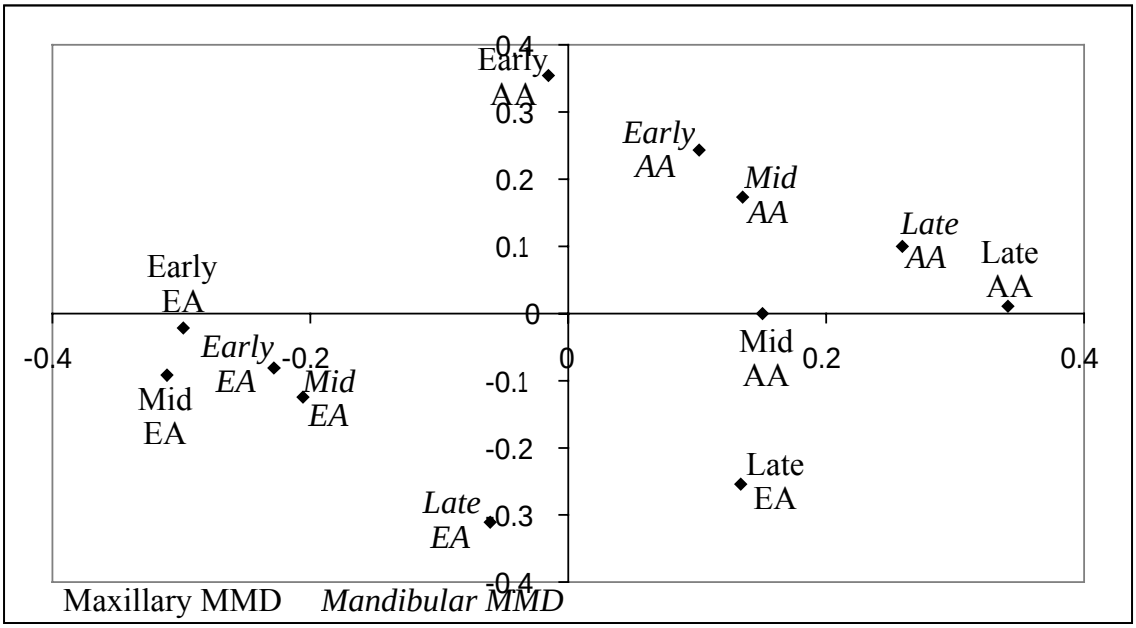

Figure 5.8. First two transformed principal coordinates for maxillary and mandibular MMDs.

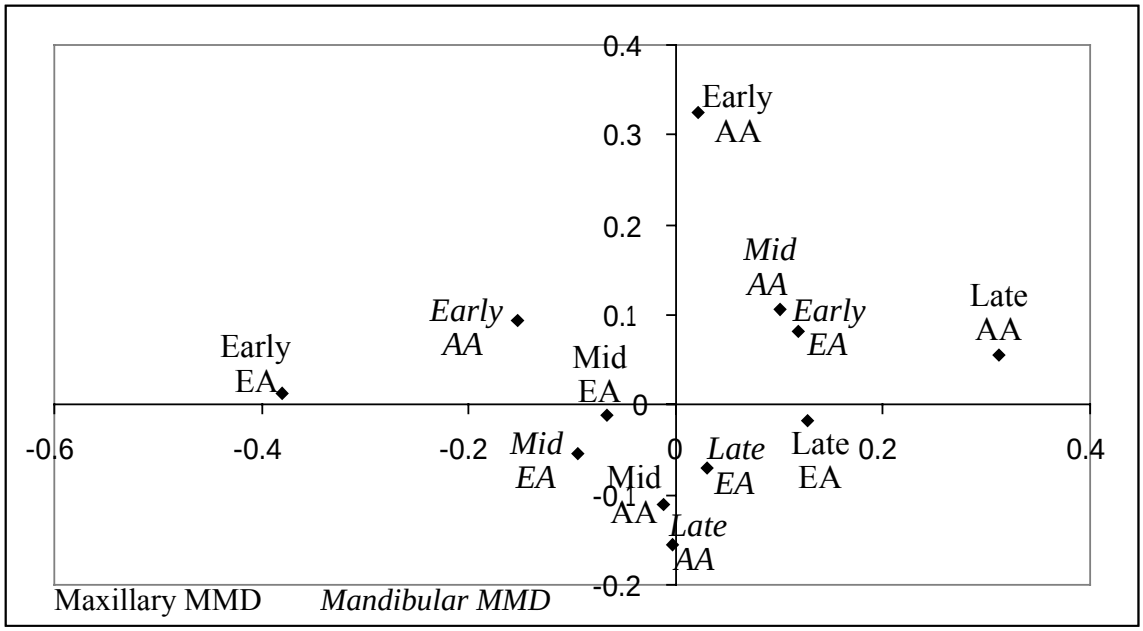

Figure 5.9. First two transformed principal coordinates for maxillary and mandibular psuedo-D^2.

Discussion

In Figure 5.8, the Procrustes transformed maxillary and mandibular MMD results for African Americans cluster together, almost wholly in the upper right quadrant of the graph. The results for the European Americans are more spread out, but still form a distinct group when compared with the African Americans. Descendants of both ancestral groups trend down and to the left over time in the graph. Whether this image indicates that they are becoming more similar to each other is debatable.

The picture is less clear among the Procrustes transformed principal coordinates for maxillary and mandibular pseudo-D^2, shown in Figure 5.9. African Americans are still more to the right of the graph, and European Americans predominate on the left. Early time period samples are still above middle and later samples. After transformation, the two graphs show similar data patterns, although these patterns can be more easily discerned in the MMD results. The results for pseudo-D^2 based on maxillary data follow clear trends, with African American samples becoming lower on the graph over time, and European American results trending toward the left of the graph over time. These trends indicate that the groups became more like each over time. These same trends are not reflected in the graphic representation of the pseudo-D^2 based on mandibular traits. One possible explanation for the lack of trends apparent for mandibular traits might be a lack of differences between the samples studied for these particular traits. In fact, among the traits used for the mandibular pseudo-D^2 analysis, there is half the average trait frequency between groups (5.54%) as there is in the maxillary pseudo-D^2 and MMD (9.95% and 10.19%), and one-quarter as much difference as in mandibular MMD (21.83%).

In Procrustes analysis, the residuals (R^2) are the variation that remains unaccounted for by scaling and rotation of the data points (Gower, 1971). The residuals between all the groups are summarized in Table 5.14. There is no test of significance for R^2, but it can be seen that all the values are relatively small except between the pseudo-D^2 for maxillary and mandibular characteristics. It is possible to simplify this table by performing a principal coordinates analysis for this R^2 matrix and display the relationships in the simplest geometric space. A graph of these coordinates shows relationships between the four methods of determining affinity. Figure 5.10 shows that the two MMD matrices have almost no residual difference. The two pseudo-D^2 matrices are different from each other, but neither is more different from the MMD matrices than the other.

	Mandibular MMD	Maxillary D^2	Mandibular D^2
Maxillary MMD	0.131	0.118	0.426
Mandibular MMD		0.336	0.640
Maxillary D^2			7.852

Table 5.14. Residuals after Procrustes transformation.

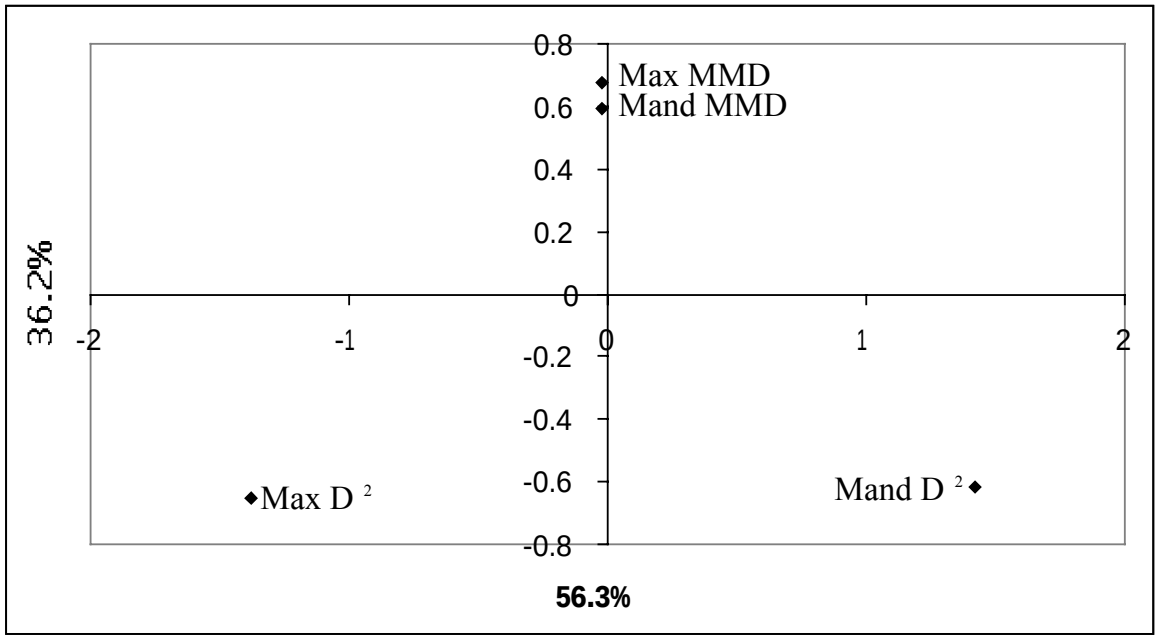

Figure 5.10. First two principal coordinates of residuals from Procrustes transformation.

Forensic Analysis

The data collected for this research can be used not only to study historical patterns of genetic relationships between groups, but also to help identify the socially determined race allocation of an unknown individual of either African American or European American ancestry. Identification of the race that a person would have been ascribed during their life is an important factor in individualizing human remains, limiting the pool of missing persons to which a match could be made for unidentified human remains. For this portion of the analysis, traits were chosen that had the most diverse frequencies in the two ancestral groups considered. The characteristics chosen

are listed in Table 5.15, along with their breakpoints for trait presence. Using these traits, probability tables based on samples of modern African Americans and European Americans were created to determine an individual's social race. Only data from modern samples were included.

UCTD 0-1 / 2-6	LP3LC 0-3 / 4-9	LP4LC 0-2 / 3-9	LM1DW 0 / 1-3
LM1MT 0 / 1	LM2C5 0 / 1-5	LM3C5 0 / 1-5	LM1C7 0 / 1-4

Table 5.15. Traits used in forensic probability tables (Appendix D) and their breakpoints.

The tables based on this analysis can be found in Appendix D. Results are presented as Bayesean predictions (BP) as well as predictions based on logistic regression probability (LP) (Bernardo and Smith, 1994; Everitt and Dunn, 1991; Hoffman and Duncan, 1988). Bayesean prediction is not considered appropriate for generalizing predictions from samples to populations (Bernardo and Smith, 1994). Logistic regression predictions are applicable to populations, but cannot be made if there are any zero frequencies for any of the trait combinations considered (Everitt and Dunn, 1991). Analysis was done with dichotomized character states for two, three and four trait combinations. It was found that socially ascribed race can be determined with upwards of 90% correct allocation using particular trait combinations.

To use these results, as many as possible of the eight traits considered should be observed in the dentition of an unknown individual. Observations should be scored using

the ASU dental anthropology system (Turner et al. 1991), then dichotomized according to Table 5.15. Then, combinations of the traits should be compared to the tables in Appendix D. It is preferable to use probabilities computed through logistic regression, as these are intended to be generalized to the population from which the samples were drawn. An assessment of social race should only be made if the probabilities for the particular unknown individual are consistently in agreement about the racial affiliation. The tables do not provide probabilities for some trait combinations. This is because those combinations did not exist in the sample data.

Testing the forensic probability method

The method of determining social race using dental morphology developed in the present study was tested using casts from the OSU dental cast collection. Ten casts were drawn from the collection, five African Americans and five European Americans. The casts were made while the individuals were alive, and their social race affiliation was documented at the time of casting. The dentitions of the European Americans used in this test were not included in the research for this dissertation. The African Americans dentitions used for this test are from the Gullah collection. They were studied for this project, but they are not included in the data from which the forensic probability tables were made. The casts were not chosen by this author, but by a fellow graduate student.

The method that was used for this test is exemplified here by the description and analysis of OSU dental cast T138. Table 5.16 shows the presence (+) and absence (-) scores for the eight forensic traits for this dentition. Notice that three traits were

unobservable (?) in the table. This is a likely situation in any forensic or historical archaeology case.

Trait	Score	Trait	Score	Trait	Score	Trait	Score
UCTD	+	LP3LC	-	LP4LC	-	LM1DW	?
LM1MT	=	LM2C5	-	LM3C5	?	LM1C7	-

Table 5.16. Scores for forensic traits for OSU dentition T138.

The combination listed above of presence and absence scores for the observable traits was compared with each of the forensic tables D.2, D.3, and D.4 so far as possible. First, the scores were compared with the four-trait probabilities in Table D.4. Four comparisons could be made, all based on Bayesian probabilities. All four comparisons indicated that the individual T136 is European American, with probabilities ranging from 0.78 to 0.91. Next, the individual was compared with the three-trait probabilities in table D.3. Ten comparisons were possible, three based on logistic regression and seven based on Bayesian probabilities. The three logistic regression probabilities all indicated that the individual was likely European American, though with probabilities ranging from only 0.56 to 0.71. The seven Bayesian probabilities ranged from 0.80 to 0.95, all in favor of European American ancestry. Lastly, the individual's scores were compared with the two-trait probabilities listed in Table D.2. Nine comparisons could be made, seven are logistic regression probabilities and two are Bayesian probabilities. The logistic regression probabilities all indicate that the individual is European American, with probabilities ranging from 0.54 to 0.96. Of the two Bayesian probabilities, one indicates

that the individual is likely European American (0.90 probability), and the other indicates that the individual is likely African American (0.96 probability). As this is the only comparison indicating that the individual is African American, it is viewed as an anomalous result, one that could occur due to chance alone. The determination can be made, then, that the individual is most likely European American, a determination later found to be accurate. Using the method described above, nine out of ten of the test dentitions were correctly ascribed to the appropriate social race category.

CHAPTER 6

CONCLUSIONS

The primary goal of this research was to test the hypothesis that, during the last 400 years, the genetically determined dental morphology of African Americans has become genetically intermediate between western Europeans and West Africans. This hypothesis lead to several predictions about the pattern and rate of flow of genes from the European gene pool into the African American gene pool. The secondary goal of the research was to create probability tables for forensic and historical archaeological application in determining ancestry, European American or African American, of an unknown individual, from his or her dental morphology alone.

To test the hypothesis and predictions and produce the probability tables, the dental morphological characteristics of 1,300 dentitions from western Europeans, West Africans, South Africans, and Americans of European and African descent were recorded. The data were analyzed with two statistical tools for measuring biological distance, the mean measure of divergence (MMD) and pseudo-Mahalanobis' D^2. The results of these analyses were compared using Procrustes transformation. In addition, Bayesian prediction and logistic regression were used to create probability tables for determining ancestry of unknown individuals.

Statistical considerations

A side benefit of this project is the comparison of two different statistics that share the same application. MMD is commonly used in biological distance studies using dental morphology data. However, this tool is limited, because it requires that traits be uncorrelated. On the other hand, pseudo-Mahalanobis' D^2 requires the traits to be correlated (Mahalanobis, 1936), and it is more cumbersome to compute.

Overall, there is very good agreement between the biological distance matrices generated using MMD and pseudo-Mahalanobis' D^2 statistics. Both statistics have their place in the analysis of biological distance, especially when using dental morphological characteristics. The MMD and pseudo-D^2 are limited by the data used in the analysis. If there is little difference between samples for the characteristics in question, the results will show small distances; if the differences are large for those particular characteristics, the distances will be large. A evaluation trait frequencies and intercorrelation should be made before attempting any measure of affinity.

When there are many traits available for analysis and they are not correlated, MMD is appropriate. When the data consist of a relatively few, correlated traits, a pseudo-Mahalanobis' D^2 is more accurately applied, as it makes no assumption about a lack of correlation between traits (Konigsberg, 1990; Mahalanobis, 1936). In a large study, the use of both statistics may allow analysis of more of the collected data. If all things are equal and either statistic is applicable, MMD is simpler to use. As it is much more frequently used (Greene, 1982; Lukacs and Hemphill, 1991; Haeussler and Turner, 1992; Irish, 1993, 1997) it is also more widely comparable.

The hypothesis and predictions

The results of this research support the main hypothesis; African Americans have become genetically closer to the average of western Europeans and West Africans since the two groups came into contact in the American colonies and later, the United States. Dental morphology reflects this change. The difference between West Africans and African Americans doubles in each time period, early, middle and late. African Americans are progressively becoming less like their West African ancestors. Also, when comparing contemporaneous early, middle, and late European Americans and African Americans, the difference shrinks over time. African Americans have tended toward the average of West Africans and western Europeans, and that this microevolutionary pattern is discernible using dental morphology. These conclusions are most clearly seen in the MMD results, but they are also generally true for pseudo-D^2 results.

While the current research supports the main hypothesis, the results give mixed support for the secondary predictions. Based on historical accounts, it was predicted that the flow of European derived genes diminished in the century following the Civil War and in the Jim Crow era (Davis, 1991; Williamson, 1980). The evidence regarding this prediction is equivocal. Both the MMD and pseudo-D^2 results show the distances between early and middle African Americans to be greater than the distance between middle and late African Americans. This would indicate that more change occurred between early and middle time periods than middle to late. However, comparisons between African Americans and European Americans indicate that African American's

progress towards intermediacy between their ancestral groups was progressive over time. This second observation may be due to the reproduction of admixed individuals within the African American population. Or, it may be that changes in the European American gene pool skewed the comparisons.

A related prediction was made about patterns of migration within the United States of admixed African Americans. Historical sources indicate that African Americans with lighter skin were more likely to migrate to urban and northern areas than their counterparts with darker skin (Davis, 1991; Williamson, 1980). If one makes the assumption that skin color difference is related to genetic admixture from European Americans, it would seem that individuals with more admixture were more likely to migrate than those who were less admixed. This prediction was tested by comparing samples of contemporaneous African Americans from rural Southern, urban Southern, and urban Northern regions. Once again, comparisons among the African American samples support the hypothesis. The two Southern groups, urban and rural, are closely related, and the greatest distance is between the rural Southern and urban northern sample. However, comparisons of these three groups with European Americans of the same time period do not lend further support. Instead, the closest relationship is between European Americans and the rural southern sample of African Americans. This relationship runs counter to prediction, and would seem to indicate that admixture is greatest in African Americans that did not migrate out of rural areas. An alternative explanation is that the migration of more admixed people described by historians cannot be seen in the rural Southern sample used in this study because the individuals in it died

before migrations took place. A series of samples that dated to a more recent time period would be necessary to address this supposition.

A prediction specific to the Gullah is that they would show little admixture and be similar to the West African samples in terms of dental morphology. This prediction was based on linguistic, cultural, anthropometric, and genetic studies that indicate low admixture in the Gullah (Pollitzer, 1999; Rogers, 2000). Previous researchers in all of these fields disagree about the geographic origins of the Gullah in West Africa (Littlefield, 1981; Pollitzer, 1993, 1999; Rogers, 2000), but there is little argument about the minor amount of admixture that that has occurred between them and European Americans.

The results of the present research show that the Gullah are statistically significantly different from West Africans, as well as African American samples from all time periods. The MMD for the Gullah and West African comparison was larger than expected (0.4361, chi-square = 329.91) and larger than for the comparisons with early, middle, or late African Americans. It is also larger than any of the comparisons of early, middle, and late African Americans with West Africans, when the Gullah are not included.

Some authors have suggested that the Gullah, unlike other African Americans, are not descended from people drawn from all over West Africa. Instead, they may be from particular areas, such as Senegal, Guinea, and Sierra Leone. This area was known as the "rice coast," and slaves brought from this area had special knowledge about the rice agriculture practiced in the outer banks where the Gullah live (Littlefield, 1981; Richardson, 1991). It may be that the large distance between the West African and

Gullah samples, described in the current research, is due to founder effect of individuals coming from a subset of the West African region, rather than the whole. However, a recent genetic and anthropometric analysis (Rogers, 2000) disputes the conclusion that the Gullah clearly descend from any specific part of West Africa. For now, it seems the question of Gullah origins remains unanswered.

A final prediction was made concerning the identification of dental characteristics that would be useful in developing probability tables for use in determining ancestry in unknown individuals. Eight such characteristics were chosen and evaluated, and were used to create tables that could be applied in forensic and historical archaeological circumstances. Using observations on the presence or absence of the eight dental traits of an unknown individual, the table provides probabilities of the individual being either of African American or European American ancestry. A test using dentitions of known social racial affiliation, but not included in the samples used to create the probability tables, showed the method to be accurate in nine of ten dentitions.

While these eight traits can be used to determine what race an individual might be ascribed, only these eight traits are useful for this purpose. With right and left observations combined, 69 separate observations of trait occurrences were possible for each individual dentition included in this study. Only 11.6% of the traits considered are different enough between African Americans and European Americans to be useful in determining affiliation of an individual. This observation points out the overwhelming similarities between these two groups, at least in terms of dental morphology.

Unexpected results and directions for the future

An interesting factor that was not anticipated was the changes over time in the dental morphology of European Americans. The sample from western Europe is more similar to the overall sample of African Americans than it is to the overall sample of European Americans. Historical studies indicate that the admixture of European genes into the African American gene pool seems to have come primarily prior to the Civil War (Williamson, 1980). This contention is supported by the present study. After the Civil War, the preponderance of Europeans immigrating to the United States were from eastern and southern Europe (Jones, 1992). These areas were excluded from the western European sample used in the present analysis. It seems that this change in migratory patterns altered the results relating to late time period European Americans. While African Americans over time have genetically become closer to the average of their two founding populations, dental morphology indicates that the pool of individuals who today are thought of as Americans of European heritage is of a somewhat different heritage than was true in previous generations. Contrary to prior thinking, new research indicates that it is also reflected the craniometrics of European immigrants to this country (Sparks and Jantz, 2002). Further comparisons of the dental morphology of modern European Americans and their European ancestors would be a valuable area of inquiry.

There are several additional avenues of research that lead from the current project. New statistical techniques, such as those derived from fuzzy set theory (McNeill and Freiberger, 1993), could be employed to better understand the patterns of social race affiliation in the United States. Fuzzy sets are ones in which membership is possible to a

degree, rather than all or not at all, as is the case with traditional "crisp sets" (McNeill and Freiberger, 1993; Willermet and Hill, 1997). An individual could be said to be affiliated with European Americans to a degree of 0.35, African Americans to a degree of 0.45, and affiliated with an unknown group to a degree of 0.20. Combined with the methods used in the current research, fuzzy set statistics may lead to a new way of thinking about the biological implications of the social phenomenon of race.

The techniques described herein could also be applied to the study of social race ascription and its relationship to biology in other areas of the world that do not use a simplistic racial scheme. It would be interesting to investigate how more complexly graduated social race structures impact on patterns of admixture. Latin American cultures recognize many more levels of admixture than does North America (Graham, 1990; Mörner, 1967). Whether these levels are purely social or reflect discernible biological differences is unknown.

The bulk of the present study has been about investigating the differences among Africans, African Americans, Europeans, and European Americans as reflected in their dental morphology. However, this exploration of the differences among these groups has served to point out the similarities among them as well. Several dental traits, such as disto-sagittal ridge and double shoveling as seen at low frequencies in all the samples studied. Other traits, such as upper second molar hypocone and lower first molar cusp five are observable with high frequency in all groups. Additionally, most traits were found at frequencies in both groups similar enough to preclude them from utility in a forensic context. While enough distinctiveness exists among these groups to allow the

possibility of the current research, it could be said that the majority of the data presented serves to indicate the overwhelming similarity of these groups.

The results of the current study show that cultural attitudes and historical events can have major impact on the microevolution of a population. Studies such as this one have a unique advantage, and a unique responsibility, when compared to studies of prehistoric peoples. More information is available about the cultural and historical factors that influence changes of modern populations in the historic era. It is possible to have an understanding of prevailing cultural beliefs, the behaviors that resulted from those beliefs, and the genetic consequences of those behaviors, as they relate to morbidity, mortality, fertility, and mating patterns. It behooves the researchers of historic populations to incorporate this information into the development of their research questions and the interpretation of their results. Humans, like all other species, are continually evolving. Unlike other species, our evolution is greatly affected by our culture. It is necessary to understand the influence of culture on microevolution to understand the past and future of human evolution.

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APPENDIX A

TRAIT FREQUENCIES

trait	N	freq %	W
DIAS	431	26.8	0.269
WING	407	2.9	2.978
UI1SS	533	8.1	1.077
UI2SS	551	33.4	1.217
UCSS	544	24.8	1.023
UI1LC	547	24.1	0.846
UI1DS	549	0.5	0.040
UI2DS	555	5.6	0.074
UI2PS	582	4.3	0.043
UM3PS	417	1.0	0.010
UI1IG	523	0.8	0.016
UI2IG	130	8.7	0.229
UI2CA	1.2	7.0	0.012
UM3CA	445	2.9	0.029
UI1TD	535	42.8	1.205
UI2TD	530	54.5	1.598
UCTD	529	79.0	2.804
UCMR	497	16.9	0.251
UCDR	484	49.4	1.267
UP3MD	536	34.0	0.656
UP4MD	521	26.1	0.533
UP3TC	565	0.4	0.004
UP4TC	559	0.2	0.002
UP3DS	557	0.4	0.016
UM1MC	553	45.2	4.464
UM2MC	547	15.9	4.080
UM3MC	388	4.1	3.507
UM1HC	551	35.2	4.361
UM2HC	531	93.8	3.162
UM3HC	374	67.6	1.907
UM1C5	522	42.3	0.635
UM2C5	509	40.3	0.660
UM3C5	357	42.0	0.857
UM1CB	526	66.0	2.815
UM2CB	533	21.4	0.588
UM3CB	380	8.7	0.256
UM1PR	454	2.0	0.020
UM2PR	477	2.3	0.055
UM3PR	273	2.6	0.078
LI1SS	555	14.8	0.157
L12SS	570	18.9	0.206
LI1CA	581	0.2	0.002
LM3CA	441	3.2	0.032
LCDR	466	28.8	0.804
LP3LC	573	82.9	5.707
LP4LC	564	97.9	6.626
LM1AF	434	37.6	1.204
LM1GP	396	90.4	1.111
LM2GP	472	64.4	1.406
LM3GP	365	37.8	1.644
LM1CN	464	19.6	5.172
LM2CN	477	57.9	4.729
LM3CN	358	87.7	5.248
LM1DW	387	48.3	0.841
LM1MT	390	28.5	0.283
LM2MT	488	23.2	0.232
LM3MT	360	18.1	0.180
LM1PS	445	31.0	0.341
LM2PS	481	21.8	0.242
LM3PS	344	9.9	0.237
LM1C5	462	97.8	3.909
LM2C5	476	57.6	1.723
LM3C5	355	87.6	3.330
LM1C6	460	19.3	0.352
LM2C6	473	16.5	0.334
LM3C6	354	37.3	0.887
LM1C7	454	44.5	0.902
LM2C7	510	21.8	0.337
LM3C7	364	20.3	0.358

N= number of observations
Freq %= frequency of trait presence
W= weighted average in ASU categorical scale

Table A.1. All AA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	10	40.0	LI1SS	22	27.3
WING	10	10.0	L12SS	26	19.2
UI1SS	15	6.7	LI1CA	28	0.0
UI2SS	19	31.6	LM3CA	24	4.2
UCSS	17	35.3	LCDR	18	61.1
UI1LC	18	16.7	LP3LC	26	73.1
UI1DS	18	0.0	LP4LC	24	91.7
UI2DS	19	21.1	LM1AF	16	62.5
UI2PS	23	4.3	LM1GP	19	89.5
UM3PS	26	0.0	LM2GP	23	56.5
UI1IG	19	0.0	LM3GP	16	43.8
UI2IG	23	13.0	LM1CN	19	47.4
UI2CA	32	0.0	LM2CN	19	68.4
UM3CA	29	10.3	LM3CN	16	0.0
UI1TD	19	26.3	LM1DW	17	4.12
UI2TD	23	39.1	LM1MT	17	11.8
UCTD	23	60.9	LM2MT	21	47.6
UCMR	16	6.3	LM3MT	16	31.3
UCDR	18	55.6	LM1PS	19	68.4
UP3MD	22	63.6	LM2PS	19	36.8
UP4MD	24	45.8	LM3PS	14	14.3
UP3TC	25	4.0	LM1C5	19	94.7
UP4TC	25	0.0	LM2C5	68	19.0
UP3DS	24	0.0	LM3C5	16	100
UM1MC	28	85.7	LM1C6	18	44.4
UM2MC	29	44.8	LM2C6	19	26.3
UM3MC	25	12.0	LM3C6	17	23.5
UM1HC	28	78.6	LM1C7	21	76.2
UM2HC	26	96.2	LM2C7	22	36.4
UM3HC	21	61.9	LM3C7	15	46.7
UM1C5	24	70.8			
UM2C5	22	63.6			
UM3C5	20	70.0			
UM1CB	25	84.0			
UM2CB	28	32.1			
UM3CB	22	9.1			
UM1PR	22	4.5			
UM2PR	29	10.3			
UM3PR	24	4.2			

Table A.2. Early AA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	36	8.3	LI1SS	371	10.5
WING	42	2.4	L12SS	381	16.3
UI1SS	358	7.5	LI1CA	389	0.0
UI2SS	372	32.5	LM3CA	373	3.5
UCSS	368	24.5	LCDR	292	17.5
UI1LC	368	28.3	LP3LC	391	81.8
UI1DS	370	0.5	LP4LC	381	98.4
UI2DS	375	7.2	LM1AF	294	40.8
UI2PS	395	4.3	LM1GP	288	91.7
UM3PS	359	0.6	LM2GP	337	64.4
UI1IG	375	1.1	LM3GP	321	38.9
UI2IG	383	9.1	LM1CN	311	19.0
UI2CA	401	0.7	LM2CN	348	56.9
UM3CA	379	2.1	LM3CN	322	87.0
UI1TD	359	47.4	LM1DW	252	51.6
UI2TD	357	57.7	LM1MT	262	34.7
UCTD	354	78.5	LM2MT	333	19.8
UCMR	334	12.6	LM3MT	309	16.8
UCDR	308	40.3	LM1PS	293	38.2
UP3MD	359	37.0	LM2PS	335	27.2
UP4MD	342	27.8	LM3PS	303	9.9
UP3TC	384	0.3	LM1C5	309	98.1
UP4TC	379	0.3	LM2C5	347	56.5
UP3DS	379	0.3	LM3C5	319	86.8
UM1MC	366	44.0	LM1C6	308	18.8
UM2MC	380	13.7	LM2C6	344	16.9
UM3MC	345	3.8	LM3C6	318	37.7
UM1HC	365	34.8	LM1C7	302	42.1
UM2HC	375	94.1	LM2C7	357	73.0
UM3HC	338	69.2	LM3C7	325	19.1
UM1C5	346	45.7			
UM2C5	365	41.1			
UM3C5	325	40.9			
UM1CB	343	65.3			
UM2CB	366	20.2			
UM3CB	338	8.9			
UM1PR	277	2.2			
UM2PR	322	2.2			
UM3PR	235	2.6			

Table A.3. Middle AA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	87	33.3	LI1SS	109	26.6
WING	104	2.9	L12SS	30	110
UI1SS	110	9.1	LI1CA	110	0.9
UI2SS	107	35.5	LM3CA	22	0.0
UCSS	106	18.9	LCDR	107	48.6
UI1LC	110	15.5	LP3LC	101	89.1
UI1DS	110	0.0	LP4LC	106	96.2
UI2DS	107	0.0	LM1AF	95	26.3
UI2PS	109	4.6	LM1GP	67	88.1
UM3PS	19	5.3	LM2GP	84	71.4
UI1IG	83	0.0	LM3GP	14	21.4
UI2IG	41	7.3	LM1CN	107	15.9
UI2CA	110	3.6	LM2CN	81	59.3
UM3CA	20	0.0	LM3CN	8	87.5
UI1TD	106	33	LM1DW	90	46.7
UI2TD	97	54.6	LM1MT	83	15.7
UCTD	99	83.8	LM2MT	99	28.3
UCMR	94	21.3	LM3MT	17	29.4
UCDR	107	71.0	LM1PS	100	8.0
UP3MD	102	23.5	LM2PS	98	6.1
UP4MD	107	25.2	LM3PS	12	8.3
UP3TC	102	0.0	LM1C5	107	97.2
UP4TC	106	0.0	LM2C5	81	59.3
UP3DS	101	0.0	LM3C5	8	87.5
UM1MC	110	34.5	LM1C6	107	15.9
UM2MC	100	18.0	LM2C6	81	11.1
UM3MC	11	0.0	LM3C6	7	42.9
UM1HC	109	25.7	LM1C7	104	45.2
UM2HC	93	92.5	LM2C7	100	21.0
UM3HC	9	44.4	LM3C7	10	10.0
UM1C5	104	32.7			
UM2C5	88	37.5			
UM3C5	7	28.6			
UM1CB	109	73.4			
UM2CB	97	27.8			
UM3CB	10	0.0			
UM1PR	107	0.9			
UM2PR	94	0.0			
UM3PR	9	0.0			

Table A.4. Late AA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	0		LI1SS	314	7.6
WING	0		L12SS	318	11.0
UI1SS	316	7.3	LI1CA	321	0.0
UI2SS	315	30.5	LM3CA	309	0.6
UCSS	326	22.7	LCDR	256	15.2
UI1LC	318	27.7	LP3LC	320	83.4
UI1DS	322	0.0	LP4LC	319	99.1
UI2DS	316	2.2	LM1AF	253	41.5
UI2PS	325	4.3	LM1GP	245	92.2
UM3PS	301	0.7	LM2GP	289	63.7
UI1IG	315	1.3	LM3GP	272	40.4
UI2IG	315	9.2	LM1CN	264	18.9
UI2CA	329	0.9	LM2CN	298	56.0
UM3CA	310	0.3	LM3CN	274	86.5
UI1TD	320	49.1	LM1DW	55	22.0
UI2TD	310	58.1	LM1MT	229	34.1
UCTD	307	80.5	LM2MT	293	19.1
UCMR	298	11.7	LM3MT	268	16.0
UCDR	273	40.7	LM1PS	252	36.1
UP3MD	311	36.0	LM2PS	288	22.9
UP4MD	298	25.8	LM3PS	261	8.8
UP3TC	325	0.0	LM1C5	263	98.9
UP4TC	319	0.3	LM2C5	300	55.7
UP3DS	324	0.3	LM3C5	274	86.5
UM1MC	306	41.2	LM1C6	264	18.6
UM2MC	316	7.6	LM2C6	299	15.7
UM3MC	285	1.4	LM3C6	273	36.3
UM1HC	306	29.7	LM1C7	259	41.7
UM2HC	314	94.6	LM2C7	306	19.3
UM3HC	281	67.3	LM3C7	277	16.6
UM1C5	299	44.1			
UM2C5	310	40.3			
UM3C5	275	39.6			
UM1CB	291	65.6			
UM2CB	309	20.7			
UM3CB	285	9.1			
UM1PR	228	2.6			
UM2PR	266	1.9			
UM3PR	188	2.1			

Table A.5. Freedman's Cemetery trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	23	8.7	LI1SS	39	35.9
WING	29	3.4	L12SS	42	57.1
UI1SS	21	14.3	LI1CA	46	0.0
UI2SS	35	42.9	LM3CA	44	25.0
UCSS	20	50.0	LCDR	19	26.3
UI1LC	28	50.0	LP3LC	45	80.0
UI1DS	26	3.8	LP4LC	39	97.4
UI2DS	36	50.0	LM1AF	24	54.2
UI2PS	44	4.5	LM1GP	28	89.3
UM3PS	34	0.0	LM2GP	29	62.1
UI1IG	37	0.0	LM3GP	31	22.6
UI2IG	43	7.0	LM1CN	29	24.1
UI2CA	45	0.0	LM2CN	30	73.3
UM3CA	44	15.9	LM3CN	30	86.7
UI1TD	20	25.0	LM1DW	19	31.6
UI2TD	25	48.0	LM1MT	20	55
UCTD	24	41.7	LM2MT	22	40.9
UCMR	15	13.3	LM3MT	26	26.9
UCDR	19	36.8	LM1PS	22	54.5
UP3MD	28	60.7	LM2PS	27	74.1
UP4MD	24	62.5	LM3PS	25	24
UP3TC	35	2.9	LM1C5	28	92.9
UP4TC	37	0.0	LM2C5	27	74.1
UP3DS	32	0.0	LM3C5	27	85.2
UM1MC	36	69.4	LM1C6	26	26.9
UM2MC	38	52.6	LM2C6	25	28.0
UM3MC	36	22.2	LM3C6	27	51.9
UM1HC	36	80.6	LM1C7	26	46.2
UM2HC	37	91.9	LM2C7	29	37.9
UM3HC	36	77.8	LM3C7	30	46.7
UM1C5	28	71.4			
UM2C5	32	59.4			
UM3C5	31	58.1			
UM1CB	30	63.3			
UM2CB	33	15.2			
UM3CB	32	6.3			
UM1PR	29	0.0			
UM2PR	33	6.1			
UM3PR	30	6.7			

Table A.6. Hamann-Todd AA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	78	32.1	LI1SS	99	26.3
WING	95	1.1	L12SS	100	31.0
UI1SS	100	7	LI1CA	100	1.0
UI2SS	97	35.1	LM3CA	21	0.0
UCSS	97	17.5	LCDR	98	52.0
UI1LC	100	14.0	LP3LC	92	90.2
UI1DS	100	0.0	LP4LC	99	96.0
UI2DS	97	0.0	LM1AF	87	24.1
UI2PS	99	5.1	LM1GP	61	93.4
UM3PS	18	5.6	LM2GP	77	70.1
UI1IG	74	0.0	LM3GP	14	21.4
UI2IG	32	6.3	LM1CN	98	14.3
UI2CA	100	4.0	LM2CN	75	58.7
UM3CA	19	0.0	LM3CN	8	87.5
UI1TD	96	33.3	LM1DW	83	47.0
UI2TD	87	57.5	LM1MT	76	15.8
UCTD	92	84.8	LM2MT	92	27.2
UCMR	89	21.3	LM3MT	16	25.0
UCDR	99	74.7	LM1PS	91	6.6
UP3MD	93	24.7	LM2PS	92	4.3
UP4MD	99	25.3	LM3PS	12	8.3
UP3TC	93	0.0	LM1C5	98	98.0
UP4TC	98	0.0	LM2C5	75	58.7
UP3DS	92	0.0	LM3C5	8	87.5
UM1MC	100	28.0	LM1C6	98	14.3
UM2MC	93	14.0	LM2C6	75	10.7
UM3MC	11	0.0	LM3C6	7	42.9
UM1HC	99	19.2	LM1C7	95	44.2
UM2HC	87	92.0	LM2C7	93	19.4
UM3HC	9	44.4	LM3C7	9	11.1
UM1C5	94	30.9			
UM2C5	82	36.6			
UM3C5	7	28.6			
UM1CB	99	71.7			
UM2CB	90	25.6			
UM3CB	9	0.0			
UM1PR	98	0.0			
UM2PR	88	0.0			
UM3PR	8	0			

Table A.7. UT Dental AA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	50	26.0	LI1SS	53	15.1
WING	51	2.0	L12SS	53	15.1
UI1SS	50	10.0	LI1CA	54	0.0
UI2SS	53	35.8	LM3CA	22	0.0
UCSS	53	35.8	LCDR	49	40.8
UI1LC	51	15.7	LP3LC	55	83.6
UI1DS	51	2.0	LP4LC	53	100.0
UI2DS	54	0.0	LM1AF	29	27.6
UI2PS	55	3.6	LM1GP	22	81.8
UM3PS	13	7.7	LM2GP	28	50.0
UI1IG	46	0.0	LM3GP	14	21.4
UI2IG	37	2.7	LM1CN	27	22.2
UI2CA	55	0.0	LM2CN	29	58.6
UM3CA	17	11.8	LM3CN	12	91.7
UI1TD	51	37.3	LM1DW	28	28.6
UI2TD	53	39.6	LM1MT	28	17.9
UCTD	53	81.1	LM2MT	35	25.7
UCMR	53	39.6	LM3MT	18	16.7
UCDR	51	58.8	LM1PS	33	15.2
UP3MD	53	20.8	LM2PS	29	3.4
UP4MD	48	6.3	LM3PS	15	6.7
UP3TC	54	0.0	LM1C5	27	100.0
UP4TC	49	0.0	LM2C5	29	58.6
UP3DS	53	1.9	LM3C5	12	91.7
UM1MC	49	55.1	LM1C6	27	22.2
UM2MC	38	10.5	LM2C6	29	20.7
UM3MC	7	0.0	LM3C6	12	41.7
UM1HC	49	34.7	LM1C7	27	44.4
UM2HC	37	91.9	LM2C7	31	29.0
UM3HC	6	33.3	LM3C7	14	28.6
UM1C5	48	25.0			
UM2C5	34	23.5			
UM3C5	5	20.0			
UM1CB	49	44.9			
UM2CB	42	9.5			
UM3CB	10	10.0			
UM1PR	48	2.1			
UM2PR	32	3.1			
UM3PR	5	0.0			

Table A.8. Gullah trait frequencies.

trait	N	freq %	W
DIAS	187	12.3	0.123
WING	216	1.9	3.104
UI1SS	221	3.2	0.92
UI2SS	223	19.7	0.892
UCSS	231	6.9	0.562
UI1LC	233	18.9	0.726
UI1DS	228	1.3	0.078
UI2DS	232	3.9	0.048
UI2PS	257	1.9	0.019
UM3PS	112	0.9	0.009
UI1IG	222	1.8	0.031
UI2IG	158	10.1	0.214
UI2CA	305	1.3	0.013
UM3CA	155	13.5	0.135
UI1TD	227	31.3	0.908
UI2TD	231	39.8	1.281
UCTD	243	39.9	1.792
UCMR	204	1.5	0.025
UCDR	203	32.0	0.822
UP3MD	243	17.3	0.348
UP4MD	248	25.0	0.494
UP3TC	260	0.0	0.000
UP4TC	271	0.4	0.004
UP3DS	252	0.0	0.000
UM1MC	281	55.9	4.612
UM2MC	278	21.9	4.093
UM3MC	103	12.6	3.779
UM1HC	276	50.4	4.602
UM2HC	267	91.0	3.141
UM3HC	97	68.0	2.132
UM1C5	252	27.0	0.573
UM2C5	245	22.9	0.333
UM3C5	91	36.3	0.869
UM1CB	268	72.4	3.088
UM2CB	270	18.1	0.482
UM3CB	91	6.6	0.264
UM1PR	258	1.9	0.04
UM2PR	258	2.7	0.064
UM3PR	86	5.8	0.127

trait	N	freq %	W
LI1SS	237	23.2	0.260
L12SS	253	22.1	0.245
LI1CA	280	0.7	0.007
LM3CA	131	14.5	0.144
LCDR	206	11.7	0.285
LP3LC	253	11.1	1.989
LP4LC	247	74.9	2.906
LM1AF	181	14.4	0.654
LM1GP	155	90.3	1.113
LM2GP	197	46.7	1.604
LM3GP	78	38.5	1.707
LM1CN	222	14.0	5.023
LM2CN	197	21.3	4.238
LM3CN	81	51.9	4.643
LM1DW	173	21.4	0.260
LM1MT	158	5.1	0.051
LM2MT	195	30.3	0.303
LM3MT	73	20.5	0.205
LM1PS	211	18.0	0.221
LM2PS	219	12.8	0.143
LM3PS	78	25.6	0.508
LM1C5	214	87.9	3.175
LM2C5	194	20.6	0.603
LM3C5	78	51.3	1.986
LM1C6	212	13.7	0.251
LM2C6	195	2.6	0.070
LM3C6	78	15.4	0.349
LM1C7	215	18.6	0.285
LM2C7	220	7.7	0.109
LM3C7	81	13.6	0.289

Table A.9. All EA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	20	10.0	LI1SS	26	34.6
WING	23	8.7	L12SS	27	40.7
UI1SS	23	4.3	LI1CA	33	0.0
UI2SS	28	32.1	LM3CA	32	12.5
UCSS	31	12.9	LCDR	25	4.0
UI1LC	26	26.9	LP3LC	33	15.2
UI1DS	24	0.0	LP4LC	28	60.7
UI2DS	27	3.7	LM1AF	12	25.0
UI2PS	33	0.0	LM1GP	16	100.0
UM3PS	26	0.0	LM2GP	28	60.7
UI1IG	30	0.0	LM3GP	22	45.5
UI2IG	33	15.2	LM1CN	19	26.3
UI2CA	41	7.3	LM2CN	22	18.2
UM3CA	36	16.7	LM3CN	28	60.7
UI1TD	28	21.4	LM1DW	8	12.5
UI2TD	32	37.5	LM1MT	7	14.3
UCTD	35	31.4	LM2MT	22	68.2
UCMR	0	26.0	LM3MT	25	32.0
UCDR	23	8.7	LM1PS	15	73.3
UP3MD	32	15.6	LM2PS	21	38.1
UP4MD	30	26.7	LM3PS	24	37.5
UP3TC	34	0.0	LM1C5	18	77.8
UP4TC	35	2.9	LM2C5	21	19.0
UP3DS	33	0.0	LM3C5	27	59.3
UM1MC	34	91.2	LM1C6	18	22.2
UM2MC	37	35.1	LM2C6	21	0.0
UM3MC	25	12.0	LM3C6	27	18.5
UM1HC	34	91.2	LM1C7	21	9.5
UM2HC	35	91.4	LM2C7	29	13.8
UM3HC	24	70.8	LM3C7	29	13.8
UM1C5	29	58.6			
UM2C5	34	32.4			
UM3C5	23	47.8			
UM1CB	31	71.0			
UM2CB	36	25.0			
UM3CB	24	8.3			
UM1PR	29	6.9			
UM2PR	32	9.4			
UM3PR	23	13.0			

Table A.10. Early EA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	36	2.8	LI1SS	58	32.8
WING	46	0.0	L12SS	72	34.7
UI1SS	44	11.4	LI1CA	92	0.0
UI2SS	42	33.3	LM3CA	83	18.1
UCSS	49	12.2	LCDR	28	17.9
UI1LC	52	32.7	LP3LC	71	9.9
UI1DS	49	6.1	LP4LC	69	71.0
UI2DS	52	13.5	LM1AF	35	14.3
UI2PS	71	1.4	LM1GP	46	78.3
UM3PS	70	0.0	LM2GP	54	44.4
UI1IG	66	6.1	LM3GP	52	34.6
UI2IG	78	11.5	LM1CN	52	11.5
UI2CA	110	0.0	LM2CN	45	24.4
UM3CA	102	14.7	LM3CN	49	49.0
UI1TD	50	10.0	LM1DW	27	18.5
UI2TD	63	38.1	LM1MT	26	23.1
UCTD	67	28.4	LM2MT	37	54.1
UCMR	35	0.0	LM3MT	38	18.4
UCDR	28	10.7	LM1PS	48	43.8
UP3MD	61	19.7	LM2PS	55	30.9
UP4MD	65	21.5	LM3PS	49	20.4
UP3TC	76	0.0	LM1C5	44	81.8
UP4TC	82	0.0	LM2C5	41	24.4
UP3DS	70	0.0	LM3C5	47	48.9
UM1MC	92	67.4	LM1C6	42	11.9
UM2MC	95	32.6	LM2C6	42	4.8
UM3MC	69	14.5	LM3C6	46	13.0
UM1HC	89	73	LM1C7	48	35.4
UM2HC	93	91.4	LM2C7	53	7.5
UM3HC	65	69.2	LM3C7	49	12.2
UM1C5	73	39.7			
UM2C5	78	35.9			
UM3C5	60	35.0			
UM1CB	83	69.9			
UM2CB	87	16.1			
UM3CB	59	5.1			
UM1PR	78	2.6			
UM2PR	84	3.6			
UM3PR	58	3.4			

Table A.11. Middle EA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	131	15.3	LI1SS	153	17.6
WING	147	1.4	L12SS	154	13.0
UI1SS	154	0.6	LI1CA	155	1.3
UI2SS	153	13.7	LM3CA	16	0.0
UCSS	151	4.0	LCDR	153	11.8
UI1LC	155	12.9	LP3LC	149	10.7
UI1DS	155	0.0	LP4LC	150	79.3
UI2DS	153	0.7	LM1AF	134	13.4
UI2PS	153	2.6	LM1GP	93	94.6
UM3PS	16	6.3	LM2GP	115	44.3
UI1IG	126	0.0	LM3GP	4	50.0
UI2IG	47	4.3	LM1CN	151	13.2
UI2CA	154	0.6	LM2CN	130	20.8
UM3CA	17	0.0	LM3CN	4	25.0
UI1TD	149	40.3	LM1DW	138	22.5
UI2TD	136	41.2	LM1MT	125	0.8
UCTD	141	47.5	LM2MT	136	24.0
UCMR	143	2.1	LM3MT	10	0.0
UCDR	152	39.5	LM1PS	148	4.1
UP3MD	150	16.7	LM2PS	143	2.1
UP4MD	153	26.1	LM3PS	5	20.0
UP3TC	150	0.0	LM1C5	152	90.8
UP4TC	154	0.0	LM2C5	132	19.7
UP3DS	149	0.0	LM3C5	4	25.0
UM1MC	155	41.3	LM1C6	152	13.2
UM2MC	146	11.6	LM2C6	132	2.3
UM3MC	9	0.0	LM3C6	5	20.0
UM1HC	153	28.1	LM1C7	146	14.4
UM2HC	139	90.6	LM2C7	138	6.5
UM3HC	8	50.0	LM3C7	4	0.0
UM1C5	150	14.7			
UM2C5	133	12.8			
UM3C5	8	12.5			
UM1CB	154	74.0			
UM2CB	147	17.7			
UM3CB	8	12.5			
UM1PR	151	0.7			
UM2PR	142	0.7			
UM3PR	5	0.0			

Table A.12. Late EA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	21	0.0	LI1SS	37	43.2
WING	30	0.0	L12SS	42	54.8
UI1SS	23	13.0	LI1CA	57	0.0
UI2SS	23	30.4	LM3CA	50	22.0
UCSS	20	5.0	LCDR	15	13.3
UI1LC	28	53.6	LP3LC	43	4.7
UI1DS	25	12.0	LP4LC	40	60.0
UI2DS	29	17.2	LM1AF	16	31.3
UI2PS	38	2.6	LM1GP	24	75.0
UM3PS	36	0.0	LM2GP	26	34.6
UI1IG	39	10.3	LM3GP	26	15.4
UI2IG	43	9.3	LM1CN	29	13.8
UI2CA	51	0.0	LM2CN	18	33.3
UM3CA	48	14.6	LM3CN	26	61.5
UI1TD	26	11.5	LM1DW	11	18.2
UI2TD	30	43.3	LM1MT	11	27.3
UCTD	35	28.6	LM2MT	14	71.4
UCMR	10	0.0	LM3MT	15	20.0
UCDR	11	9.1	LM1PS	27	44.4
UP3MD	21	23.8	LM2PS	27	40.7
UP4MD	26	30.8	LM3PS	25	20.0
UP3TC	32	0.0	LM1C5	21	81.0
UP4TC	38	0.0	LM2C5	14	35.7
UP3DS	24	0.0	LM3C5	24	66.7
UM1MC	29	71.8	LM1C6	19	15.8
UM2MC	42	38.1	LM2C6	15	6.7
UM3MC	32	28.1	LM3C6	22	18.2
UM1HC	37	83.8	LM1C7	24	58.3
UM2HC	39	89.7	LM2C7	26	11.5
UM3HC	29	79.3	LM3C7	24	16.7
UM1C5	26	42.3			
UM2C5	29	48.3			
UM3C5	26	46.2			
UM1CB	33	75.8			
UM2CB	35	11.4			
UM3CB	23	8.7			
UM1PR	29	3.4			
UM2PR	34	2.9			
UM3PR	22	4.5			

Table A.13. Hamann-Todd EA trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	79	12.7	LI1SS	101	14.9
WING	93	0.0	L12SS	101	14.9
UI1SS	101	0.0	LI1CA	101	1.0
UI2SS	101	12.9	LM3CA	12	0.0
UCSS	100	1.0	LCDR	100	12.0
UI1LC	101	9.9	LP3LC	99	14.1
UI1DS	101	0.0	LP4LC	99	76.8
UI2DS	101	0.0	LM1AF	84	7.1
UI2PS	101	2.0	LM1GP	51	94.1
UM3PS	11	9.1	LM2GP	79	46.8
UI1IG	85	0.0	LM3GP	4	50.0
UI2IG	29	6.9	LM1CN	97	13.4
UI2CA	101	0.0	LM2CN	92	16.0
UM3CA	13	0.0	LM3CN	4	25.0
UI1TD	99	41.4	LM1DW	89	23.6
UI2TD	93	43.0	LM1MT	76	0.0
UCTD	97	51.5	LM2MT	91	16.5
UCMR	97	1.0	LM3MT	8	0.0
UCDR	101	48.5	LM1PS	96	2.1
UP3MD	96	14.6	LM2PS	99	3.0
UP4MD	100	20	LM3PS	5	20.0
UP3TC	96	0.0	LM1C5	98	89.8
UP4TC	101	0.0	LM2C5	93	16.1
UP3DS	96	0.0	LM3C5	4	25.0
UM1MC	101	32.7	LM1C6	98	13.3
UM2MC	98	8.2	LM2C6	93	3.2
UM3MC	6	0.0	LM3C6	5	20.0
UM1HC	99	16.2	LM1C7	96	10.4
UM2HC	96	87.5	LM2C7	98	2.0
UM3HC	5	60.0	LM3C7	3	0.0
UM1C5	98	14.3			
UM2C5	93	10.8			
UM3C5	5	0.0			
UM1CB	100	81			
UM2CB	97	22.7			
UM3CB	5	20.0			
UM1PR	100	0.0			
UM2PR	97	1.0			
UM3PR	3	0.0			

Table A.14. UT Dental EA trait frequencies.

trait	N	freq %	W
DIAS	34	20.6	0.206
WING	32	6.3	2.843
UI1SS	26	3.8	1.036
UI2SS	54	37.0	1.277
UCSS	96	34.4	1.188
UI1LC	30	23.3	0.966
UI1DS	29	0.0	0.034
UI2DS	57	26.3	0.282
UI2PS	75	6.7	0.067
UM3PS	162	0.6	0.006
UI1IG	58	0.0	0.000
UI2IG	75	4.0	0.091
UI2CA	180	0.0	0.000
UM3CA	178	0.6	0.006
UI1TD	42	33.3	1.119
UI2TD	63	50.8	1.683
UCTD	103	80.6	3.079
UCMR	91	33.0	0.605
UCDR	65	41.5	1.491
UP3MD	128	25.8	0.500
UP4MD	109	34.9	0.735
UP3TC	155	0.0	0.000
UP4TC	158	0.6	0.006
UP3DS	155	0.0	0.000
UM1MC	165	86.7	4.958
UM2MC	171	38.6	4.369
UM3MC	154	3.2	3.697
UM1HC	166	71.7	4.844
UM2HC	168	93.5	3.626
UM3HC	151	78.1	2.491
UM1C5	85	56.5	1.099
UM2C5	128	52.3	0.901
UM3C5	132	66.7	1.355
UM1CB	114	68.4	3.086
UM2CB	146	14.4	0.357
UM3CB	151	17.2	0.558
UM1PR	129	5.4	0.054
UM2PR	160	1.9	0.019
UM3PR	146	2.1	0.091

trait	N	freq %	W
LI1SS	48	12.5	0.146
L12SS	68	35.3	0.399
LI1CA	135	0.0	0.000
LM3CA	142	1.4	0.014
LCDR	64	42.2	1.284
LP3LC	110	80.9	5.824
LP4LC	110	99.1	6.900
LM1AF	79	67.1	1.899
LM1GP	111	95.5	1.038
LM2GP	129	71.3	1.377
LM3GP	128	53.9	1.466
LM1CN	111	23.4	5.216
LM2CN	104	62.5	4.837
LM3CN	110	84.5	5.292
LM1DW	54	51.9	1.036
LM1MT	49	32.7	0.327
LM2MT	98	51.0	0.455
LM3MT	108	26.9	0.420
LM1PS	95	52.6	0.560
LM2PS	118	44.1	0.441
LM3PS	121	26.4	0.462
LM1C5	109	98.2	4.438
LM2C5	103	62.1	2.086
LM3C5	110	84.5	3.172
LM1C6	110	24.5	0.444
LM2C6	103	21.4	0.428
LM3C6	110	46.4	0.953
LM1C7	101	51.5	1.159
LM2C7	127	27.6	0.355
LM3C7	124	39.5	0.556

Table A.15. WA trait frequencies.

trait	N	freq %	W	trait	N	freq %	W
DIAS	54	11.1	0.111	LI1SS	92	3.3	0.033
WING	55	1.8	2.876	L12SS	104	2.9	0.029
UI1SS	82	1.2	0.548	LI1CA	121	0.0	0.000
UI2SS	41	19.4	0.803	LM3CA	110	12.7	0.127
UCSS	102	4.9	0.47	LCDR	98	8.2	0.223
UI1LC	78	20.5	0.871	LP3LC	107	19.6	2.410
UI1DS	83	0	0.012	LP4LC	101	84.2	3.663
UI2DS	97	2.1	0.021	LM1AF	54	29.6	0.910
UI2PS	98	3.1	0.031	LM1GP	69	91.3	1.058
UM3PS	82	3.7	0.037	LM2GP	97	36.1	1.620
UI1IG	91	2.2	0.055	LM3GP	66	34.8	1.600
UI2IG	100	31	0.300	LM1CN	86	10.5	4.970
UI2CA	130	2.3	0.023	LM2CN	99	24.2	4.258
UM3CA	116	15.5	0.155	LM3CN	65	63.1	4.672
UI1TD	73	35.6	0.999	LM1DW	55	20.0	0.291
UI2TD	85	45.9	1.331	LM1MT	45	13.3	0.133
UCTD	101	55.4	1.963	LM2MT	69	39.1	0.325
UCMR	100	2.0	0.040	LM3MT	64	20.3	0.277
UCDR	88	9.1	0.224	LM1PS	59	69.5	0.712
UP3MD	101	23.8	0.387	LM2PS	85	22.4	0.224
UP4MD	88	17.0	0.340	LM3PS	76	13.2	0.132
UP3TC	120	0.0	0.000	LM1C5	83	85.5	3.227
UP4TC	119	0.0	0.000	LM2C5	99	24.2	0.635
UP3DS	111	0.0	0.000	LM3C5	65	61.5	2.538
UM1MC	119	61.3	4.631	LM1C6	85	9.4	0.153
UM2MC	116	14.7	4.064	LM2C6	98	3.1	0.050
UM3MC	74	2.7	3.611	LM3C6	64	9.4	0.222
UM1HC	106	63.2	4.667	LM1C7	84	16.4	0.335
UM2HC	109	85.3	3.078	LM2C7	101	12.9	0.159
UM3HC	72	52.8	1.542	LM3C7	74	8.1	0.151
UM1C5	81	37.0	0.470				
UM2C5	92	26.1	0.389				
UM3C5	64	34.4	0.954				
UM1CB	83	72.3	2.844				
UM2CB	103	9.7	0.216				
UM3CB	71	8.5	0.252				
UM1PR	89	0.0	0.000				
UM2PR	111	3.6	0.099				
UM3PR	72	0.0	0.000				

Table A.16. EU trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	54	11.1	LI1SS	92	3.3
WING	55	1.8	L12SS	104	2.9
UI1SS	82	1.2	LI1CA	121	0.0
UI2SS	98	19.4	LM3CA	110	12.7
UCSS	102	4.9	LCDR	98	8.2
UI1LC	78	20.5	LP3LC	107	19.6
UI1DS	83	0.0	LP4LC	101	85.0
UI2DS	97	2.1	LM1AF	54	29.6
UI2PS	98	3.1	LM1GP	69	91.3
UM3PS	82	3.7	LM2GP	97	36.1
UI1IG	91	2.2	LM3GP	66	34.8
UI2IG	100	13.0	LM1CN	86	10.5
UI2CA	130	2.3	LM2CN	99	24.9
UM3CA	116	15.5	LM3CN	65	63.1
UI1TD	73	35.6	LM1DW	55	20.0
UI2TD	85	45.9	LM1MT	45	13.3
UCTD	101	55.4	LM2MT	69	39.1
UCMR	100	2.0	LM3MT	64	20.3
UCDR	88	9.1	LM1PS	59	69.5
UP3MD	101	23.8	LM2PS	85	22.4
UP4MD	88	17.0	LM3PS	76	13.2
UP3TC	120	0.0	LM1C5	83	85.5
UP4TC	119	0.0	LM2C5	99	24.2
UP3DS	119	0.0	LM3C5	65	61.5
UM1MC	111	61.3	LM1C6	85	9.4
UM2MC	116	14.7	LM2C6	98	3.1
UM3MC	74	2.7	LM3C6	64	9.4
UM1HC	106	63.2	LM1C7	84	16.7
UM2HC	109	85.3	LM2C7	101	12.9
UM3HC	72	52.8	LM3C7	74	8.1
UM1C5	81	37.0			
UM2C5	92	26.1			
UM3C5	64	34.4			
UM1CB	83	72.3			
UM2CB	103	9.7			
UM3CB	71	8.5			
UM1PR	89	0.0			
UM2PR	111	3.6			
UM3PR	72	0.0			

Table A.17. EU excluding Poundbury trait frequencies.

trait	N	freq %	trait	N	freq %
DIAS	37	10.8	LI1SS	60	1.7
WING	39	0.0	L12SS	64	0.0
UI1SS	55	1.8	LI1CA	64	0.0
UI2SS	60	11.7	LM3CA	57	10.5
UCSS	54	3.7	LCDR	58	10.3
UI1LC	55	14.5	LP3LC	59	25.4
UI1DS	57	0.0	LP4LC	57	86.0
UI2DS	60	0.0	LM1AF	29	31.0
UI2PS	60	0.0	LM1GP	36	97.2
UM3PS	41	7.3	LM2GP	58	41.4
UI1IG	59	3.4	LM3GP	34	35.3
UI2IG	620	16.7	LM1CN	56	7.1
UI2CA	67	1.5	LM2CN	59	27.1
UM3CA	56	16.1	LM3CN	35	57.1
UI1TD	45	33.3	LM1DW	30	23.3
UI2TD	51	54.9	LM1MT	23	13.0
UCTD	47	61.7	LM2MT	39	33.3
UCMR	47	2.1	LM3MT	32	9.4
UCDR	45	11.1	LM1PS	32	62.5
UP3MD	56	25.0	LM2PS	52	21.2
UP4MD	40	15.0	LM3PS	41	14.6
UP3TC	64	0.0	LM1C5	54	83.3
UP4TC	58	0.0	LM2C5	59	27.1
UP3DS	63	0.0	LM3C5	34	55.9
UM1MC	60	55.0	LM1C6	56	7.1
UM2MC	59	10.2	LM2C6	58	3.4
UM3MC	35	0.0	LM3C6	34	14.7
UM1HC	58	67.2	LM1C7	52	21.2
UM2HC	57	87.7	LM2C7	57	15.8
UM3HC	34	52.9	LM3C7	37	8.1
UM1C5	45	42.2			
UM2C5	52	23.1			
UM3C5	30	23.3			
UM1CB	42	69.0			
UM2CB	49	12.2			
UM3CB	33	9.1			
UM1PR	47	0.0			
UM2PR	58	3.4			
UM3PR	35	0.0			

Table A.18. Poundbury trait frequencies.

trait	N	freq %	W
DIAS	34	23.5	0.235
WING	34	2.9	2.998
UI1SS	34	5.9	0.824
UI2SS	35	20.0	1.062
UCSS	34	17.6	0.793
UI1LC	34	26.5	1.028
UI1DS	34	0.0	0.059
UI2DS	35	5.7	0.057
UI2PS	35	0.0	0.000
UM3PS	5	0.0	0.000
UI1IG	34	2.9	0.029
UI2IG	31	16.1	0.357
UI2CA	35	0.0	0.000
UM3CA	6	0.0	0.000
UI1TD	34	8.8	0.381
UI2TD	34	14.7	0.676
UCTD	34	64.7	2.503
UCMR	34	29.4	0.382
UCDR	34	82.4	3.026
UP3MD	35	17.1	0.258
UP4MD	35	34.3	0.658
UP3TC	35	0.0	0.000
UP4TC	35	0.0	0.000
UP3DS	35	0.0	0.000
UM1MC	35	88.6	4.995
UM2MC	34	47.1	4.442
UM3MC	3	33.3	3.996
UM1HC	35	82.9	5.138
UM2HC	32	93.8	3.319
UM3HC	2	50.0	2.000
UM1C5	35	62.9	1.114
UM2C5	33	51.5	0.820
UM3C5	2	50.0	1.000
UM1CB	35	68.6	2.832
UM2CB	35	25.7	0.694
UM3CB	2	50.0	2.500
UM1PR	34	0.0	0.000
UM2PR	33	0.0	0.000
UM3PR	3	0.0	0.000

trait	N	freq %	W
LI1SS	34	17.6	0.176
L12SS	34	26.5	0.265
LI1CA	35	0.0	0.000
LM3CA	6	0.0	0.000
LCDR	34	88.2	2.885
LP3LC	35	71.4	5.568
LP4LC	35	97.1	5.836
LM1AF	34	73.5	2.205
LM1GP	35	97.1	1.029
LM2GP	34	52.9	1.530
LM3GP	4	50.0	1.500
LM1CN	35	60	5.600
LM2CN	33	69.7	5.000
LM3CN	4	100.0	5.750
LM1DW	29	44.8	0.724
LM1MT	31	45.2	0.452
LM2MT	35	51.4	0.514
LM3MT	5	20.0	0.200
LM1PS	35	11.4	0.144
LM2PS	35	11.4	0.144
LM3PS	4	0.0	0.000
LM1C5	35	100	4.286
LM2C5	33	72.7	2.362
LM3C5	4	100.0	4.250
LM1C6	35	57.1	1.030
LM2C6	33	30.3	0.424
LM3C6	4	75.0	1.250
LM1C7	35	77.1	1.342
LM2C7	35	54.3	0.686
LM3C7	4	75.0	0.750

Table A. 19. SA trait frequencies.

APPENDIX B

LEFT AND RIGHT OBSERVATIONS COMPARED

	maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	113	9	+	215.60	0.001	121	30	+	218.99	0.001
UI2SS	109	42	+	206.47	0.001	127	20	+	218.05	0.001
UCSS	123	9	+	161.90	0.001	142	9	+	221.27	0.001
UI1LC	125	9	+	132.99	0.001	127	16	+	163.18	0.001
UI1DS	132	1	+	24.14	0.001	136			0.00	
UI2DS	119	1	+	6.02	0.014	131	1	+	16.88	0.001
UI2PS	125	1	+	16.69	0.001	141	1	+	3.66	0.056
UM3PS	125			0.00		111			0.00	
UI1IG	115	1	+	11.48	0.001	118	2	+	8.78	0.012
UI2IG	100	4	+	14.90	0.005	111	16	+	18.75	0.282
UI2CA	131	1	+	11.74	0.001	144			0.00	
UM3CA	129			0.00		122			0.00	
UI1TD	108	30	+	167.70	0.001	113	30	+	132.61	0.001
UI2TD	103	25	+	165.50	0.001	116	36	+	157.02	0.001
UCTD	113	36	+	262.52	0.001	120	25	+	255.37	0.001
UCMR	102	6	+	63.40	0.001	115	9	+	42.56	0.001
UCDR	84	9	+	72.11	0.001	103	12	+	127.20	0.001
UP3TC	132			0.00		137			0.00	
UP4TC	126			0.00		130			0.00	
UP3DS	132			0.00		137			0.00	
UM1MC	112	4	+	101.19	0.001	121	4	+	86.33	0.001
UM2MC	130	4	+	63.48	0.001	135	4	+	82.75	0.001
UM3MC	114	15	+	144.19	0.001	99	9	+	84.26	0.001
UM1HC	112	9	+	115.70	0.001	121	16	+	98.63	0.001
UM2HC	129	25	+	193.45	0.001	137	25	+	239.92	0.001
UM3HC	115	16	+	139.51	0.001	97	16	+	154.54	0.001
UM1C5	104	9	+	80.68	0.001	119	16	+	94.92	0.001
UM2C5	123	9	+	96.73	0.001	134	16	+	111.94	0.001
UM3C5	108	20	+	126.98	0.001	99	16	+	114.10	0.001
UM1CB	92	49	+	227.65	0.001	112	49	+	219.40	0.001
UM2CB	116	30	+	97.26	0.001	132	25	+	62.59	0.001
UM3CB	109	24	+	54.16	0.001	99	25	+	39.96	0.029
UM1PR	37			0.00		39			0.00	
UM2PR	48			0.00		66			0.00	
UM3PR	27			0.00		32			0.00	
UP3MD	116	9	+	59.11	0.001	125	9	+	141.01	0.001
UP4MD	109	9	+	89.86	0.001	117	9	+	111.30	0.001

Continued.

Table B.1. Freedman's Cemetery left and right observations compared.

Table B.1. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	118	4	+	41.40	0.001	128	4	+	75.02	0.001
L12SS	116	4	+	79.45	0.001	127	4	+	83.56	0.001
LI1CA	130			0.00		134			0.00	
LM3CA	128			0.00		134	1	+	20.79	0.001
LCDR	78	16	+	80.38	0.001	83	9	+	48.98	0.001
LP3LC	129	81	+	327.57	0.001	134	81	+	371.13	0.001
LP4LC	121	64	+	246.65	0.001	135	64	+	349.66	0.001
LM1AF	80	16	+	122.63	0.001	99	12	+	108.35	0.001
LM1GP	77	4	+	10.73	0.030	96	2	+	20.54	0.001
LM2GP	94	9	+	45.64	0.001	109	4	+	48.37	0.001
LM3GP	104	4	+	35.07	0.001	99	4	+	34.45	0.001
LM1CN	89	4	+	80.65	0.001	103	4	+	90.73	0.001
LM2CN	105	9	+	161.21	0.001	118	4	+	107.28	0.001
LM3CN	106	9	+	107.89	0.001	109	4	+	75.62	0.001
LM1DW	62	9	+	57.52	0.001	83	9	+	69.94	0.001
LM1MT	66	4	+	40.99	0.001	90	1	+	48.12	0.001
LM2MT	96	1	+	10.35	0.001	94	1	+	10.00	0.002
LM3MT	101	1	+	14.32	0.001	90	1	+	4.46	0.035
LM1PS	65	1	+	21.25	0.001	89	3	+	22.84	0.001
LM2PS	91	1	+	3.183	0.074	107	1	+	2.11	0.146
LM3PS	97	4	+	23.85	0.001	89	4	+	6.14	0.189
LM1C5	89	25	+	114.07	0.001	101	16	+	121.20	0.001
LM2C5	105	25	+	188.13	0.001	118	25	+	160.14	0.001
LM3C5	106	20	+	92.43	0.001	110	25	+	118.00	0.001
LM1C6	88	9	+	94.36	0.001	103	9	+	110.99	0.001
LM2C6	105	9	+	95.18	0.001	118	9	+	71.14	0.001
LM3C6	106	12	+	93.55	0.001	108	12	+	71.06	0.001
LM1C7	84	16	+	100.45	0.001	100	16	+	103.34	0.001
LM2C7	114	12	+	51.20	0.001	119	9	+	94.66	0.001
LM3C7	112	20	+	72.68	0.001	108	8	+	35.03	0.001

	maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	13	16	+	36.73	0.001	29	9	+	69.84	0.001
UI2SS	10	9	+	17.82	0.037	30	9	+	60.04	0.001
UCSS	13	4	+	23.69	0.002	34	9	+	51.65	0.001
UI1LC	14	4	+	11.80	0.019	30	4	+	26.69	0.001
UI1DS	14			0.00		31	4	+	17.60	0.001
UI2DS	11			0.00		33			0.00	
UI2PS	33			0.00		33	1	+	8.96	0.003
UM3PS	5			0.00		1			0.00	
UI1IG	13			0.00		26			0.00	
UI2IG	6			0.00		14			0.00	
UI2CA	15			0.00		34			0.00	
UM3CA	5			0.00		5	1	-	0.51	0.477
UI1TD	14	4	+	18.48	0.001	31	6	+	23.26	0.001
UI2TD	12			0.00		32	12	+	25.81	0.011
UCTD	15	9	+	27.09	0.001	33	25	+	49.20	0.003
UCMR	14	4	+	11.15	0.025	33	9	+	32.46	0.001
UCDR	11	4	+	14.48	0.006	31	6	+	34.26	0.001
UP3TC	12			0.00		31			0.00	
UP4TC	13			0.00		25			0.00	
UP3DS	11			0.00		30			0.00	
UM1MC	10	1	+	8.46	0.004	27	2	+	6.71	0.035
UM2MC	10	1	+	3.73	0.053	16	1	+	0.58	0.440
UM3MC	0					0				
UM1HC	10	2	+	8.86	0.012	26	4	+	17.8	0.001
UM2HC	7	4	+	10.61	0.031	12	9	+	25.86	0.002
UM3HC	1			0.00		0				
UM1C5	8	1	+	3.26	0.071	22	4	+	9.8	0.044
UM2C5	6			0.00		10	4	+	12.22	0.016
UM3C5	0					0				
UM1CB	10	4	+	16.04	0.003	27	20	+	46.21	0.001
UM2CB	10			0.00		16	1	+	7.48	0.006
UM3CB	3			0.00		11			0.00	
UM1PR	6			0.00		24			0.00	
UM2PR	7			0.00		11			0.00	
UM3PR	1			0.00		0				
UP3MD	12	2	+	12	0.002	28	4	+	38.3	0.001
UP4MD	11			0.00		23	1	+	8.23	0.004

Continued.

Table B.2. Gullah left and right observations compared.

Table.B2. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	14	1	+	14.55	0.001	33	4	+	24.38	0.001
L12SS	15	1	+	7.96	0.005	31	1	+	12.98	0.001
LI1CA	15			0.00		34			0.00	
LM3CA	9			0.00		8			0.00	
LCDR	13	4	+	15.06	0.005	28	12	+	42.5	0.001
LP3LC	16	25	+	41.025	0.023	34	64	+	98.23	0.004
LP4LC	14	24	+	38.39	0.032	28	49	+	89.26	0.001
LM1AF	9	4	+	12.37	0.015	12	6	+	11.36	0.078
LM1GP	6			0.00		8	1	+	10.59	0.001
LM2GP	4	1	+	4.50	0.034	7	1	+	2.83	0.092
LM3GP	3			0.00		1			0.00	
LM1CN	8	1	+	10.59	0.001	10	1	+	3.73	0.053
LM2CN	7	4	+	14.06	0.007	9	4	+	8.55	0.073
LM3CN	5	1	+	6.73	0.009	2	1	+	2.77	0.096
LM1DW	7	1	+	8.38	0.004	10	6	+	10.83	0.094
LM1MT	7	1	+	5.74	0.017	10	1	+	1.21	0.272
LM2MT	5			0.00		3			0.00	
LM3MT	4			0.00		4	1	-	0.68	0.410
LM1PS	9	2	+	6.28	0.043	11	1	+	12.89	0.001
LM2PS	5	1	+	5.00	0.025	6			0.00	
LM3PS	4	1	+	4.50	0.034	2			0.00	
LM1C5	8	4	+	12.82	0.012	10	4	+	7.78	0.100
LM2C5	7	4	+	14.06	0.007	9	12	+	17.91	0.118
LM3C5	5	4	+	6.73	0.151	2	1	+	2.77	0.096
LM1C6	8	4	+	14.4	0.006	10	1	+	3.73	0.053
LM2C6	7	1	+	1.22	0.270	9	4	+	6.57	0.161
LM3C6	5	4	+	10.55	0.032	2			0.00	
LM1C7	6	4	+	7.64	0.106	9	9	+	15.14	0.087
LM2C7	6			0.00		8	2	+	9.00	0.011
LM3C7	3			0.00		1			0.00	

	Maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	11	9	+	19.25	0.023	3	1	+	1.05	0.306
UI2SS	18	16	+	46.00	0.001	4	4	+	8.32	0.081
UCSS	11	9	+	28.48	0.001	3	4	+	6.59	0.159
UI1LC	11	9	+	22.29	0.008	3	4	+	6.59	0.159
UI1DS	10	1	+	3.73	0.053	2	1	+	2.77	0.096
UI2DS	19	4	+	28.75	0.001	4	4	+	8.32	0.081
UI2PS	27	1	+	14.26	0.001	6			0.00	
UM3PS	24			0.00		3			0.00	
UI1IG	23			0.00		5			0.00	
UI2IG	30			0.00		7			0.00	
UI2CA	34			0.00		7			0.00	
UM3CA	34	1	+	24.63	0.001	6	1	+	2.63	0.105
UI1TD	13	12	+	21.28	0.046	4			0.00	
UI2TD	15	16	+	24.04	0.089	5	1	+	5.00	.250
UCTD	15	9	+	34.12	0.001	5	4	+	9.50	0.050
UCMR	6			0.00		1			0.00	
UCDR	9	6	+	15.28	0.018	2	1	+	2.77	0.096
UP3TC	23			0.00		2			0.00	
UP4TC	19			0.00		4			0.00	
UP3DS	20			0.00		1			0.00	
UM1MC	16	4	+	14.89	0.005	3	1	+	3.82	0.051
UM2MC	23	4	+	16.64	0.001	1			0.00	
UM3MC	22	9	+	18.25	0.003	2			0.00	
UM1HC	15	4	+	17.51	0.002	4	2	+	5.55	0.135
UM2HC	22	20	+	52.36	0.001	1			0.00	
UM3HC	19	30	+	43.66	0.051	2			0.00	
UM1C5	8	2	+	6.59	0.037	3	2	+	3.82	0.148
UM2C5	14	12	+	28.97	0.004	1			0.00	
UM3C5	16	20	+	40.4	0.004	2	1	+	2.77	0.096
UM1CB	13	36	+	41.74	0.236	3	1	+	3.82	0.051
UM2CB	15	6	+	14.55	0.024	1			0.00	
UM3CB	18			0.00		2			0.00	
UM1PR	29			0.00		9			0.00	
UM2PR	12			0.00		1			0.00	
UM3PR	14			0.00		2			0.00	
UP3MD	16	6	+	31.18	0.001	2			0.00	
UP4MD	11	1	+	15.16	0.001	3	1	+	1.05	0.306

Continued.

Table B.3. Hamann-Todd AA left and right observations compared.

Table B.3. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	25	4	+	31.34	0.001	5	1	+	6.73	0.009
L12SS	25	4	+	28.72	0.001	8	1	+	6.09	0.014
LI1CA	2			0.00		1			0.00	
LM3CA	30	1	+	8.62	0.003	7	1	+	4.56	0.033
LCDR	10	12	+	19.00	0.088	2	1	+	2.77	0.096
LP3LC	25	30	+	84.96	0.001	7	9	+	16.15	0.064
LP4LC	19	16	+	53.62	0.001	5	4	+	7.78	0.181
LM1AF	8	9	+	24.00	0.004	2			0.00	
LM1GP	7			0.00		3			0.00	
LM2GP	15	4	+	11.70	0.02	3	1	+	0.75	0.386
LM3GP	12	4	+	10.81	0.029	2	1	+	2.77	0.096
LM1CN	10	4	+	12.78	0.012	4	1	+	4.50	0.034
LM2CN	13	4	+	8.00	0.093	3	4	+	6.59	0.159
LM3CN	10	4	+	15.19	0.004	2	1	+	2.77	0.096
LM1DW	5	2	+	5.00	0.082	3	1	+	3.82	0.665
LM1MT	5	1	+	6.73	0.009	2	1	+	2.77	0.096
LM2MT	9	1	+	2.81	0.094	1			0.00	
LM3MT	9	1	+	2.23	0.135	1			0.00	
LM1PS	7	1	+	9.56	0.002	3	1	+	1.05	0.306
LM2PS	12	1	+	1.74	0.188	3	1	+	3.82	0.051
LM3PS	9	1	+	3.51	0.061	1			0.00	
LM1C5	10	4	+	6.81	0.035	4	1	+	5.55	0.019
LM2C5	12	20	+	28.09	0.107	3	4	+	6.59	0.159
LM3C5	10	12	+	20.28	0.062	2	1	+	2.77	0.096
LM1C6	10	1	+	6.50	0.011	4	1	+	4.50	0.034
LM2C6	12	9	+	14.06	0.120	3	1	+	3.82	0.051
LM3C6	9	6	+	12.34	0.054	2			0.00	
LM1C7	7	8	+	11.15	0.082	3	1	+	3.00	0.083
LM2C7	14	8	+	28.00	0.001	3	1	+	3.82	0.051
LM3C7	11	6	+	12.40	0.054	2			0.00	

	maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	49	9	+	99.05	0.001	48	9	+	110.63	0.001
UI2SS	46	16	+	96.72	0.001	44	9	+	98.04	0.001
UCSS	46	6	+	84.13	0.001	47	4	+	81.00	0.001
UI1LC	50	9	+	69.25	0.001	48	9	+	80.80	0.001
UI1DS	50			0.00		48			0.00	
UI2DS	47			0.00		44			0.00	
UI2PS	49	1	-	0.042	0.838	46	1	+	6.86	0.009
UM3PS	6			0.00		5			0.00	
UI1IG	33			0.00		34			0.00	
UI2IG	8			0.00		12			0.00	
UI2CA	50			0.00		49	1	+	5.94	0.015
UM3CA	6			0.00		5			0.00	
UI1TD	47	16	+	58.29	0.001	46	12	+	51.06	0.001
UI2TD	42	25	+	68.00	0.001	38	25	+	56.23	0.001
UCTD	38	30	+	94.24	0.001	46	20	+	69.36	0.001
UCMR	38	1	+	15.63	0.001	42	6	+	17.41	0.008
UCDR	47	20	+	66.37	0.001	48	8	+	52.02	0.001
UP3TC	44			0.00		47			0.00	
UP4TC	46			0.00		47			0.00	
UP3DS	43			0.00		47			0.00	
UM1MC	50	1	+	45.81	0.001	49	4	+	61.91	0.001
UM2MC	40	4	+	33.05	0.001	47	4	+	64.23	0.001
UM3MC	5			0.00		4			0.00	
UM1HC	49	4	+	52.35	0.001	48	6	+	56.56	0.001
UM2HC	37	16	+	69.37	0.001	39	16	+	62.70	0.001
UM3HC	2	1	+	2.77	0.157	3	4	+	6.59	0.159
UM1C5	43	6	+	36.62	0.001	42	4	+	43.65	0.001
UM2C5	28	6	+	28.47	0.001	32	8	+	31.52	0.001
UM3C5	0					3	1	+	3.82	0.051
UM1CB	49	36	+	89.37	0.001	49	25	+	74.74	0.001
UM2CB	38	12	+	29.39	0.003	43	4	+	59.78	0.001
UM3CB	3			0.00		2			0.00	
UM1PR	48			0.00		49			0.00	
UM2PR	39			0.00		42			0.00	
UM3PR	3			0.00		1			0.00	
UP3MD	44	4	+	12.87	0.012	44	6	+	10.27	0.114
UP4MD	47	9	+	27.51	0.001	47	4	+	7.66	0.105

Continued.

Table B.4. UT Dental AA left and right observations compared.

Table B.4. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	49	1	+	45.30	0.001	49	4	+	50.27	0.001
L12SS	47	1	+	55.43	0.001	49	4	+	43.50	0.001
LI1CA	50	1	+	9.80	0.002	49			0.00	
LM3CA	8			0.00		10			0.00	
LCDR	46	16	+	56.13	0.001	46	16	+	70.17	0.001
LP3LC	44	49	+	139.16	0.001	46	64	+	146.24	0.001
LP4LC	49	64	+	151.30	0.001	47	56	+	150.25	0.001
LM1AF	33	12	+	51.65	0.001	39	4	+	63.99	0.001
LM1GP	18	1	+	1.39	0.238	18	1	-	0.243	0.622
LM2GP	30	2	+	5.17	0.075	23	2	+	6.06	0.048
LM3GP	4			0.00		2			0.00	
LM1CN	45	1	+	12.59	0.001	47	4	+	47.94	0.001
LM2CN	34	4	+	28.11	0.001	34	4	+	35.8	0.001
LM3CN	4	2	+	5.55	0.063	3	1	+	3.82	0.083
LM1DW	28	9	+	45.46	0.001	34	6	+	35.56	0.001
LM1MT	24	1	+	9.20	0.002	33	1	+	6.19	0.013
LM2MT	5	1	+	5.00	0.025	4	1	-	0.68	0.410
LM3MT	5	1	+	2.23	0.135	4	1	+	1.73	0.189
LM1PS	40	1	+	6.58	0.010	40	1	+	0.158	0.691
LM2PS	34			0.00		45	1	+	4.09	0.043
LM3PS	3			0.00		1			0.00	
LM1C5	45	9	+	41.39	0.001	46	16	+	79.56	0.001
LM2C5	34	16	+	44.96	0.001	34	16	+	45.58	0.001
LM3C5	4			0.00		3	1	+	3.82	0.051
LM1C6	45	6	+	21.61	0.001	47	4	+	34.09	0.001
LM2C6	34	6	+	18.63	0.005	34	2	+	9.02	0.011
LM3C6	4	4	+	8.32	0.081	2			0.00	
LM1C7	39	12	+	40.25	0.001	43	16	+	63.01	0.001
LM2C7	42	4	+	52.89	0.001	44	2	+	38.56	0.001
LM3C7	4	1	+	4.50	0.034	3			0.00	

	maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	27	9	+	38.90	0.001	25	4	+	54.60	0.001
UI2SS	23	4	+	24.78	0.001	25	4	+	38.02	0.001
UCSS	21	4	+	25.42	0.001	22	4	+	14.55	0.006
UI1LC	27	9	+	32.88	0.001	26	4	+	25.89	0.001
UI1DS	27			0.00		26	1	+	8.48	0.004
UI2DS	25			0.00		25			0.00	
UI2PS	26			0.00		26			0.00	
UM3PS	4			0.00		0				
UI1IG	19			0.00		21			0.00	
UI2IG	3			0.00		8			0.00	
UI2CA	26			0.00		27	1	+	8.55	0.003
UM3CA	3			0.00		0				
UI1TD	36	25	+	64.66	0.001	24	9	+	38.50	0.001
UI2TD	19	16	+	57.00	0.001	20	20	+	43.82	0.002
UCTD	20	12	+	37.92	0.001	17	12	+	16.24	0.180
UCMR	21			0.00		21	2	+	8.04	0.018
UCDR	22	4	+	15.16	0.004	22	9	+	26.62	0.002
UP3TC	27			0.00		27			0.00	
UP4TC	24			0.00		26			0.00	
UP3DS	25			0.00		27			0.00	
UM1MC	27	+	+	37.10	0.001	27	4	+	24.60	0.001
UM2MC	18	12	+	37.55	0.001	21	1	+	5.68	0.017
UM3MC	2	1	+	2.77	0.096	0				
UM1HC	27	9	+	35.42	0.001	27	4	+	41.67	0.001
UM2HC	18	6	+	32.32	0.001	19	9	+	36.45	0.001
UM3HC	2	1	+	2.77	0.096	0				
UM1C5	26	1	+	10.28	0.001	25	2	+	14.53	0.001
UM2C5	16	6	+	12.06	0.061	12	1	+	6.88	0.009
UM3C5	2	1	+	2.77	0.096	0				
UM1CB	26	20	+	49.75	0.001	26	36	+	72.59	0.001
UM2CB	19			0.00		24	4	+	16.54	0.002
UM3CB	2			0.00		0				
UM1PR	21			0.00		25	1	+	8.40	0.004
UM2PR	17			0.00		19			0.00	
UM3PR	0					0				
UP3MD	25	6	+	19.31	0.004	26	2	+	2.15	0.342
UP4MD	18	9	+	25.73	0.002	26	3	+	8.48	0.037

Continued.

Table B.5. Bolton Brush EA left and right observations compared.

Table B.5. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	23	1	+	17.80	0.001	27	1	+	18.95	0.001
L12SS	25	1	+	13.94	0.001	26	1	+	4.66	0.031
LI1CA	27	1	+	8.55	0.003	27			0.00	
LM3CA	1			0.00		1			0.00	
LCDR	24	1	+	4.60	0.032	26	1	+	8.48	0.004
LP3LC	18	9	+	33.86	0.001	25	6	+	22.46	0.001
LP4LC	22	20	+	65.13	0.001	24	16	+	50.06	0.001
LM1AF	20	6	+	23.73	0.001	24	4	+	33.44	0.001
LM1GP	12	1	+	12.00	0.001	11	1	+	1.38	0.24
LM2GP	11	6	+	14.42	0.025	11	1	+	7.22	0.007
LM3GP	0					0				
LM1CN	23	9	+	23.79	0.005	25	4	+	8.58	0.073
LM2CN	13	1	+	8.78	0.003	12	4	+	17.40	0.002
LM3CN	0					0				
LM1DW	19	4	+	12.79	0.012	22	1	+	15.86	0.001
LM1MT	16	1	+	7.48	0.006	24			0.00	
LM2MT	0					0				
LM3MT	1			0.00		0				
LM1PS	20	1	+	7.94	0.005	24	1	+	9.95	0.002
LM2PS	12			0.00		20			0.00	
LM3PS	0					0				
LM1C5	23	16	+	39.61	0.001	25	16	+	43.15	0.001
LM2C5	14	6	+	28.00	0.001	15	6	+	18.83	0.004
LM3C5	0					0				
LM1C6	23	4	+	15.04	0.005	25	4	+	8.48	0.075
LM2C6	14			0.00		15			0.00	
LM3C6	0					0				
LM1C7	17	4	+	12.32	0.015	22	4	+	25.78	0.001
LM2C7	14			0.00		15	1	+	12.39	0.001
LM3C7	0					0				

	Maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	51	4	+	93.47	0.001	50	4	+	86.56	0.001
UI2SS	50	4	+	66.41	0.001	49	4	+	58.15	0.001
UCSS	50	1	+	38.21	0.001	48	4	+	41.46	0.001
UI1LC	51	4	+	37.38	0.001	49	4	+	56.97	0.001
UI1DS	51			0.00		50			0.00	
UI2DS	51			0.00		50			0.00	
UI2PS	51			0.00		50			0.00	
UM3PS	48			0.00		47			0.00	
UI1IG	30			0.00		43			0.00	
UI2IG	9	1	+	9.54	0.002	9			0.00	
UI2CA	51			0.00		50			0.00	
UM3CA	5			0.00		3			0.00	
UI1TD	49	12	+	49.78	0.001	47	6	+	30.68	0.001
UI2TD	41	12	+	75.37	0.001	40	6	+	33.16	0.001
UCTD	43	16	+	106.95	0.001	43	20	+	70.46	0.001
UCMR	43	1	+	9.50	0.002	43			0.00	
UCDR	51	9	+	64.79	0.001	49	12	+	63.31	0.001
UP3TC	48			0.00		47			0.00	
UP4TC	50			0.00		49			0.00	
UP3DS	48			0.00		47			0.00	
UM1MC	50	1	+	27.31	0.001	48	1	+	23.56	0.001
UM2MC	47	6	+	46.23	0.001	50	4	+	52.86	0.001
UM3MC	2			0.00		1			0.00	
UM1HC	49	4	+	49.60	0.001	48	4	+	20.90	0.001
UM2HC	44	16	+	76.51	0.001	46	16	+	68.51	0.001
UM3HC	1			0.00		1			0.00	
UM1C5	48	4	+	22.44	0.001	42	2	+	13.30	0.001
UM2C5	38	2	+	12.67	0.002	41			0.00	
UM3C5	1			0.00		1			0.00	
UM1CB	50	36	+	122.40	0.001	48	30	+	102.02	0.001
UM2CB	46	12	+	46.70	0.001	49	16	+	37.73	0.002
UM3CB	2			0.00		2			0.00	
UM1PR	50			0.00		48			0.00	
UM2PR	46			0.00		48			0.00	
UM3PR	1			0.00		1			0.00	
UP3MD	45	6	+	35.08	0.001	47	2	-	0.088	0.957
UP4MD	49	9	+	19.92	0.018	48	6	+	19.00	0.004

Continued.

Table B.6. UT Dental EA left and right observations compared.

Table B.6. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	51	1	+	22.30	0.001	49	1	+	26.90	0.001
L12SS	51	1	+	38.03	0.001	48	1	+	36.17	0.001
LI1CA	51			0.00		50			0.00	
LM3CA	6			0.00		4			0.00	
LCDR	48	4	+	52.43	0.001	49	4	+	23.26	0.001
LP3LC	48	25	+	180.74	0.001	47	25	+	127.04	0.001
LP4LC	48	25	+	165.39	0.001	46	64	+	141.69	0.001
LM1AF	39	4	+	62.08	0.001	32	1	+	36.03	0.001
LM1GP	17	1	-	0.23	0.611	23	16	+	32.91	0.008
LM2GP	28	2	+	8.35	0.015	24	9	+	24.88	0.003
LM3GP	2	1	+	2.77	0.096	0				
LM1CN	47	4	+	34.28	0.001	43	4	+	35.13	0.001
LM2CN	39	4	+	19.70	0.001	42	4	+	24.19	0.001
LM3CN	2			0.00		1			0.00	
LM1DW	40	4	+	22.99	0.001	42	1	+	14.01	0.001
LM1MT	37			0.00		28			0.00	
LM2MT	2			0.00		3			0.00	
LM3MT	3			0.00		2			0.00	
LM1PS	45			0.00		45			0.00	
LM2PS	42	1	+	16.08	0.001	48	1	+	9.72	0.002
LM3PS	1			0.00		0				
LM1C5	47	16	+	86.87	0.001	46	12	+	67.95	0.001
LM2C5	39	16	+	23.39	0.104	44	6	+	50.08	0.001
LM3C5	2			0.00		1			0.00	
LM1C6	47	4	+	12.82	0.012	46	6	+	32.9	0.001
LM2C6	39	6	+	18.55	0.005	44			0.00	
LM3C6	2			0.00		1			0.00	
LM1C7	47	9	+	102.70	0.001	37	1	+	6.42	0.011
LM2C7	41			0.00		46			0.00	
LM3C7	1			0.00		1			0.00	

	males only										
	maxilla					mandible					
trait	total	df	phi	G2	Prob	trait	total	df	phi	G2	Prob
UI1SS	1			0.00		LI1SS	2			0.00	
UI2SS	4	4	+	8.32	0.081	L12SS	2			0.00	
UCSS	4	1	+	5.55	0.019	LI1CA	8			0.00	
UI1LC	2	1	+	0.00	1	LM3CA	6	1	+	5.41	0.020
UI1DS	2	1	+	0.00	1	LCDR	0				
UI2DS	3	1	+	0.19	0.665	LP3LC	2	1	+	2.00	0.157
UI2PS	5			0.00		LP4LC	2	1	-	2.00	0.157
UM3PS	4			0.00		LM1AF	2			0.00	
UI1IG	2			0.00		LM1GP	1			0.00	
UI2IG	5			0.00		LM2GP	2			0.00	
UI2CA	29			0.00		LM3GP	4	1	+	0.68	0.410
UM3CA	28	1	+	3.50	0.061	LM1CN	2			0.00	
UI1TD	2	1	+	2.77	0.096	LM2CN	2	1	+	2.77	0.096
UI2TD	6	4	+	12.14	0.016	LM3CN	3	1	+	3.00	0.083
UCTD	7	1	+	2.97	0.085	LM1DW	2			0.00	
UCMR	5					LM1MT	2			0.00	
UCDR	4			0.00		LM2MT	0				
UP3TC	12			0.00		LM3MT	1			0.00	
UP4TC	14			0.00		LM1PS	2			0.00	
UP3DS	12			0.00		LM2PS	2			0.00	
UM1MC	21	4	+	29.78	0.001	LM3PS	3	1	+	1.05	0.306
UM2MC	19	1	+	19.59	0.001	LM1C5	1			0.00	
UM3MC	7	6	+	13.38	0.037	LM2C5	2	1	+	2.00	0.157
UM1HC	20	4	+	17.38	0.002	LM3C5	2	1	+	2.00	0.157
UM2HC	19	25	+	50.93	0.002	LM1C6	2			0.00	
UM3HC	5	6	+	6.67	0.353	LM2C6	2			0.00	
UM1C5	18	9	+	24.32	0.004	LM3C6	3			0.00	
UM2C5	18	2	+	9.44	0.009	LM1C7	2	1	+	2.77	0.096
UM3C5	5	1	+	5.00	0.025	LM2C7	2			0.00	
UM1CB	18	30	+	47.42	0.023	LM3C7	3			0.00	
UM2CB	19	4	+	28.88	0.001						
UM3CB	6			0.00							
UM1PR	21			0.00							
UM2PR	18			0.00							
UM3PR	6			0.00							
UP3MD	11	2	+	5.03	0.081						
UP4MD	12	1	+	12.00	0.001						

Table B.7. Civil War collection left and right observations compared.

	males only										
	maxilla					mandible					
trait	total	df	phi	G2	Prob	trait	total	df	phi	G2	Prob
UI1SS	9	4	+	19.10	0.001	LI1SS	8	2	+	6.23	0.044
UI2SS	98	4	+	10.59	0.032	L12SS	8	1	+	6.09	0.014
UCSS	9	1	+	9.54	0.002	LI1CA	8			0.00	
UI1LC	10	1	+	12.22	0.001	LM3CA	7			0.00	
UI1DS	8	1	+	6.03	0.014	LCDR	4			0.00	
UI2DS	8			0.00		LP3LC	7	4	+	14	0.007
UI2PS	10			0.00		LP4LC	7			0.00	
UM3PS	6			0.00		LM1AF	0				
UI1IG	11			0.00		LM1GP	2			0.00	
UI2IG	8			0.00		LM2GP	6	1	+	3.82	0.051
UI2CA	13			0.00		LM3GP	3			0.00	
UM3CA	10	1	+	3.73	0.053	LM1CN	3	1	+	3.82	0.051
UI1TD	9			0.00		LM2CN	5	1	+	2.23	0.135
UI2TD	8	6	1	14.4	0.025	LM3CN	3	4	+	6.59	0.159
UCTD	11	4	+	13.2	0.01	LM1DW	0				
UCMR	7			0.00		LM1MT	0				
UCDR	7	1	+	5.74	0.017	LM2MT	3			0.00	
UP3TC	10			0.00		LM3MT	3			0.00	
UP4TC	9			0.00		LM1PS	3			0.00	
UP3DS	10			0.00		LM2PS	5	1	+	2.23	0.135
UM1MC	5	1	+	5.00	0.025	LM3PS	2	1	+	2.00	0.157
UM2MC	8	1	+	9.00	0.003	LM1C5	3	1	+	1.05	0.306
UM3MC	5			0.00		LM2C5	5	2	+	5.00	0.082
UM1HC	7	4	+	14.06	0.007	LM3C5	3	4	+	6.00	0.199
UM2HC	8	20	+	21.13	0.389	LM1C6	3	4	+	6.59	0.159
UM3HC	5	9	+	15.00	0.091	LM2C6	5			0.00	
UM1C5	6	1	+	2.40	0.121	LM3C6	3	1	+	3.82	0.051
UM2C5	8	1	+	11.09	0.001	LM1C7	2	1	+	2.77	0.096
UM3C5	5	1	-	0.31	0.576	LM2C7	6			0.00	
UM1CB	5	6	+	10.55	0.103	LM3C7	3	1	+	3.82	0.051
UM2CB	7	4	+	11.15	0.025						
UM3CB	5	2	+	5.00	0.082						
UM1PR	3			0.00							
UM2PR	7			0.00							
UM3PR	5			0.00							
UP3MD	8	4	+	11.77	0.019						
UP4MD	9	6	+	15.28	0.018						

Table B.8. Fort William Henry left and right observations compared.

	males only										
	maxilla					mandible					
trait	total	df	phi	G2	Prob	trait	total	df	phi	G2	Prob
UI1SS	10	6	+	9.87	0.130	LI1SS	26	4	+	35.85	0.001
UI2SS	11	9	+	14.42	0.108	L12SS	26	4	+	25.72	0.001
UCSS	10	1	+	8.46	0.004	LI1CA	53			0.00	
UI1LC	13	9	+	25.64	0.002	LM3CA	38	1	+	9.39	0.002
UI1DS	12	3	+	10.81	0.013	LCDR	6	1	+	5.41	0.02
UI2DS	13	4	+	13.94	0.008	LP3LC	22	12	+	54.85	0.001
UI2PS	28			0.00		LP4LC	19	25	+	56.21	0.001
UM3PS	20			0.00		LM1AF	3	4	+	6.00	0.199
UI1IG	24	2	-	0.273	0.872	LM1GP	9	1	+	6.28	0.012
UI2IG	31	3	+	6.06	0.109	LM2GP	9	4	+	4.73	0.316
UI2CA	48			0.00		LM3GP	8	1	+	3.43	0.064
UM3CA	33	1	+	16.74	0.001	LM1CN	10	1	+	10.00	0.002
UI1TD	13	2	+	13.00	0.002	LM2CN	9	1	+	11.46	0.001
UI2TD	22	30	+	47.23	0.024	LM3CN	7	4	+	11.15	0.025
UCTD	20	9	+	41.50	0.001	LM1DW	3			0.00	
UCMR	5			0.00		LM1MT	2	1	+	0.00	
UCDR	5			0.00		LM2MT	5			0.00	
UP3TC	14			0.00		LM3MT	2			0.00	
UP4TC	16			0.00		LM1PS	10	1	-	0.48	0.49
UP3DS	8			0.00		LM2PS	9	4	+	6.82	0.146
UM1MC	17	4	+	14.70	0.005	LM3PS	7			0.00	
UM2MC	21	2	+	21.00	0.001	LM1C5	8	2	+	1.07	0.587
UM3MC	14	4	+	20.98	0.001	LM2C5	8	9	+	24.00	0.004
UM1HC	18	4	+	10.78	0.029	LM3C5	7	16	+	15.11	0.517
UM2HC	18	25	+	34.49	0.098	LM1C6	7	1	+	5.74	0.017
UM3HC	9	15	+	27.00	0.029	LM2C6	7			0.00	
UM1C5	9	4	+	18.00	0.001	LM3C6	8	1	+	6.03	0.014
UM2C5	12	9	+	18.05	0.035	LM1C7	8	1	+	0.17	0.676
UM3C5	10	9	+	17.08	0.047	LM2C7	11			0.00	
UM1CB	14	24	+	47.60	0.003	LM3C7	5			0.00	
UM2CB	17	2	+	17.00	0.001						
UM3CB	7			0.00							
UM1PR	10			0.00							
UM2PR	14			0.00							
UM3PR	11			0.00							
UP3MD	8	4	+	12.82	0.012						
UP4MD	9	6	+	12.50	0.052						

Table B.9. Hamann-Todd EA left and right observations compared.

	maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	8	4	+	11.09	0.026	4	1	+	4.50	0.034
UI2SS	11	9	+	23.98	0.004	7	4	+	15.11	0.004
UCSS	16	4	+	19.88	0.001	10	1	+	4.46	0.035
UI1LC	6	2	+	2.63	0.268	4	1	+	5.55	0.019
UI1DS	6			0.00		4			0.00	
UI2DS	10			0.00		7			0.00	
UI2PS	11			0.00		7	1	+	5.74	0.017
UM3PS	18			0.00		5			0.00	
UI1IG	11			0.00		5			0.00	
UI2IG	12			0.00		7			0.00	
UI2CA	40			0.00		18	1	+	7.73	0.005
UM3CA	38	1	+	6.42	0.011	17	1	+	15.84	0.001
UI1TD	7	9	+	13.38	0.146	3	2	+	3.82	0.223
UI2TD	11	12	+	18.98	0.089	6	2	+	7.064	0.022
UCTD	17	25	+	40.12	0.028	10	16	+	23.87	0.092
UCMR	15			0.00		11			0.00	
UCDR	9			0.00		8	1	-	0.29	0.592
UP3TC	25			0.00		9			0.00	
UP4TC	25			0.00		8			0.00	
UP3DS	23			0.00		9			0.00	
UM1MC	22	4	+	27.52	0.001	11	1	+	8.39	0.004
UM2MC	24	6	+	32.40	0.001	15	4	+	15.01	0.005
UM3MC	16	4	+	31.18	0.001	5	4	+	10.55	0.032
UM1HC	21	4	+	26.34	0.001	11	1	+	9.42	0.002
UM2HC	23	20	+	40.16	0.005	13	16	+	33.96	0.006
UM3HC	15	16	+	46.92	0.001	5	3	+	5.00	0.172
UM1C5	16	1	+	8.24	0.004	8	1	+	3.26	0.071
UM2C5	20	2	+	15.15	0.001	11	1	+	3.93	0.047
UM3C5	12	12	+	18.87	0.092	5	16	+	16.09	0.446
UM1CB	16	36	+	47.85	0.089	9	30	+	27.41	0.602
UM2CB	24			0.00		14	2	+	3.39	0.066
UM3CB	16	1	+	7.21	0.007	5	1	+	5.00	0.025
UM1PR	19			0.00		9			0.00	
UM2PR	24	2	+	9.40	0.009	14			0.00	
UM3PR	18			0.00		5			0.00	
UP3MD	20	4	+	25.56	0.001	6	2	+	5.41	0.067
UP4MD	17	4	+	24.93	0.001	5	4	+	9.50	0.050

Continued.

Table B.10. EU excluding Poundbury left and right observations compared.

Table. B 10. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	12			0.00		6			0.00	
L12SS	17	1	+	12.32	0.001	6			0.00	
LI1CA	34			0.00		15			0.00	
LM3CA	28	1	+	13.05	0.001	10	1	+	10.00	0.002
LCDR	8	6	+	11.77	0.067	5			0.00	
LP3LC	22	16	+	58.49	0.001	7	9	+	11.08	0.270
LP4LC	18	16	+	33.33	0.007	5	16	+	16.09	0.446
LM1AF	13	4	+	14.27	0.006	2	1	+	2.77	0.096
LM1GP	16	1	+	4.75	0.032	3			0.00	
LM2GP	13	4	+	7.25	0.123	5			0.00	
LM3GP	15	2	+	10.72	0.005	3	1	+	3.82	0.051
LM1CN	11	4	+	16.71	0.002	5			0.00	
LM2CN	13	1	+	7.05	0.008	8	2	+	11.09	0.004
LM3CN	13	4	+	12.32	0.015	4	1	+	1.73	0.189
LM1DW	11	1	+	6.70	0.010	3			0.00	
LM1MT	9	1	+	6.28	0.012	4	1	+	4.5	0.034
LM2MT	7	1	-	0.06	0.81	2			0.00	
LM3MT	9	1	+	2.81	0.094	4			0.00	
LM1PS	14	1	+	7.82	0.005	3			0.00	
LM2PS	12	1	+	0.715	0.398	7	1	+	5.74	0.017
LM3PS	16			0.00		3			0.00	
LM1C5	11	16	+	28.48	0.028	5	2	+	6.73	0.035
LM2C5	13	1	+	7.05	0.008	8	9	+	16.64	0.055
LM3C5	13	12	+	16.28	0.179	4	4	+	5.55	0.0236
LM1C6	11	4	+	13.20	0.010	5			0.00	
LM2C6	13			0.00		8			0.00	
LM3C6	13	1	+	7.05	0.008	4			0.00	
LM1C7	17			0.00		3			0.00	
LM2C7	17			0.00		8	1	+	3.26	0.071
LM3C7	17	1	+	7.61	0.001	4			0.00	

	maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	15	2	+	20.19	0.001	17	4	+	27.48	0.001
UI2SS	14	4	+	22.38	0.001	16	2	+	12.99	0.002
UCSS	16	4	+	22.49	0.001	14	1	+	11.48	0.001
UI1LC	16	9	+	31.47	0.001	18	4	+	24.95	0.001
UI1DS	16			0.00		18			0.00	
UI2DS	15			0.00		16			0.00	
UI2PS	8			0.00		15			0.00	
UM3PS	11			0.00		10	1	+	6.50	0.011
UI1IG	18			0.00		19			0.00	
UI2IG	15	2	+	7.35	0.025	17	2	+	4.83	0.089
UI2CA	21			0.00		26	6		0.00	
UM3CA	20	1	+	7.94	0.005	16	1	+	1.19	0.276
UI1TD	12	9	+	18.05	0.035	11	2	+	12.89	0.002
UI2TD	13	12	+	20.91	0.049	11	9	+	21.89	0.009
UCTD	10	16	+	25.60	0.060	12	9	+	21.31	0.011
UCMR	10			0.00		12			0.00	
UCDR	5			0.00		12	1	+	4.11	0.043
UP3TC	18			0.00		19			0.00	
UP4TC	16			0.00		17			0.00	
UP3DS	17			0.00		19			0.00	
UM1MC	15	4	+	17.4	0.002	17	1	+	13.08	0.001
UM2MC	18			0.00		17	4	+	14.27	0.006
UM3MC	10	1	+	3.56	0.059	8	1	+	10.59	0.001
UM1HC	13	4	+	10.33	0.035	18	4	+	27.92	0.001
UM2HC	15	16	+	29.78	0.019	16	12	+	33.22	0.001
UM3HC	10	9	+	20.59	0.015	8	9	+	17.32	0.044
UM1C5	5	2	+	6.73	0.035	14	4	+	16.75	0.002
UM2C5	14	9	+	12.22	0.202	14	1	-	0.154	0.695
UM3C5	9	9	+	18.05	0.035	7			0.00	
UM1CB	4	1	+	4.50	0.034	13	16	+	33.05	0.007
UM2CB	12			0.00		14			0.00	
UM3CB	8			0.00		9			0.00	
UM1PR	6			0.00		12			0.00	
UM2PR	17	2	+	7.61	0.022	15			0.00	
UM3PR	10			0.00		7			0.00	
UP3MD	12	2	+	6.99	0.030	14	2	+	7.21	0.027
UP4MD	3			0.00		12	2	+	6.88	0.032

Continued.

Table B.11. Poundbury left and right observations compared.

Table B. 11. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	15	1	+	7.35	0.007	21			0.00	
L12SS	17			0.00		23			0.00	
LI1CA	22			0.00		26			0.00	
LM3CA	18					24	1	+	4.50	0.034
LCDR	6			0.00		17			0.00	
LP3LC	15	36	+	56.97	0.014	20	25	+	65.60	0.001
LP4LC	14	20	+	37.29	0.011	17	36	+	46.71	0.109
LM1AF	1			0.00		5	6	+	7.78	0.255
LM1GP	6			0.00		13			0.00	
LM2GP	13	1	+	1.99	0.158	15	4	+	2.86	0.582
LM3GP	11	1	+	4.89	0.027	8	4	+	9.00	0.061
LM1CN	11	4	+	13.20	0.010	15	1	+	15.01	0.001
LM2CN	13	1	+	16.05	0.001	16	4	+	11.01	0.026
LM3CN	11	9	+	20.16	0.017	12	4	+	10.93	0.027
LM1DW	1			0.00		9	2	+	9.54	0.009
LM1MT	0					7	1	+	5.74	0.017
LM2MT	6			0.00		7	1	+	1.24	0.265
LM3MT	6	1	-	0.40	0.526	5	1	+	2.23	0.135
LM1PS	4			0.00		8	2	+	4.36	0.113
LM2PS	10	1	+	12.22	0.001	11	1	+	3.93	0.047
LM3PS	14	1	-	0.321	0.571	11			0.00	
LM1C5	11	9	+	19.97	0.001	15	12	+	39.64	0.001
LM2C5	13	4	+	21.59	0.001	16	3	+	7.48	0.001
LM3C5	11	12	+	21.21	0.047	12	6	+	17.32	0.008
LM1C6	11	1	+	6.70	0.01	15			0.00	
LM2C6	13			0.00		16			0.00	
LM3C6	11	4	+	9.39	0.052	11			0.00	
LM1C7	8	4	+	11.77	0.019	15	6	+	18.83	0.004
LM2C7	14	1	+	4.43	0.035	14			0.00	
LM3C7	12			0.00		12	4	+	7.08	0.0131

	maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	11	9	+	22.80	0.007	5	1	+	6.73	0.025
UI2SS	18	12	+	32.82	0.001	6	1	+	7.64	0.006
UCSS	26	4	+	47.09	0.001	12	4	+	20.86	0.001
UI1LC	13	2	+	17.95	0.001	6	4	+	12.14	0.016
UI1DS	13			0.00		5			0.00	
UI2DS	17	4	+	8.8	0.066	7	1	+	2.97	0.085
UI2PS	27	1	+	8.55	0.003	9			0.00	
UM3PS	70			0.00		31			0.00	
UI1IG	25			0.00		8			0.00	
UI2IG	27	1	-	0.08	0.781	10			0.00	
UI2CA	93			0.00		51			0.00	
UM3CA	92			0.00		48	1	+	9.72	0.002
UI1TD	17	16	+	30.10	0.017	6	6	+	12.14	0.059
UI2TD	23	36	+	61.60	0.005	9	16	+	22.92	0.116
UCTD	28	25	+	67.80	0.001	12	20	+	29.82	0.073
UCMR	21	6	+	18.48	0.005	12	4	+	11.04	0.026
UCDR	12	12	+	13.18	0.356	9	9	+	16.32	0.06
UP3TC	69			0.00		31			0.00	
UP4TC	63			0.00		29			0.00	
UP3DS	68			0.00		33			0.00	
UM1MC	65	4	+	52.25	0.001	39	4	+	30.70	0.001
UM2MC	74	9	+	80.51	0.001	40	4	+	33.23	0.001
UM3MC	58	9	+	64.21	0.001	31	4	+	22.48	0.001
UM1HC	67	4	+	67.50	0.001	41	6	+	67.14	0.001
UM2HC	72	25	+	125.67	0.001	38	30	+	74.54	0.001
UM3HC	54	25	+	90.28	0.001	29	25	+	41.37	0.021
UM1C5	30	25	+	67.07	0.001	20	16	+	47.27	0.001
UM2C5	45	12	+	61.94	0.001	32	9	+	35.95	0.001
UM3C5	44	25	+	52.36	0.001	25	12	+	34.67	0.001
UM1CB	39	30	+	81.94	0.001	28	36	+	76.16	0.001
UM2CB	57	15	+	36.92	0.001	35	6	+	15.40	0.017
UM3CB	53	20	+	35.62	0.017	29	6	+	14.56	0.024
UM1PR	45	1	+	16.36	0.001	36			0.00	
UM2PR	64	1	+	4.79	0.029	38			0.00	
UM3PR	56			0.00		30			0.00	
UP3MD	48	6	+	47.31	0.001	24	9	+	31.29	0.001
UP4MD	30	9	+	27.78	0.001	19	9	+	25.10	0.003

Continued.

Table B.12. West Africans left and right observations compared.

Table B. 12. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	24	4	+	29.57	0.001	4			0.00	
L12SS	22	1	+	10.06	0.002	6	1	+	2.63	0.105
LI1CA	74			0.00		36			0.00	
LM3CA	77			0.00		36	1	+	6.37	0.012
LCDR	21	12	+	37.37	0.001	7	6	+	9.33	0.156
LP3LC	43	36	+	117.7	0.001	14	20	+	42.35	0.002
LP4LC	41	49	+	226.99	0.001	14	25	+	43.94	0.011
LM1AF	27	9	+	66.82	0.001	19	16	+	42.21	0.001
LM1GP	41	1	+	12.16	0.001	23	1	+	8.23	0.004
LM2GP	51	4	+	19.34	0.001	25	4	+	16.92	0.008
LM3GP	51	4	+	19.41	0.001	21	4	+	15.42	0.004
LM1CN	45	1	+	35.34	0.001	24	1	+	21.63	0.001
LM2CN	41	4	+	55.14	0.001	26	4	+	24.18	0.001
LM3CN	46	9	+	58.26	0.001	20	4	+	17.40	0.002
LM1DW	14	6	+	18.76	0.001	11	9	+	19.48	0.021
LM1MT	13	1	+	11.16	0.001	13	1	+	17.32	0.001
LM2MT	37	1	+	8.49	0.004	23	1	+	1.06	0.304
LM3MT	28	1	+	0.77	0.379	17	1	+	2.78	0.095
LM1PS	36	4	+	44.82	0.001	24	1	+	8.55	0.003
LM2PS	48	1	+	34.16	0.001	29	1	+	26.55	0.001
LM3PS	52	1	+	5.61	0.018	22	6	+	7.08	0.314
LM1C5	43	1	+	22.96	0.001	25	4	+	27.29	0.001
LM2C5	41	25	+	93.39	0.001	26	25	+	54.41	0.001
LM3C5	46	20	+	74.64	0.001	20	20	+	34.87	0.004
LM1C6	44	9	+	49.85	0.001	24	4	+	26.13	0.001
LM2C6	41	9	+	41.56	0.001	26	2	+	5.79	0.055
LM3C6	46	12	+	56.90	0.001	20	6	+	14.47	0.025
LM1C7	40	16	+	67.41	0.001	22	16	+	47.86	0.001
LM2C7	50	9	+	33.74	0.001	28	4	+	29.10	0.001
LM3C7	51	16	+	53.82	0.001	23	9	+	22.98	0.006

	maxilla									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
UI1SS	18	4	+	27.03	0.001	15	4	+	29.73	0.001
UI2SS	19	12	+	45.15	0.001	16	4	+	31.18	0.001
UCSS	19	4	+	35.28	0.001	15	4	+	26.76	0.001
UI1LC	18	9	+	35.32	0.001	15	9	+	39.69	0.001
UI1DS	18			0.00		15			0.00	
UI2DS	19			0.00		16	1	+	7.48	0.006
UI2PS	19			0.00		16			0.00	
UM3PS	2			0.00		0				
UI1IG	18	1	+	7.72	0.005	14			0.00	
UI2IG	17	4	+	12.32	0.015	11	1	-	0.2	0.654
UI2CA	19			0.00		16			0.00	
UM3CA	2			0.00		1			0.00	
UI1TD	18	4	+	12.56	0.014	15	9	+	18.83	0.027
UI2TD	19	4	+	11.74	0.019	15	9	+	16.35	0.06
UCTD	19	16	+	41.43	0.001	15	36	+	50.38	0.056
UCMR	19	4	+	12.62	0.013	15	2	+	7.96	0.019
UCDR	19	20	+	39.27	0.006	15	20	+	29.78	0.073
UP3TC	19			0.00		16			0.00	
UP4TC	19			0.00					0.00	
UP3DS	19			0.00		16			0.00	
UM1MC	19	2	+	19.56	0.001	16	1	+	18.00	0.001
UM2MC	17	4	+	29.79	0.001	16	1	+	21.93	0.001
UM3MC	1			0.00		0				
UM1HC	19	4	+	13.47	0.009	16	4	+	16.67	0.002
UM2HC	17	16	+	36.50	0.002	15	9	+	31.34	0.001
UM3HC	1			0.00		0				
UM1C5	19	9	+	34.97	0.001	16	12	+	24.76	0.016
UM2C5	17	4	+	16.92	0.002	14	9	+	30.75	0.001
UM3C5	1			0.00		0				
UM1CB	19	49	+	47.58	0.531	16	25	+	44.00	0.011
UM2CB	19	12	+	23.17	0.026	16	9	+	22.49	0.007
UM3CB	1			0.00		0				
UM1PR	18			0.00		16			0.00	
UM2PR	17			0.00		15			0.00	
UM3PR	1			0.00		1				
UP3MD	19	4	+	24.06	0.001	16	1	+	12.06	0.001
UP4MD	19	9	+	36.16	0.001	14	4	+	16.75	0.002

Continued.

Table B.13. SA left and right observations compared.

Table B.13. Continued.

	mandible									
	male					female				
trait	total	df	phi	G2	Prob	total	df	phi	G2	Prob
LI1SS	18	1	+	16.22	0.001	16	1	+	15.44	0.001
L12SS	17	1	+	20.60	0.001	16	1	+	18.00	0.001
LI1CA	19			0.00		16			0.00	
LM3CA	3			0.00		3			0.00	
LCDR	16	20	+	33.45	0.030	13	16	+	24.23	0.085
LP3LC	18	30	+	52.05	0.008	14	30	+	37.62	0.160
LP4LC	18	49	+	63.82	0.076	15	30	+	46.28	0.029
LM1AF	19	9	+	35.50	0.001	15	16	+	35.87	0.003
LM1GP	15	1	-	0.65	0.422	14			0.00	
LM2GP	17	4	-	11.43	0.022	15	4	+	6.30	0.178
LM3GP	1			0.00		2	1	-	2.77	0.096
LM1CN	19	1	+	19.59	0.001	15	1	+	10.51	0.001
LM2CN	16	4	+	32.77	0.001	14	4	+	30.61	0.001
LM3CN	1			0.00		2			0.00	
LM1DW	12	2	+	10.72	0.009	13	4	+	9.70	0.046
LM1MT	15	1	+	13.69	0.001	13	1	+	6.29	0.012
LM2MT	2			0.00		3	1	+	1.05	0.306
LM3MT	2			0.00		3	1	+	3.82	0.051
LM1PS	19	1	-	0.11	0.739	16			0.00	
LM2PS	17	1	+	4.83	0.028	16	2	+	7.48	0.024
LM3PS	2			0.00		1			0.00	
LM1C5	19	4	+	21.90	0.001	15	4	+	21.21	0.001
LM2C5	17	25	+	49.23	0.003	14	16	+	36.44	0.003
LM3C5	1			0.00		2	1	+	2.77	0.096
LM1C6	19	4	+	31.04	0.001	15	6	+	25.28	0.001
LM2C6	17	4	+	23.05	0.001	14	4	+	24.98	0.001
LM3C6	1			0.00		2			0.00	
LM1C7	17	9	+	27.16	0.001	15	9	+	28.74	0.001
LM2C7	18	4	+	34.49	0.001	14	4	+	19.12	0.001
LM3C7	1			0.00		1			0.00	

APPENDIX C

TRAIT FREQUENCIES IN MALES AND FEMALES COMPARED

trait	total	df	phi	G2	Prob
WING	0				
DIAS	0				
UI1SS	287	6	-	4.64	0.59
UI2SS	285	6	+	4.60	0.60
UCSS	296	3	+	0.12	0.44
UI1LC	289	4	-	5.35	0.25
UI1DS	292	1	+	5.83	0.02
UI2DS	286	1	+	0.02	0.90
UI2PS	295	1	-	0.87	0.35
UM3PS	274	1	-	2.82	0.09
UI1IG	288	1	-	0.98	0.32
UI2IG	287	4	-	3.95	0.41
UI2CA	300	1	+	0.40	0.53
UM3CA	283	1	-	1.37	0.24
UI1TD	291	6	+	6.72	0.35
UI2TD	281	7	+	11.68	0.11
UCTD	278	6	+	10.16	0.12
UCMR	270	3	+	2.60	0.46
UCDR	244	4	-	5.19	0.27
UP3MD	286	3	-	2.50	0.48
UPRMD	273	3	-	1.80	0.62
UP3TC	299			0.00	
UP4TC	290	1	-	1.36	0.24
UP3DS	298	1	-	1.35	0.25
UM1MC	279	3	+	3.37	0.34
UM2MC	286	3	+	1.91	0.59
UM3MC	261	4	-	4.84	0.30
UM1HC	279	4	-	5.26	0.26
UM2HC	284	5	+	11.6	0.04
UM3HC	257	4	+	8.83	0.07
UM1C5	274	4	+	4.26	0.37
UM2C5	281	4	-	4.10	0.72
UM3C5	254	6	+	16.37	0.01
UM1CB	267	7	+	14.46	0.04
UM2CB	279	7	+	4.25	0.75
UM3CB	261	6	-	3.11	0.80
UM1PR	210	1	+	0.41	0.52
UM2PR	242	4	+	7.00	0.14
UM3PR	169	3	+	4.07	0.26

trait	total	df	phi	G2	Prob
LI1SS	286	2	-	1.28	0.53
L12SS	290	2	+	1.50	0.47
LI1CA	293			0.00	
LM3CA	284	1	-	2.73	0.10
LCDR	232	5	+	9.56	0.09
LP3LC	292	9	+	15.87	0.07
LP4LC	292	9	+	5.81	0.76
LM1AF	231	4	-	5.22	0.27
LM1GP	173	1	-	0.49	0.48
LM2GP	203	3	-	3.25	0.35
LM3GP	203	3	+	3.33	0.34
LM1CN	245	2	+	0.453	0.80
LM2CN	275	3	+	6.34	0.10
LM3CN	253	3	+	5.13	0.16
LM1DW	202	3	-	5.12	0.16
LM1MT	212	2	-	3.50	0.17
LM2MT	281	1	-	1.46	0.23
LM3MT	279	1	+	0.34	0.85
LM1PS	235	3	+	2.87	0.41
LM2PS	263	2	+	1.50	0.47
LM3PS	241	2	-	4.22	0.12
LM1C5	244	5	+	3.47	0.63
LM2C5	276	5	+	8.83	0.12
LM3C5	253	5	+	24.51	0.00
LM1C6	245	3	+	2.13	0.55
LM2C6	275	4	+	2.23	0.69
LM3C6	252	5	-	3.29	0.66
LM1C7	240	4	+	7.81	0.10
LM2C7	283	5	-	3.87	0.57
LM3C7	257	5	+	1.99	0.85

Table C.1. Freedman's Cemetery male and female observations compared.

trait	total	df	phi	G2	Prob
WING	94	3	+	7.55	0.06
DIAS	77	1	-	2.13	0.15
UI1SS	99	3	+	1.5	0.68
UI2SS	96	5	-	4.8	0.44
UCSS	96	3	-	2.47	0.48
UI1LC	99	3	-	4.13	0.25
UI1DS	99			0.00	
UI2DS	96			0.00	
UI2PS	98	1	-	0.26	0.61
UM3PS	18	1	-	1.45	0.23
UI1IG	73			0.00	
UI2IG	31	1	+	3.05	0.08
UI2CA	99	1	-	1.13	0.29
UM3CA	19			0.00	
UI1TD	19	6	-	12.86	0.05
UI2TD	86	6	+	3.16	0.79
UCTD	91	6	+	3.54	0.74
UCMR	88	3	-	5.45	0.14
UCDR	98	4	+	5.41	0.25
UP3MD	92	3	+	2.96	0.40
UPRMD	98	3	+	3.56	0.31
UP3TC	92			0.00	
UP4TC	97			0.00	
UP3DS	91			0.00	
UM1MC	99	2	-	4.05	0.13
UM2MC	92	2	-	4.06	0.13
UM3MC	11	1	-	1.30	0.34
UM1HC	98	2	+	1.44	0.49
UM2HC	86	4	+	0.67	0.96
UM3HC	9	3	-	3.00	0.39
UM1C5	93	3	+	3.10	0.38
UM2C5	81	4	-	2.38	0.67
UM3C5	7	2	-	2.83	0.24
UM1CB	98	6	+	6.92	0.33
UM2CB	89	4	+	6.03	0.20
UM3CB	9			0.00	
UM1PR	97			0.00	
UM2PR	87			0.00	
UM3PR	8			0.00	

trait	total	df	phi	G2	Prob
LI1SS	98	2	-	1.48	0.48
L12SS	99	2	+	1.51	0.47
LI1CA	99	1	+	1.38	0.24
LM3CA	21			0.00	
LCDR	97	4	+	20.59	0.00
LP3LC	91	9	+	12.09	0.21
LP4LC	98	8	+	5.37	0.72
LM1AF	86	4	+	6.16	0.19
LM1GP	36	1	+	1.42	0.23
LM2GP	53	1	-	2.34	0.13
LM3GP	6	1	-	0.91	0.34
LM1CN	97	2	+	3.93	0.14
LM2CN	74	2	+	0.57	0.75
LM3CN	8	2	+	1.73	0.42
LM1DW	82	3	+	1.24	0.74
LM1MT	75	1	+	2.02	0.16
LM2MT	90	1	-	0.16	0.69
LM3MT	83	1	-	0.14	0.71
LM1PS	90	1	-	0.73	0.39
LM2PS	91	1	-	0.96	0.33
LM3PS	12	1	-	1.88	0.17
LM1C5	97	4	+	3.73	0.44
LM2C5	74	4	+	2.79	0.59
LM3C5	8	2	-	6.59	0.04
LM1C6	97	3	+	3.41	0.33
LM2C6	74	3	+	3.51	0.32
LM3C6	7	2	+	1.24	0.57
LM1C7	94	4	+	6.17	0.19
LM2C7	92	4	-	9.25	0.06
LM3C7	9	1	+	1.28	0.26

Table C.2. UT Dental AA male and female observations compared.

trait	total	df	phi	G2	Prob
WING	93	1	+	1.41	0.234
DIAS	79	1	-	2.51	0.113
UI1SS	101	2	+	2.46	0.292
UI2SS	101	2	+	2.16	0.340
UCSS	100	2	+	2.74	0.255
UI1LC	101	2	+	1.80	0.408
UI1DS	101			0.00	
UI2DS	101			0.00	
UI2PS	101	1	-	0.00	0.976
UM3PS	11	1	-	1.30	0.255
UI1IG	85			0.00	
UI2IG	29	1	+	2.24	0.134
UI2CA	101			0.00	
UM3CA	13			0.00	
UI1TD	99	4	+	8.80	0.066
UI2TD	93	4	+	3.97	0.411
UCTD	97	5	+	6.52	0.259
UCMR	97	1	+	1.34	0.248
UCDR	101	4	-	2.64	0.620
UP3MD	96	3	+	8.39	0.039
UPRMD	100	3	+	1.39	0.708
UP3TC	96			0.976	
UP4TC	101			0.976	
UP3DS	96			0.976	
UM1MC	101	1	-	0.08	0.778
UM2MC	98	2	+	0.66	0.719
UM3MC	6	1	-	3.82	0.051
UM1HC	99	2	+	1.54	0.463
UM2HC	96	4	+	14.26	0.007
UM3HC	5	3	+	6.73	0.081
UM1C5	98	2	-	5.49	0.064
UM2C5	93	2	+	3.57	0.168
UM3C5	5			0.976	
UM1CB	100	6	+	5.61	0.468
UM2CB	97	5	-	3.88	0.568
UM3CB	5	1	-	2.23	0.135
UM1PR	100			0.976	
UM2PR	97	1	+	1.42	0.234
UM3PR	3			0.976	

trait	total	df	phi	G2	Prob
LI1SS	101	1	+	0.64	0.423
L12SS	101	1	+	0.64	0.423
LI1CA	101	1	-	1.42	0.234
LM3CA	12			0.00	
LCDR	100	2	+	4.36	0.113
LP3LC	99	6	+	9.42	0.151
LP4LC	99	8	+	11.20	0.193
LM1AF	84	2	+	8.43	0.015
LM1GP	40	4	-	6.06	0.195
LM2GP	52	3	-	7.05	0.070
LM3GP	2			0.00	
LM1CN	95	2	-	1.43	0.490
LM2CN	92	4	+	7.18	0.127
LM3CN	4	1	-	1.73	0.189
LM1DW	90	2	+	0.69	0.707
LM1MT	76			0.00	
LM2MT	87	1	-	0.00	0.969
LM3MT	81	1	+	0.00	0.963
LM1PS	96	1	-	0.00	0.976
LM2PS	99	1	+	0.37	0.542
LM3PS	5	1	+	1.19	0.276
LM1C5	98	4	+	13.8	0.008
LM2C5	93	5	+	9.7	0.084
LM3C5	4	1	-	1.73	0.189
LM1C6	98	3	-	4.22	0.239
LM2C6	93	3	+	4.46	0.216
LM3C6	4			0	
LM1C7	96	3	+	4.31	0.230
LM2C7	98	1	-	0	0.977
LM3C7	3			0	

Table C.3. UT Dental EA male and female observations compared.

trait	total	df	phi	G2	Prob
WING	15	3	+	3.82	0.282
DIAS	15	1	+	0.07	0.788
UI1SS	25	2	+	2.09	0.351
UI2SS	36	4	+	1.90	0.754
UCSS	46	3	-	1.77	0.621
UI1LC	21	3	-	2.62	0.454
UI1DS	25			0.976	
UI2DS	36	1	+	1.68	0.195
UI2PS	36	1	+	0.976	0.001
UM3PS	40			0.976	
UI1IG	30			0.976	
UI2IG	38	2	+	1.05	0.592
UI2CA	60	1	-	0.30	0.584
UM3CA	58	1	-	0.18	0.675
UI1TD	26	4	+	1.16	0.885
UI2TD	32	4	+	4.43	0.351
UCTD	51	6	+	8.24	0.221
UCMR	51	1	+	0.82	0.365
UCDR	42	2	-	4.72	0.094
UP3MD	43	3	-	2.65	0.449
UPRMD	46	3	-	1.17	0.76
UP3TC	53			0.976	
UP4TC	58			0.976	
UP3DS	53			0.976	
UM1MC	48	2	-	0.97	0.616
UM2MC	54	3	-	1.10	0.776
UM3MC	38	3	+	4.58	0.205
UM1HC	45	2	+	1.41	0.494
UM2HC	50	5	+	8.25	0.143
UM3HC	37	4	-	5.36	0.252
UM1C5	35	2	-	2.99	0.224
UM2C5	38	2	+	1.70	0.428
UM3C5	33	5	-	7.07	0.215
UM1CB	40	7	-	11.29	0.126
UM2CB	53	1	-	3.06	0.080
UM3CB	37	3	-	4.06	0.255
UM1PR	40			0.976	
UM2PR	51	1	-	0.19	0.664
UM3PR	36			0.976	

trait	total	df	phi	G2	Prob
LI1SS	29	1	-	0.22	0.640
L12SS	35	1	+	2.13	0.145
LI1CA	51			0.976	
LM3CA	47	1	+	0.976	0.970
LCDR	35	3	+	3.57	0.312
LP3LC	43	6	+	7.18	0.305
LP4LC	40	7	+	11.5	0.119
LM1AF	24	3	-	9.38	0.025
LM1GP	19	1	+	0.73	0.393
LM2GP	18	2	-	1.44	0.486
LM3GP	18	1	-	0.18	0.668
LM1CN	28	2	+	6.58	0.037
LM2CN	36	2	-	6.14	0.047
LM3CN	26	2	-	1.03	0.599
LM1DW	24	1	+	0.976	.001
LM1MT	21	1	-	1.64	0.200
LM2MT	31	1	+	3.09	0.079
LM3MT	33	1	+	1.08	0.298
LM1PS	26	1	-	0.01	0.94
LM2PS	31	1	+	1.60	0.206
LM3PS	29	1	-	0.05	0.822
LM1C5	27	4	+	6.70	0.152
LM2C5	36	4	-	7.18	0.127
LM3C5	27	4	-	3.14	0.535
LM1C6	27	2	+	3.10	0.213
LM2C6	36	1	-	2.26	0.133
LM3C6	26	1	+	0.75	0.385
LM1C7	30	1	-	2.37	0.124
LM2C7	39	1	-	0.72	0.396
LM3C7	32	2	-	1.20	0.550

Table C.4. EU excluding Poundbury male and female observations compared.

trait	total	df	phi	G2	Prob
WING	30	2	+	3.95	0.139
DIAS	30	1	-	0.85	0.358
UI1SS	22	3	-	4.03	0.259
UI2SS	47	4	+	2.74	0.602
UCSS	77	3	-	0.87	0.833
UI1LC	26	3	-	3.38	0.337
UI1DS	25	1	+	0.46	0.499
UI2DS	50	2	+	0.629	0.730
UI2PS	67	1	-	0.89	0.346
UM3PS	134			0.976	
UI1IG	50			0.976	
UI2IG	67	2	+	0.94	0.625
UI2CA	148			0.976	
UM3CA	147	1	-	2.17	0.141
UI1TD	35	5	-	2.16	0.827
UI2TD	57	6	+	4.25	0.643
UCTD	84	6	+	14.13	0.028
UCMR	75	3	+	7.65	0.054
UCDR	49	5	-	2.44	0.786
UP3MD	101	3	+	1.39	0.708
UPRMD	92	3	+	3.90	0.272
UP3TC	127			0.00	
UP4TC	132	1	+	0.79	0.373
UP3DS	126			0.00	
UM1MC	133	2	-	1.58	0.455
UM2MC	140	3	-	1.08	0.780
UM3MC	127	4	+	6.75	0.150
UM1HC	134	2	+	1.65	0.438
UM2HC	138	6	+	7.48	0.279
UM3HC	124	5	+	4.27	0.512
UM1C5	68	5	+	9.25	0.099
UM2C5	102	4	+	3.88	0.422
UM3C5	107	5	+	7.51	0.185
UM1CB	91	6	+	16.38	0.012
UM2CB	118	5	+	3.38	0.642
UM3CB	123	6	+	10.4	0.109
UM1PR	106	1	+	0.00	1
UM2PR	131	1	+	0.53	0.468
UM3PR	120	2	+	1.59	0.452

trait	total	df	phi	G2	Prob
LI1SS	42	1	+	1.44	0.231
L12SS	55	2	+	0.84	0.656
LI1CA	111			0.976	
LM3CA	117	1	-	1.68	0.195
LCDR	50	4	-	2.25	0.690
LP3LC	91	9	+	12.9	0.169
LP4LC	92	8	+	10.8	0.213
LM1AF	63	4	-	2.63	0.622
LM1GP	64	1	+	0.01	0.923
LM2GP	76	2	-	0.35	0.838
LM3GP	72	2	+	6.12	0.047
LM1CN	92	2	+	2.80	0.247
LM2CN	87	2	+	2.95	0.228
LM3CN	91	3	+	4.70	0.195
LM1DW	44	3	-	1.30	0.729
LM1MT	40	1	-	0.44	0.506
LM2MT	90	1	-	0.57	0.451
LM3MT	90	1	-	2.07	0.151
LM1PS	78	3	+	1.80	0.615
LM2PS	96	1	+	2.21	0.137
LM3PS	99	2	-	6.60	0.037
LM1C5	90	3	+	4.40	0.222
LM2C5	87	5	+	4.08	0.539
LM3C5	91	5	+	2.56	0.768
LM1C6	91	3	+	5.15	0.161
LM2C6	87	3	+	8.23	0.041
LM3C6	91	4	+	6.27	0.180
LM1C7	85	4	+	3.55	0.470
LM2C7	106	3	+	1.54	0.670
LM3C7	101	4	-	5.57	0.234

Table C.5. West African male and female observations compared.

APPENDIX D

FORENSIC PROBABILITY TABLES

How to use these tables:

1. Record observations of the dental traits listed in table 5.15. The traits should be score as present, absent, or unobservable, according to the breakpoints also listed in table 5.15.

2. Compare the scores with tables D.2, D.3, and D.4. Table D.1 provides the frequency of each individual trait in the samples. Tables D2, D3, and D.4 provide probabilities of presence and absence combinations for two, three, and four trait combinations, respectively. In the tables, "0" refers to a trait observed to be absent, and "1" refers to a trait observed to be present. For each comparison that can be made, record the probability that the individual would be classified in each race. Also, record whether the probability given is a Bayesian probability (BP) or a logistic regression probability (LP). Probabilities computed by logistic regression are preferable, but are not always computable.

3. Choose an acceptable level of probability (I used 85.0%) and note the race assigned by each result above that level. The determination of social race affiliation should be based on these probabilities.

UCTD	0	1	TOT
AA	16	83	99
EA	74	67	141
TOT	90	150	240
AA BP	0.18	0.55	
EA BP	0.82	0.45	

LM2C5	0	1	TOT
AA	33	48	81
EA	106	26	132
TOT	139	74	213
AA BP	0.24	0.65	
EA BP	0.76	0.35	

LP3LC	0	1	TOT
AA	11	90	101
EA	133	16	149
TOT	144	106	250
AA BP	0.08	0.85	
EA BP	0.92	0.15	

LM3C5	0	1	TOT
AA	1	7	8
EA	3	1	4
TOT	4	8	12
AA BP	0.25	0.88	
EA BP	0.75	0.13	

LP4LC	0	1	TOT
AA	4	102	106
EA	31	119	150
TOT	35	221	256
AA BP	0.11	0.46	
EA BP	0.89	0.54	

LM1C7	0	1	TOT
AA	57	47	104
EA	125	21	146
TOT	182	68	250
AA BP	0.31	0.69	
EA BP	0.69	0.31	

LM1DW	0	1	TOT
AA	48	42	90
EA	107	31	138
TOT	155	73	228
AA BP	0.31	0.58	
EA BP	0.69	0.42	

LM1MT	0	1	TOT
AA	70	13	83
EA	124	1	125
TOT	194	14	208
AA BP	0.36	0.93	
EA BP	0.64	0.07	

Table D.1. Single trait forensic probabilities.

UCTD	0		1		
LP3LC	0	1	0	1	TOT
AA	2	12	8	70	92
EA	67	5	54	11	137
TOT	69	17	62	81	229
AA BP	0.03	0.71	0.13	0.86	
EA BP	0.97	0.29	0.87	0.14	
AA RP	0.03	0.75	0.14	0.86	
EA RP	0.97	0.25	0.87	0.14	

UCTD	0		1		
LP4LC	0	1	0	1	TOT
AA	1	15	3	78	97
EA	20	53	10	54	137
TOT	21	68	13	132	234
AA BP	0.05	0.22	0.23	0.59	
EA BP	0.95	0.78	0.77	0.41	
AA RP	0.03	0.24	0.36	0.57	
EA RP	0.97	0.76	0.64	0.43	

UCTD	0		1		
LM1DW	0	1	0	1	TOT
AA	6	6	36	34	82
EA	51	15	45	14	125
TOT	57	21	81	48	207
AA BP	0.11	0.29	0.44	0.71	
EA BP	0.89	0.71	0.56	0.29	
AA RP	0.1	0.33	0.46	0.69	
EA RP	0.9	0.67	0.54	0.31	

UCTD	0		1		
LM1MT	0	1	0	1	TOT
AA	9	1	54	12	76
EA	61	0	50	1	112
TOT	70	1	104	13	188
AA BP	0.13	1	0.52	0.92	
EA BP	0.87	0	0.48	0.08	

Continued.

Table D.2. Two trait forensic probabilities.

Table D.2. Continued.

UCTD	0		1		
LM2C5	0	1	0	1	TOT
AA	6	6	23	38	73
EA	0	1	1	6	8
TOT	6	7	24	44	81
AA BP	1	0.86	0.96	0.86	
EA BP	0	0.14	0.04	0.14	

UCTD	0		1		
LM3C5	0	1	0	1	TOT
AA	52	17	48	7	124
EA	1	0	2	1	4
TOT	53	17	50	8	128
AA BP	0.98	1	0.96	0.88	
EA BP	0.02	0	0.04	0.13	

UCTD	0		1		
LM1C7	0	1	0	1	TOT
AA	10	4	44	35	93
EA	62	7	52	12	133
TOT	72	11	96	47	226
AA BP	0.14	0.36	0.46	0.74	
EA BP	0.86	0.64	0.54	0.26	
AA RP	0.14	0.41	0.46	0.74	
EA RP	0.87	0.59	0.54	0.26	

LP3PC	0		1		
LM1DW	0	1	0	1	TOT
AA	6	2	37	39	84
EA	91	27	11	3	132
TOT	97	29	48	42	216
AA BP	0.06	0.07	0.77	0.93	
EA BP	0.94	0.93	0.23	0.07	
AA RP	0.05	0.11	0.84	0.9	
EA RP	0.95	0.89	0.16	0.1	

Continued.

Table D.2. Continued.

LP3PC	0		1		
LP4LC	0	1	0	1	TOT
AA	2	9	2	85	98
EA	29	101	1	14	145
TOT	31	110	3	99	243
AA BP	0.06	0.08	0.67	0.86	
EA BP	0.94	0.92	0.33	0.14	
AA RP	0.06	0.08	0.83	0.86	
EA RP	0.94	0.92	0.17	0.14	

LP3PC	0		1		
LM2C5	0	1	0	1	TOT
AA	4	5	26	41	76
EA	89	22	13	3	127
TOT	93	27	39	44	203
AA BP	0.04	0.19	0.67	0.93	
EA BP	0.96	0.81	0.33	0.07	
AA RP	0.04	0.24	0.72	0.92	
EA RP	0.96	0.76	0.28	0.08	

LP3PC	0		1		
LM1MT	0	1	0	1	TOT
AA	8	0	59	12	79
EA	108	0	12	0	120
TOT	116	0	71	12	199
AA BP	0.07		0.83	1	
EA BP	0.93		0.17	0	

LP3PC	0		1		
LM1C7	0	1	0	1	TOT
AA	6	5	47	38	96
EA	110	15	11	5	141
TOT	116	20	58	43	237
AA BP	0.05	0.25	0.81	0.88	
EA BP	0.95	0.75	0.19	0.12	
AA RP	0.06	0.17	0.79	0.9	
EA RP	0.95	0.83	0.21	0.1	

Continued.

Table D.2. Continued.

LP4LC	0		1		
LM1MT	0	1	0	1	TOT
AA	3	0	64	12	79
EA	26	0	93	1	120
TOT	29	0	157	13	199
AA BP	0.1		0.41	0.92	
EA BP	0.9		0.59	0.08	

LP4LC	0		1		
LM1DW	0	1	0	1	TOT
AA	2	1	43	40	86
EA	22	6	80	25	133
TOT	24	7	123	65	219
AA BP	0.08	0.14	0.35	0.62	
EA BP	0.92	0.86	0.65	0.38	
AA RP	0.06	0.28	0.36	0.59	
EA RP	0.94	0.72	0.64	0.41	

LP4LC	0		1		
LM2C5	0	1	0	1	TOT
AA	3	1	29	46	79
EA	23	4	81	21	129
TOT	26	5	110	67	208
AA BP	0.12	0.2	0.26	0.69	
EA BP	0.88	0.8	0.74	0.31	
AA RP	0.08	0.28	0.47	0.66	
EA RP	0.92	0.72	0.54	0.34	

LP4LC	0		1		
LM1C7	0	1	0	1	TOT
AA	3	0	53	44	100
EA	26	1	95	20	142
TOT	29	1	148	64	242
AA BP	0.1	0	0.36	0.69	
EA BP	0.9	1	0.64	0.31	

Continued.

Table D.2. Continued.

LM1DW	0		1		
LM2C5	0	1	0	1	TOT
AA	16	16	12	20	64
EA	76	16	19	7	118
TOT	92	32	31	27	182
AA BP	0.17	0.5	0.39	0.74	
EA BP	0.83	0.5	0.61	0.26	
AA RP	0.17	0.4	0.51	0.73	
EA RP	0.83	0.6	0.49	0.27	

LM1DW	0		1		
LM1MT	0	1	0	1	TOT
AA	40	2	30	11	83
EA	92	0	28	1	121
TOT	132	2	58	12	204
AA BP	0.3	1	0.52	0.92	
EA BP	0.7	0	0.48	0.08	

LM1DW	0		1		
LM1C7	0	1	0	1	TOT
AA	25	23	24	18	90
EA	90	12	22	8	132
TOT	115	35	46	26	222
AA BP	0.22	0.66	0.52	0.69	
EA BP	0.78	0.34	0.48	0.31	
AA RP	0.24	0.45	0.58	0.8	
EA RP	0.76	0.55	0.42	0.21	

LM1MT	0		1		
LM2C5	0	1	0	1	TOT
AA	23	26	3	8	60
EA	83	21	1	0	105
TOT	106	47	4	8	165
AA BP	0.22	0.55	0.75	1	
EA BP	0.78	0.45	0.25	0	

Continued.

Table D.2. Continued.

LM1MT	0		1		
LM2C5	0	1	0	1	TOT
AA	23	26	3	8	60
EA	83	21	1	0	105
TOT	106	47	4	8	165
AA BP	0.22	0.55	0.75	1	
EA BP	0.78	0.45	0.25	0	

LM1MT	0		1		
LM1C7	0	1	0	1	TOT
AA	37	33	9	4	83
EA	102	17	1	0	120
TOT	139	50	10	4	203
AA BP	0.27	0.66	0.9	1	
EA BP	0.73	0.34	0.1	0	

LM2C5	0		1		
LM1C7	0	1	0	1	TOT
AA	18	13	26	19	76
EA	86	14	22	3	125
TOT	104	27	48	22	201
AA BP	0.17	0.48	0.54	0.86	
EA BP	0.83	0.52	0.46	0.14	
AA RP	0.17	0.49	0.55	0.86	
EA RP	0.83	0.51	0.46	0.14	

UCTD	0				1				
LP3LC	0		1		0		1		
LP4LC	0	1	0	1	0	1	0	1	TOT
AA	1	1	0	12	1	7	2	66	90
EA	19	47	0	5	9	43	1	9	133
TOT	20	48	0	17	10	50	3	75	223
AA BP	0.05	0.02		0.71	0.1	0.14	0.67	0.88	
EA BP	0.95	0.98		0.29	0.9	0.86	0.33	0.12	

UCTD	0				1				
LP3LC	0		1		0		1		
LM1DW	0	1	0	1	0	1	0	1	TOT
AA	0	1	5	5	5	1	29	32	78
EA	46	14	3	1	36	11	8	2	121
TOT	46	15	8	6	41	12	37	34	199
AA BP	0	0.07	0.63	0.83	0.12	0.08	0.78	0.94	
EA BP	1	0.93	0.38	0.17	0.88	0.92	0.22	0.06	

UCTD	0				1				
LP3LC	0		1		0		1		
LM1MT	0	1	0	1	0	1	0	1	TOT
AA	1	0	8	1	6	0	47	11	74
EA	55	0	4	0	42	0	8	0	109
TOT	56	0	12	1	48	0	55	11	183
AA BP	0.02		0.67	1	0.13		0.85	1	
EA BP	0.98		0.33	0	0.88		0.15	0	

UCTD	0				1				
LP3LC	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	1	1	5	4	3	3	18	34	69
EA	47	15	4	1	37	5	9	2	120
TOT	48	16	9	5	40	8	27	36	189
AA BP	0.02	0.06	0.56	0.8	0.08	0.38	0.67	0.94	
EA BP	0.98	0.94	0.44	0.2	0.93	0.63	0.33	0.06	
AA RP	0.01	0.09	0.15	0.23	0.03	0.22	0.83	0.92	
EA RP	0.99	0.91	0.85	0.77	0.97	0.78	0.17	0.08	

Continued.

Table D.3. Three trait forensic probabilities.

Table D.3. Continued.

UCTD	0				1				
LP3LC	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	1	1	9	2	5	3	35	31	87
EA	58	4	3	2	42	9	8	3	129
TOT	59	5	12	4	47	12	43	34	216
AA BP	0.02	0.2	0.75	0.5	0.11	0.25	0.81	0.91	
EA BP	0.98	0.8	0.25	0.5	0.89	0.75	0.19	0.09	
AA RP	0.02	0.12	0.88	0.5	0.29	0.19	0.81	0.91	
EA RP	0.98	0.89	0.12	0.5	0.71	0.81	0.19	0.09	

UCTD	0				1				
LP4LC	0		1		0		1		
LM1DW	0	1	0	1	0	1	0	1	TOT
AA	0	1	6	5	2	0	32	34	80
EA	13	4	37	11	8	2	34	12	121
TOT	13	5	43	16	10	2	66	46	201
AA BP	0	0.2	0.14	0.31	0.2	0	0.48	0.74	
EA BP	1	0.8	0.86	0.69	0.8	1	0.52	0.26	

UCTD	0				1				
LP4LC	0		1		0		1		
LM1MT	0	1	0	1	0	1	0	1	TOT
AA	1	0	8	1	2	0	51	11	74
EA	16	0	44	0	9	0	38	1	108
TOT	17	0	52	1	11	0	89	12	182
AA BP	0.06		0.15	1	0.18		0.57	0.92	
EA BP	0.94		0.85	0	0.82		0.43	0.08	

UCTD	0				1				
LP4LC	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	1	0	5	6	2	1	20	36	71
EA	15	3	37	13	8	1	38	6	121
TOT	16	3	42	19	10	2	58	42	192
AA BP	0.06	0	0.12	0.32	0.2	0.5	0.34	0.86	
EA BP	0.94	1	0.88	0.68	0.8	0.5	0.66	0.14	

Continued.

Table D.3. Continued.

UCTD	0				1				
LP4LC	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	1	0	9	4	2	0	41	34	91
EA	17	0	44	7	8	1	41	11	129
TOT	18	0	53	11	10	1	82	45	220
AA BP	0.06		0.17	0.36	0.2	0	0.5	0.76	
EA BP	0.94		0.83	0.64	0.8	1	0.5	0.24	

UCTD	0				1				
LM1DW	0		1		0		1		
LM1MT	0	1	0	1	0	1	0	1	TOT
AA	4	0	5	1	31	2	23	10	76
EA	44	0	14	0	37	0	12	1	108
TOT	48	0	19	1	68	2	35	11	184
AA BP	0.08		0.26	1	0.46	1	0.66	0.91	
EA BP	0.92		0.74	0	0.54	0	0.34	0.09	

UCTD	0				1				
LM1DW	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	0	3	6	0	13	11	6	20	59
EA	36	11	10	4	35	4	8	3	111
TOT	36	14	16	4	48	15	14	23	170
AA BP	0	0.21	0.38	0	0.27	0.73	0.43	0.87	
EA BP	1	0.79	0.63	1	0.73	0.27	0.57	0.13	

UCTD	0				1				
LM1DW	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	5	1	4	2	19	17	19	15	82
EA	47	3	10	4	35	7	10	4	120
TOT	52	4	14	6	54	24	29	19	202
AA BP	0.1	0.25	0.29	0.33	0.35	0.71	0.66	0.79	
EA BP	0.9	0.75	0.71	0.67	0.65	0.29	0.34	0.21	
AA RP	0.09	0.28	0.31	0.41	0.3	0.6	0.63	0.82	
EA RP	0.91	0.72	0.69	0.59	0.6	0.4	0.37	0.18	

Continued.

Table D.3. Continued.

UCTD	0				1				
LM1MT	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	5	2	1	0	16	22	2	8	56
EA	43	14	0	0	34	6	1	0	98
TOT	48	16	1	0	50	28	3	8	154
AA BP	0.1	0.13	1		0.32	0.79	0.67	1	
EA BP	0.9	0.88	0		0.68	0.21	0.33	0	

UCTD	0				1				
LM1MT	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	7	2	1	0	28	26	8	4	76
EA	53	6	0	0	39	9	1	0	108
TOT	60	8	1	0	67	35	9	4	184
AA BP	0.12	0.25	1		0.42	0.74	0.89	1	
EA BP	0.88	0.75	0		0.58	0.26	0.11	0	

UCTD	0				1				
LM2C5	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	4	2	3	2	13	8	22	14	68
EA	44	5	15	1	38	7	5	2	117
TOT	48	7	18	3	51	15	27	16	185
AA BP	0.08	0.29	0.17	0.67	0.25	0.53	0.81	0.88	
EA BP	0.92	0.71	0.83	0.33	0.75	0.47	0.19	0.13	
AA RP	0.05	0.26	0.34	0.63	0.3	0.58	0.67	0.88	
EA RP	0.96	0.74	0.66	0.37	0.7	0.42	0.33	0.12	

LP3LC	0				1				
LP4LC	0		1		0		1		
LM1DW	0	1	0	1	0	1	0	1	TOT
AA	1	1	5	1	1	0	34	38	81
EA	21	5	67	22	0	1	10	2	128
TOT	22	6	72	23	1	1	44	40	209
AA BP	0.05	0.17	0.07	0.04	1	0	0.77	0.95	
EA BP	0.95	0.83	0.93	0.96	0	1	0.23	0.05	

Continued.

Table D.3. Continued.

LP3LC	0				1				
LP4LC	0		1		0		1		
LM1MT	0	1	0	1	0	1	0	1	TOT
AA	2	0	6	0	1	0	56	11	76
EA	24	0	81	0	1	0	10	0	116
TOT	26	0	87	0	2	0	66	11	192
AA BP	0.08		0.07		0.5		0.85	1	
EA BP	0.92		0.93		0.5		0.15	0	

LP3LC	0				1				
LP4LC	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	2	0	2	5	1	1	24	39	74
EA	22	3	66	18	1	0	11	3	124
TOT	24	3	68	23	2	1	35	42	198
AA BP	0.08	0	0.03	0.22	0.5	1	0.69	0.93	
EA BP	0.92	1	0.97	0.78	0.5	0	0.31	0.07	

LP3LC	0				1				
LP4LC	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	2	0	4	5	1	0	45	36	93
EA	24	1	83	14	1	0	9	5	137
TOT	26	1	87	19	2	0	54	41	230
AA BP	0.08	0	0.05	0.26	0.5		0.83	0.88	
EA BP	0.92	1	0.95	0.74	0.5		0.17	0.12	

LP3PC	0				1				
LM1DW	0		1		0		1		
LM1MT	0	1	0	1	0	1	0	1	TOT
AA	6	0	2	0	31	2	28	10	79
EA	79	0	26	0	9	0	2	0	116
TOT	85	0	28	0	40	2	30	10	195
AA BP	0.07		0.07		0.78	1	0.93	1	
EA BP	0.93		0.93		0.23	0	0.07	0	

Continued.

Table D.3. Continued.

LP3PC	0				1				
LM1DW	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	2	3	1	0	12	12	11	20	61
EA	63	14	17	5	10	1	1	2	113
TOT	65	17	18	5	22	13	12	22	174
AA BP	0.03	0.18	0.06	0	0.55	0.92	0.92	0.91	
EA BP	0.97	0.82	0.94	1	0.45	0.08	0.08	0.09	

LP3PC	0				1				
LM1DW	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	3	3	2	0	21	16	21	18	84
EA	79	8	20	6	8	3	1	2	127
TOT	82	11	22	6	29	19	22	20	211
AA BP	0.04	0.27	0.09	0	0.72	0.84	0.95	0.9	
EA BP	0.96	0.73	0.91	1	0.28	0.16	0.05	0.1	

LP3PC	0				1				
LM1MT	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	3	3	0	0	18	23	3	8	58
EA	71	18	0	0	10	2	0	0	101
TOT	74	21	0	0	28	25	3	8	159
AA BP	0.04	0.14			0.64	0.92	1	1	
EA BP	0.96	0.86			0.36	0.08	0	0	

LP3PC	0				1				
LM1MT	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	5	3	0	0	31	28	8	4	79
EA	91	13	0	0	9	3	0	0	116
TOT	96	16	0	0	40	31	8	4	195
AA BP	0.05	0.19			0.78	0.9	1	1	
EA BP	0.95	0.81			0.23	0.1	0	0	

Continued.

Table D.3. Continued.

LP3PC	0				1				
LM2C5	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	4	0	1	4	12	12	24	14	71
EA	73	10	20	1	10	3	1	2	120
TOT	77	10	21	5	22	15	25	16	191
AA BP	0.05	0	0.05	0.8	0.55	0.8	0.96	0.88	
EA BP	0.95	1	0.95	0.2	0.45	0.2	0.04	0.13	

LP4LC	0				1				
LM1DW	0		1		0		1		
LM1MT	0	1	0	1	0	1	0	1	TOT
AA	2	0	1	0	36	1	28	11	79
EA	20	0	6	0	67	0	22	1	116
TOT	22	0	7	0	103	1	50	12	195
AA BP	0.09		0.14		0.35	1	0.56	0.92	
EA BP	0.91		0.86		0.65	0	0.44	0.08	

LP4LC	0				1				
LM1DW	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	2	0	1	0	13	15	11	20	62
EA	16	2	6	0	58	13	13	7	115
TOT	18	2	7	0	71	28	24	27	177
AA BP	0.11	0	0.14		0.18	0.54	0.46	0.74	
EA BP	0.89	1	0.86		0.82	0.46	0.54	0.26	

LP4LC	0				1				
LM1DW	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	2	0	1	0	22	21	23	17	86
EA	19	1	5	0	67	11	17	8	128
TOT	21	1	6	0	89	32	40	25	214
AA BP	0.1	0	0.17		0.25	0.66	0.58	0.68	
EA BP	0.9	1	0.83		0.75	0.34	0.43	0.32	

Continued.

Table D.3. Continued.

LP4LC	0				1				
LM1MT	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	3	0	0	0	20	25	2	8	58
EA	21	2	0	0	60	18	1	0	102
TOT	24	2	0	0	80	43	3	8	160
AA BP	0.13	0			0.25	0.58	0.67	1	
EA BP	0.88	1			0.75	0.42	0.33	0	

LP4LC	0				1				
LM1MT	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	3	0	0	0	34	30	8	4	79
EA	23	1	0	0	75	16	1	0	116
TOT	26	1	0	0	109	46	9	4	195
AA BP	0.12	0			0.31	0.65	0.89	1	
EA BP	0.88	1			0.69	0.35	0.11	0	

LP4LC	0				1				
LM2C5	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	3	0	0	0	14	13	26	18	74
EA	21	0	3	0	63	14	18	3	122
TOT	24	0	3	0	77	27	44	21	196
AA BP	0.13		0		0.18	0.48	0.59	0.86	
EA BP	0.88		1		0.82	0.52	0.41	0.14	

LM1DW	0				1				
LM1MT	0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	TOT
AA	14	13	1	1	9	13	2	7	60
EA	63	15	0	0	17	6	1	0	102
TOT	77	28	1	1	26	19	3	7	162
AA BP	0.18	0.46	1	1	0.35	0.68	0.67	1	
EA BP	0.82	0.54	0	0	0.65	0.32	0.33	0	

Continued.

Table D.3. Continued.

LM1DW	0				1				
LM1MT	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	22	18	1	1	15	15	8	3	83
EA	78	11	0	0	21	6	1	0	117
TOT	100	29	1	1	36	21	9	3	200
AA BP	0.22	0.62	1	1	0.42	0.71	0.89	1	
EA BP	0.78	0.38	0	0	0.58	0.29	0.11	0	

LM1DW	0				1				
LM2C5	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	10	6	8	8	5	7	13	7	64
EA	62	11	16	0	15	3	4	3	114
TOT	72	17	24	8	20	10	17	10	178
AA BP	0.14	0.35	0.33	1	0.25	0.7	0.76	0.7	
EA BP	0.86	0.65	0.67	0	0.75	0.3	0.24	0.3	

LM1MT	0				1				
LM2C5	0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	TOT
AA	12	11	15	11	2	1	5	3	60
EA	67	12	19	2	1	0	0	0	101
TOT	79	23	34	13	3	1	5	3	161
AA BP	0.15	0.48	0.44	0.85	0.67	1	1	1	
EA BP	0.85	0.52	0.56	0.15	0.33	0	0	0	

UCTD	0								1								
LP3LC	0				1				0				1				
LP4LC	0		1		0		1		0		1		0		1		
LM1MT	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	1	0	0	0	0	0	8	1	1	0	5	0	1	0	45	10	72
EA	15	0	39	0	0	0	4	0	8	0	32	0	1	0	6	0	105
TOT	16	0	39	0	0	0	12	1	9	0	37	0	2	0	51	10	177
AA BP	0.1		0				0.7	1	0.1		0.1		0.5		0.9	1	
EA BP	0.9		1				0.3	0	0.9		0.9		0.5		0.1	0	

UCTD	0								1								
LP3LC	0				1				0				1				
LP4PC	0		1		0		1		0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	1	0	0	1	0	0	5	4	1	0	2	3	1	1	16	32	67
EA	15	2	32	12	0	0	4	1	7	1	29	4	1	0	7	2	117
TOT	16	2	32	13	0	0	9	5	8	1	31	7	2	1	23	34	184
AA BP	0.1	0	0	0.1			0.6	0.8	0.1	0	0.1	0.4	0.5	1	0.7	0.9	
EA BP	0.9	1	1	0.9			0.4	0.2	0.9	1	0.9	0.6	0.5	0	0.3	0.1	

Continued.

Table D.4. Four trait forensic probabilities.

Table D.4. Continued.

UCTD	0								1								
LP3LC	0				1				0				1				
LP4LC	0		1		0		1		0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	1	0	0	1	0	0	9	2	1	0	4	3	1	0	33	30	85
EA	16	0	41	4	0	0	3	2	7	1	33	8	1	0	6	3	125
TOT	17	0	41	5	0	0	12	4	8	1	37	11	2	0	39	33	210
AA BP	0.1		0	0.2			0.8	0.5	0.1	0	0.1	0.3	0.5		0.8	0.9	
EA BP	0.9		1	0.8			0.3	0.5	0.9	1	0.9	0.7	0.5		0.2	0.1	

UCTD	0								1								
LP3LC	0				1				0				1				
LM1MT	0		1		0		1		0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	1	0	0	0	4	2	1	0	2	2	0	0	13	20	2	8	55
EA	39	12	0	0	3	1	0	0	27	5	0	0	7	1	0	0	95
TOT	40	12	0	0	7	3	1	0	29	7	0	0	20	21	2	8	150
AA BP	0	0			0.6	0.7	1		0.1	0.3			0.7	1	1	1	
EA BP	1	1			0.4	0.3	0		0.9	0.7			0.4	0	0	0	

Continued.

Table D.4. Continued.

UCTD	0								1								
LP3LC	0				1				0				1				
LM1MT	0		1		0		1		0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	1	0	0	0	6	2	1	0	4	2	0	0	23	24	7	4	74
EA	50	3	0	0	2	2	0	0	32	8	0	0	7	1	0	0	105
TOT	51	3	0	0	8	4	1	0	36	10	0	0	30	25	7	4	179
AA BP	0	0			0.8	0.5	1		0.1	0.2			0.8	1	1	1	
EA BP	1	1			0.3	0.5	0		0.9	0.8			0.2	0	0	0	

UCTD	0								1								
LP4LC	0				1				0				1				
LM1MT	0		1		0		1		0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	1	0	0	0	4	2	1	0	2	0	0	0	14	21	1	8	54
EA	14	1	0	0	29	12	0	0	7	1	0	0	25	5	1	0	95
TOT	15	1	0	0	33	14	1	0	9	1	0	0	39	26	2	8	149
AA BP	0.1	0			0.1	0.1	1		0.2	0			0.4	0.8	0.5	1	
EA BP	0.9	1			0.9	0.9	0		0.8	1			0.6	0.2	0.5	0	

Continued.

Table D.4. Continued.

UCTD	0								1								
LP4LC	0				1				0				1				
LM1MT	0		1		0		1		0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	1	0	0	0	6	2	1	0	2	0	0	0	26	25	7	4	74
EA	15	0	0	0	37	6	0	0	7	1	0	0	29	8	1	0	104
TOT	16	0	0	0	43	8	1	0	9	1	0	0	55	33	8	4	178
AA BP	0.1				0.1	0.3	1		0.2	0			0.5	0.8	0.9	1	
EA BP	0.9				0.9	0.8	0		0.8	1			0.5	0.2	0.1	0	

UCTD	0								1								
LP4LC	0				1				0				1				
LM2C5	0		1		0		1		0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	1	0	0	0	3	2	3	2	2	0	0	0	10	8	22	13	66
EA	14	0	2	0	30	5	12	1	7	0	1	0	29	7	4	2	114
TOT	15	0	2	0	33	7	15	3	9	0	1	0	39	15	26	15	180
AA BP	0.1		0		0.1	0.3	0.2	0.7	0.2		0		0.3	0.5	0.8	0.9	
EA BP	0.9		1		0.9	0.7	0.8	0.3	0.8		1		0.7	0.5	0.2	0.1	

Continued.

Table D.4. Continued.

UCTD	0								1								
LM1MT	0				1				0				1				
LM2C5	0		1		0		1		0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	3	2	2	0	1	0	0	0	9	7	12	10	1	1	5	3	56
EA	37	4	13	1	0	0	0	0	26	6	5	1	1	0	0	0	94
TOT	40	6	15	1	1	0	0	0	35	13	17	11	2	1	5	3	150
AA BP	0.1	0.3	0.1	0	1				0.3	0.5	0.7	0.9	0.5	1	1	1	
EA BP	0.9	0.7	0.9	1	0				0.7	0.5	0.3	0.1	0.5	0	0	0	

LP3LC	0								1								
LP4LC	0				1				0				1				
LM1MT	0		1		0		1		0		1		0		1		
LM2C5	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	2	0	0	0	1	3	0	0	1	0	0	0	17	22	2	8	56
EA	20	1	0	0	50	16	0	0	1	0	0	0	8	2	0	0	98
TOT	22	1	0	0	51	19	0	0	2	0	0	0	25	24	2	8	154
AA BP	0.1	0			0	0.2			0.5				0.7	0.9	1	1	
EA BP	0.9	1			1	0.8			0.5				0.3	0.1	0	0	

Continued.

Table D.4. Continued.

LP3LC	0								1								
LP4LC	0				1				0				1				
LM1MT	0		1		0		1		0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	2	0	0	0	3	3	0	0	1	0	0	0	30	26	7	4	76
EA	21	1	0	0	67	12	0	0	1	0	0	0	7	3	0	0	112
TOT	23	1	0	0	70	15	0	0	2	0	0	0	37	29	7	4	188
AA BP	0.1	0			0	0.2			0.5				0.8	0.9	1	1	
EA BP	0.9	1			1	0.8			0.5				0.2	0.1	0	0	

LP3LC	0								1								
LP4LC	0				1				0				1				
LM2C5	0		1		0		1		0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	2	0	0	0	2	0	1	4	1	0	0	0	10	12	24	13	69
EA	20	0	2	0	52	10	17	1	1	0	0	0	8	3	1	2	117
TOT	22	0	2	0	54	10	18	5	2	0	0	0	18	15	25	15	186
AA BP	0.1		0		0	0	0.1	0.8	0.5				0.6	0.8	1	0.9	
EA BP	0.9		1		1	1	0.9	0.2	0.5				0.4	0.2	0	0.1	

Continued.

Table D.4. Continued.

LP4LC	0								1								
LM1MT	0				1				0				1				
LM2C5	0		1		0		1		0		1		0		1		
LM1C7	0	1	0	1	0	1	0	1	0	1	0	1	0	1	0	1	TOT
AA	3	0	0	0	9	11	15	10	1	1	5	3	15	2	32	12	119
EA	19	0	2	0	0	0	0	0	46	12	16	2	1	0	0	0	98
TOT	22	0	2	0	9	11	15	10	47	13	21	5	16	2	32	12	217
AA BP	0.1		0		1	1	1	1	0	0.1	0.2	0.6	0.9	1	1	1	
EA BP	0.9		1		0	0	0	0	1	0.9	0.8	0.4	0.1	0	0	0	