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POPULATION STRUCTURE OF LOWER NUBIA INTHE MESOLITHIC-CHRISTIAN GROUPS

A Dissertation
Presented for the
Doctor of Philosophy
Degree
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Kanya Mia Godde
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DEDICATION

This dissertation is dedicated to my mother, Sheila Wilson, who made this possible. Thank you for everything you have done for me.

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ABSTRACT

For almost 100 years, population structure in Nubians has been speculated upon. Initially, most scholars contended that Nubian biological evolution was the product of biological diffusion, or extraregional gene flow, from the different populations they came into contact with. In 1968, Adams put forth a new way to look at the archaeological record. He argued that the archaeological record was reflective of an in situ change, where Nubians evolved culturally without influences from other populations. Later, Carlson and Van Gerven (1979) hypothesized that the same forces that formed the archaeological record were also operating biologically. Since Adams and Carlson and Van Gerven suggested an alternative way to look at Nubian cultural and biological evolution, most research (with the exception of DNA studies) have concurred with their conclusions.

The body of research into Nubian biological evolution is vast and incorporates DNA, craniometrics, dental metrics, and dental nonmetrics. However, very little work has been done with cranial discrete traits. In this dissertation, seven questions and their corollaries of Nubian population structure will be examined utilizing cranial discrete traits. Population genetics statistics for quantitative traits have become popular in craniometric data studies. Because of their effectiveness in deciphering subtle aspects of population structure, this dissertation will adapt the continuous population genetics statistics for use with categorical or discrete data.

The results of the inquiry into Nubian population structure depict a complex pattern of biological evolution that suggests in situ evolution did not operate alone. Rather, sometimes in situ evolution occurred, while other times biological diffusion influenced their

evolution. These interesting results mainly support the DNA evidence, which found evidence of multiple migrations across Nubia (Fox 1997; Krings et al. 1999). Sample size may have affected these results, as several of the samples numbered less than 30. However, small samples should not be ignored because they can contribute much information about past populations. Furthermore, this dissertation successfully modified and applied population genetics statistics to categorical data and can serve as a stepping stone for more sophisticated techniques to be applied to the methodology employed within.

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Chapter 1

Introduction

Researchers employing discrete trait analyses have struggled over the years to apply a population genetics approach to their methodology. The closest discrete analyses have been to providing a population genetics methodology involved estimations of R matrices and F_{st}. The application of other population genetics parameters, such as estimations of gene flow, has remained elusive. The desire to estimate population genetics parameters has strengthened, and thus some studies have erroneously applied RMET (the statistical program for continuous, quantitative traits) to discrete data. In this study, I would like to achieve a successfully application of a population genetics approach. Thus, I will utilize population genetics statistics that incorporate estimates of gene flow to analyze population structure in Nubians.

Two hypotheses have been put forth to explain Nubian biological evolution. The first, biological diffusion (e.g. Elliot Smith and Wood-Jones 1910), states that Nubians evolved because of contact with other populations (gene flow). A later hypothesis was

proposed by Adams (1968, 1977) and Carlson and Van Gerven (1979) where Nubians were thought to have evolved in situ, with little influence from gene flow. Currently, most skeletal biology and archaeological data supports in situ biological evolution. However, the designs of the studies testing the hypothesis are not adequate for two reasons. First, they are sometimes conducted on a large number of samples (which may act to obscure details of population structure), or second, they are performed on select samples whose results should not be extrapolated to the greater population. This study boasts a large number of samples that span the Mesolithic through Christian time periods, and from locations ranging from the 1st through below the 4th cataract. This multifaceted dataset will allow for several manifestations of the investigations into Nubian population structure. Not only can the samples be pooled for an analysis on overall population structure, but they can also be divided into meaningful subsets designed to test particular aspects of Nubian history.

Several statistics will be generated to assess population structure in Nubians. First, the application of a biological distance estimator (Mahalanobis D^2) to the data will be completed in order to elucidate the relationship among the samples. Next, principal coordinates analysis will be applied in order to graphically depict the relationships of the various groups to one another. R matrices and F_{st} estimates will be derived from biological distances in order to describe the variation found within the population and to set the methodological foundation for estimations of gene flow. Finally, the Relethford-Blangero analysis for continuous, quantitative data will be adapted for categorical data so that estimates of gene flow can be produced.

In order to conduct the population genetics methodology outlined above, data from 19 nonmetric traits were collected or obtained from other authors. As a result of the dataset containing multiple authors' data, interobserver error will be tested for using Fisher's exact test and removal of traits will be completed on those traits with high differences among observers. Other possible biases have been identified in discrete trait analyses including age, sex, and intertrait correlations. Selection of traits will be conducted among those that have been tested to be nearly free of age dependency in adults. Further, to prevent erroneous conclusions, samples will be limited to adults, and juveniles will be avoided. Some traits are sex dependant and care must be exercised to ensure traits are not sex dependant in a particular sample. Thus, sexes will be pooled if, after sex differences are tested for with chi-square analyses, a large disparity exists. Finally, intertrait correlations are not an issue when utilizing Mahalanobis distances for nonmetric traits and tests to identify the correlations are not necessary. The statistic takes into account these correlations and prevents the need for elimination of traits that influence one another.

At the moment, heritability in discrete traits is a topic that is at the forefront of the subject. In 2006, Carson published a paper with low estimates of narrow heritabilities in discrete traits of the human cranium. Prior work had established that narrow heritability estimates were similar in discrete traits (Sjϕvold 1984) to craniometrics in humans and some perceptions were that her article negated this body of research. However, narrow heritability estimates reflect genetic and environmental influences and are specific to a certain population living in a particular environment. Thus, her results are not to be extrapolated beyond her sample and heritability estimates produced from macaques and mice are probably still valid

(Cheverud 1981; Cheverud and Buikstra 1981a; Cheverud and Buikstra 1981b; Cheverud and Buikstra 1982; McGrath et al. 1984; Richtsmeier and McGrath 1986). A more in-depth discussion that illustrates why Carson's (2006) and Sjϕvold's (1984) results are so different, despite their observation of the same Austrian sample, will be developed in Chapter 2.

Some nonmetric traits are at least partially controlled by the environment (e.g. auditory exostosis). These traits will be avoided as their presence in a biological distance study serves to add an environmental component to a study of genetics. Cranial modification can change the frequency of discrete traits, but the effect is minimal and affects traits near the modification. As Konigsberg et al. (1993) notes, modified skulls can still be input into biological distance studies without severely skewing the results.

Biological distances can be used in a multitude of ways, including with applications to post-marital residence patterns (e.g. Lane and Sublett 1972), cemetery analyses (e.g. Bondioli et al. 1986), and bioarchaeological studies (e.g. Buikstra 1980). Most importantly, biological distances can uncover relationships among populations and shed some light on population histories. Further, R matrices are generated from Mahalanobis distances, and thus biological distances enable the calculation of population genetic statistics. Therefore, the inclusion of biological distances into this dissertation is crucial for population genetics parameter estimations and for insight into the Nubians' biological affinities.

Seven hypotheses regarding Nubian evolution will be explored in this dissertation, in an effort to investigate various aspects of Nubian population history using the population genetics methodology outlined above. Data from 13 samples representing 8 time periods and 7 sites will be utilized for both an overall picture of Nubian evolution and for dispersing into

meaningful subsets. The subsets will incorporate only those samples that pertain to the testing of specific questions. Seven questions, some with accompanying corollaries, have been formulated for testing in this dissertation that are based on certain aspects of the archaeological record or previous biological studies on Nubians:

1. Is the *in situ* hypothesis reflective in the overall picture of Nubian evolution?
2. Was there a population replacement after the Paleolithic, but prior to the A-Group as some authors have contended? Furthermore, was there continuity between the A- and C-Groups in spite of the hiatus between their disappearance and their subsequent reappearance in the archaeological record?
3. Were the three contemporary Nubian groups (C-Group, Pan-Grave, and Kerma) with distinctly different material culture really one biologically homogeneous group with a highly variable material culture?
4. After the 1,000-year hiatus of Lower Nubia (prior to the Meroites), did Nubians return to Lower Nubia, or was it some other population?
5. The X-Group has been identified as a Nubian group comprised of several populations as a result of their extensive contact with these foreign people. Is this the case, or did the X-Group remain biologically Nubian despite the large amount of contact with other populations?
6. How did time affect the three samples at Semna South? Did the three groups representing three successive time periods evolve into one another, or was there gene flow from other populations?

7. How did space affect four samples from the same time period?

In order to address the questions above, this dissertation will provide a background of the methodology in nonmetric traits, biological distance, and population genetics on quantitative traits (Chapter 2). Next, the archaeological and biological evidence from the time periods and geographic locations of the samples included in this study will be presented (Chapter 3) as they pertain to *in situ* evolution. The Materials chapter (4) gives an overview of the archaeology specific to each of the samples used in this dissertation. The Methods chapter (5) describes the methodology in this dissertation and, specifically, a new technique in population genetics statistics that allow for categorical data to be processed. A brief review of the results is included next (Chapter 6) to summarize the results for the overall dissertation, and thus do not pertain to specific questions about *in situ* evolution in Nubians (e.g. sample trait frequencies, interobserver error rates, etc.). Chapters 7-13 are comprised of the results and discussion of each of the seven questions, above. The archaeological and biological evidence are synthesized in these seven chapters to portray the mode of biological evolution in Nubians. Finally, the concluding chapter (14) summarizes all of the findings in this dissertation, spanning from those that deal strictly with the methodology employed within, to the results from each of the seven questions on population structure in Nubians.

Chapter 2

Literature Review

Nonmetric traits, or discrete traits, are characteristics that can be observed, but not measured on a metric scale. Their presence or absence is noted, and in some cases the level of expression is recorded, and their manifestation is later quantified with statistics. As it stands, discrete trait analyses typically take a model-free approach to estimating population relationships. Relethford and Lees (1982) described model-bound and model-free approaches, where model-bound studies seek to estimate population genetics parameters, while model-free studies explore population structure without estimating specific population genetics parameters. Model-bound approaches are uncommon in discrete trait analyses, as of yet. Although it is not the standard, this dissertation strives to be model-bound. Because this dissertation seeks to investigate hypotheses revolving around population structure in Nubians by applying population genetics statistics, a background of discrete traits and their

methodology will be presented. Subsequently, model-bound techniques will be introduced to synthesize the use of discrete data with population genetics approaches.

Heritabilites and Environmental Influences

In order to discuss heritiability estimates as they relate to discrete traits, a short discussion of heritability statistics and the conditions surrounding them, are in order. Vitzthum (2003) outlines the erroneous assumptions related to heritability estimates and clarifies the meaning and interpretability of heritabilites. Heritability, as a statistical estimate, is, "the proportion of the total phenotypic variance that is associated with genetic variance in a specific sample with a specific genetic composition and environmental context" (Vitzthum 2003:541). Heritability can be split into two coefficients: 1. broad heritabilities, and 2. narrow heritabilities.

The most important component of heritability is that it is not applicable across populations or environment (Vitzthum 2003). Although some traits' heritabilities have been calculated as low, this may be due to the particular sample, and population utilized (Vitzthum 2003). Vitzthum (2003) clearly summarizes this concept:

> A heritability estimate is always specific to that sample. Change the environment and the same sample of individuals with exactly the same genotypes will have a different heritability estimate. Because of this, heritability estimates cannot be directly compared from samples not having either identical [genetic] or environmental composition (at least as regards those environmental factors that would influence the phenotype under study). Heritability does not indicate the mode of inheritance, the number of loci, the location or product of any locus, the functional effect of that product on the phenotype, or the extent to which that phenotype is "controlled" by the genes (545).

Vitzthum (2003) explicates narrow heritability with a description of heritabilities of heights in women. She emphasizes that if a narrow heritability estimate of height is .75, the statistic is interpreted as 75% of height variation is due to genetic variation (Vitzthum 2003: 547). Therefore, as Vitzhum exemplifies, if heights in women in one city have a smaller heritability than heights of women in another city, the narrow heritability estimate does not mean that less or different genetic forces are operating on the two separate samples of women (Vitzthum 2003: 547). Instead, the heritability estimate indicates there is more environmental variation in the sample with the lower narrow heritability estimate (Vitzthum, 2003: 547-8).

Grüneberg (1952) first calculated on mice. His study confirmed that discrete traits could be passed down from parent to offspring. Later, under the assumption of heritability, Berry and Berry (1967) utilized nonmetric traits to calculate biological distance among several human populations. Heritabilities were further assessed on a non-human proxy by Cheverud (1981) and Cheverud and Buikstra (1981a,b; 1982) who calculated narrow heritabilities on Rhesus Macaques from Cayo Santiago that boasted a documented matrilineal pedigree. From this unusually useful dataset, the authors concluded that many discrete traits were highly heritable. Specifically, Cheverud and Buikstra (1982) determined the mean heritability for nonmetric traits as 0.528, a value similar to Devor's (1987) estimation of a 0.55 for heritability of craniofacial metric traits. The high numbers indicate that craniofacial metrics and cranial nonmetrics have an underlying genetic component, which makes them appropriate to explore biological relationships among populations.

Around this time, Richtsmeier and McGrath (1986) independently calculated heritabilities on mice and generated smaller heritabilities that conflicted with the results from Cheverud and Buikstra (1982). In the time between the Cheverud and Buikstra and Richtsmeier and McGrath studies, Sjϕvold (1984) calculated heritabilities in human crania from documented Austrian pedigrees. His data led Sjϕvold (1984) to conclude that certain nonmetric traits had a relatively high heritability in humans and could be used in biological distance studies with meaningful results.

Over the years, many advances were made in statistics and by 2006 it was time to reassess heritability information with new, more powerful equations. Carson (2006) reevaluated discrete trait heritability by collecting nonmetric data on the same Austrian pedigreed collection as Sjϕvold (1984). Even though she employed essentially the same dataset, Carson's (2006) conclusions were very different from Sjϕvold (1984); her heritability estimates were much lower. In some cases, her heritiability estimates were zero. Carson (2006) attributed the discrepancy between the two studies' results to the application of different statistics.

Even though Carson (2006) produced low heritability estimates, nonmetric trait investigations have demonstrated repeatedly that their results can identify families (Alt et al. 1997), are similar to relationships elucidated from craniometrics (Corruccini 1974; Corruccini 1976; Ossenberg 1977; Stefan and Chapman 2003; Wijsman and Neves 1986), and correspond well to the archaeological and/or linguistic record (Conner 1990; Stefan and Chapman 2003). Furthermore, Carson's sample was only one human sample in a certain environment. As has already been established in the summarization of Vitzthum (2003),

Carson's results are particular to her sample and cannot be necessarily extrapolated other human samples. Therefore, nonmetrics as a whole should not be disregarded and labeled as ineffective in estimating population relationships; rather, the heritabilities are merely reflective of Carson's specific study. Nonmetric information is probably still valuable in estimating population affinities and this dissertation seeks to demonstrate their utility to do so.

Antithetical to Conner (1990) and Chapman (2003), from above, who find discrete traits correspond well to the archaeological and linguistic data, some studies demonstrated that their discrete data did not support other forms of evidence (Christensen 1998; Neves and Pucciarelli 1991). Interestingly, Rightmire (1972) explored both craniometric and cranial discrete traits in an effort to trace their relationship with archaeological and linguistic data. Results from his analysis suggested craniometrics coincided well with non-biological data, but nonmetrics did not. Conversely, DNA analyses have yielded results consistent with alternative data sources (Klaric 2000). Differences of opinion regarding whether or not discrete traits produce information consistent with other forms of evidence may be due to the disparities in methodology and trait selection. Moreover, some authors (Shimada et al. 2004) assert that material evidence needs to be interpreted in relation to biological evidence, which may be a better approach to handling different data types. Thus, the archaeological and biological record should be interpreted together and conclusions and hypotheses can be formed from both types of data, rather than one form of evidence treated as the type to compare all others to.

Certain discrete traits are influenced by factors other than genetic control. In her research on Wormians, Ossenberg (1970) noted that environmental factors, e.g. cranial modification, could affect nonmetric traits. As cranial modification is a common practice in many cultures, it is important to understand how modification will affect cranial landmarks, and subsequently, distance studies utilizing these landmarks. Scholars have investigated discrete character frequency changes in modified and non-modified crania with differing opinions as to modification's effects. Ossenberg (1970) examined Hopewell modified crania and determined that some areas of the skull displayed increases in Wormians, while other areas experienced decreases. As a result of the differences in frequencies of Wormians after modification, Ossenberg (1970) concluded that modified crania should not be included in biological distance studies.

In response to Ossenberg's (1970) findings, El-Najjar and Dawson (1977) presented evidence from fetal crania where Wormian formation was not necessarily environmentally induced. The presence of Wormians in a fetal sample suggested that accessory cranial bones can form in the womb, where there has been little possibility of environmental influence (El-Najjar and Dawson 1977). Therefore, genes were probably responsible for the formation of these fetal Wormians, rather than environmental factors (El-Najjar and Dawson 1977). Gottlieb (1978) also studied Wormian formation, but in Southwest Indian crania. The results from her data were not consistent with genetic inheritance (Gottlieb 1978), and as Godde (2004) suggested, the differences between Gottlieb (1978) and El-Najjar and Dawson's (1977) conclusions may be attributable to Gottlieb's small sample size.

Later, Konigsberg et al. (1993) revisited this problem with modified Hopi, Nootka, Kwakiutl, and prehistoric Peruvian skulls. Like Ossenberg (1970), Konigsberg and his coworkers did note increases and decreases in Wormians, however, Konigsberg et al. (1993) concluded the frequency changes were low and would not drastically affect biological distance studies. From their research, Konigsberg et al. (1993) deduced there were two rules associated with deformation. First, modification will not change the appearance and frequency of developmentally complete traits. Second, only traits near the deformation can be influenced by the modification.

Other authors have subsequently observed an environmental component to nonmetric trait presence/absence (e.g. Corruccini et al. 1982; Richtsmeier and McGrath 1986; Sellevold 1980; Trinkaus 1978). Environmentally induced traits are beneficial; a trait spurred from an environmental component can yield information about subsistence strategies and social practices, among other information about past lifeways. Out of the probable environmentally induced traits, one particular trait has been identified as possessing a strong environmental component that can be interpreted for information about past lifeways: auditory exostosis.

The anatomical/medical literature has linked auditory exostoses to individuals experiencing prolonged water exposure (e.g. swimmers). Many anthropological investigations have utilized auditory exostoses to reconstruct ancient population subsistence strategies (e.g. Frayer 1988; Kennedy 1986; Standen et al. 1997; Velasco-Vasquez 2000) and have attributed the appearance of exostoses to diving for marine resources. Additional work has associated exostoses with social practices, specifically in individuals who frequented Roman baths (Ascenzi and Balistreri 1975; Manzi et al. 1991). More recently, Okumura et

al. (2007 a,b) cited evidence that auditory exostoses are influenced by air temperature in addition to water exposure in tropical and subtropical environments. Okumura and her colleagues also discussed the interpretive value of the characteristic in skeletons and cautioned against deducing all auditory exostoses are linked to water.

While water exposure may be one of the causes of exostoses in the ear canal, it is not the only possible origin. Hutchison et al. (1997) presented evidence from the medical literature that suggests alternative etiologies for auditory exostoses, e.g. trauma and systemic conditions. Godde (2006; 2009b) substantiated Hutchison et al.'s (1997) claims with her brief study of exostoses in Nubians. In her research, she discovered auditory exostoses in a population with limited water exposure. With inconclusive evidence for the definite etiology of auditory exostoses, it is best not to include it in biodistance studies as other authors have (e.g. as Hanihara et al. (2003) did in their study of global populations).

Potential Biases in Nonmetric Data: Sex, Age, and Intertrait Correlations

Both cranial and postcranial discrete traits have been mapped in the skeleton. Postcranial traits are utilized much less frequently in biological distance studies, e.g. (Donlon 2000). Tyrell (2000) does not suggest producing biodistances from postcranial discrete traits. Although, Tyrell (2000) concedes they are good traits, he reasons that due to remodeling, functional modification, effects of canalization, and lack of a good understanding of their development, their use should be minimized.

Cranial discrete trait investigators have determined that some characteristics exhibit sex-specific frequencies (Berry 1975; Corruccini 1974; Lundy 1980; Mouri 1976; Perizonius 1979), while others have not detected any (Berry and Berry 1967; Sawyer et al. 1990; Sawyer and Kiely 1987). Sex specific frequencies have been reported by Berry (1975) who observed significant sex differences between her St. Bride's Church samples. Moreover, Corruccini (1974) recognized the degree of sex differences differed among populations, specifically between American Whites and Blacks. In Mouri's (1976) investigation of individuals from the Kinki district in Japan, he narrowed sex differences to three specific nonmetric traits: epipteric bone, ossicle at asterion, and pterygospinous foramen. Perizonius (1979) also noted sex differences in 7 out of 45 discrete traits that he studied. While these studies identified sex dependancies, other work has not uncovered any differences between the sexes. For example, Berry and Berry (1967) tested for sex differences in their study of Egyptian and Nubian relationships, among other populations, and found no evident sex differences. Sawyer and Kiely (1987) and Sawyer et al. (1990) ascertained that mylohyoid bridging and jugular foramen bridging were not biased by sex in populations of Asian Indians and Chilean samples, respectively.

Two sex-specific classifications of nonmetric traits have been put forth by Ossenberg (1970): hypostotic and hyperostotic traits. Hypostotic traits are the result of an under-ossification of bone, while hyperostotic traits are due to over-ossification of bone. Ossenberg (1970) hypothesized that hypostotic traits are usually linked to females and hyperostotic traits to males. This classification is helpful for describing not only the type of trait, but also the processes associated with its formation. In sum, as the above outline of research into sex-

specific traits illustrates, some nonmetrics are sex-specific, and thus can skew the results when they are included. As a result, most studies only utilize those characteristics that have been shown to be free of, or only slightly affected by, sex bias.

Age is another confounding factor in nonmetric trait analyses. Some traits, e.g. atlas bridging and clinoid bridging, have been shown to develop during adolescence, with few changes affecting the traits during adulthood (Saunders and Popovich 1978), while other traits have been identified with some sort of age dependency (e.g. Perizonius 1979). Perizonius (1979) noted two discrete traits that were age dependent (epipteric bone and foramen zygomaticotemporale), but concluded that age was not a strong influence overall with nonmetric traits. Berry (1975) was consistent with Perizonius (1979) in concluding that age is not a significant factor in most nonmetric trait development in adults. However, Berry (1975) did identify one age dependant trait: foramen of Huschke (tympanic dehiscence). Later, Humphrey and Scheuer (2006) revisited age as it relates to tympanic dehiscence and discovered that there is no age dependency in the trait in adults. Understanding age dependency is important because traits that appear at different stages in life can bias biological distances by emitting false negatives in younger individuals. Because of the possible effects of age on nonmetric trait frequency, Saunders (1989) suggested elimination of subadults to avoid this issue. Thus, many studies use only adult individuals in their studies (e.g. Hanihara et al. 2003).

Intertrait correlations are another potential bias in discrete trait analyses that can affect the results. Intertrait correlations occur when one trait's appearance or absence, or lack there of, influences another trait's presence or absence. These correlations can yield an

inaccurate picture of the variation between samples if the statistic the researcher selected is affected by these correlations. The nature of intertrait correlations was explored by Hertzog (1968) who found traits that are closer to one another are more likely to be shaped by intertrait correlations than those traits that are further apart. When utilizing the statistic Mean Measure of Divergence (MMD), intertrait correlations can be addressed by performing simple chi-square tests on the data to identify any intertrait correlations (Sjφvold 1977). Usually traits that have high correlations with other traits are dropped from subsequent analyses. As discussed later in the Methods chapter, employing the statistic Mahalanobis D^2 with a tetrachoric matrix (which is robust to correlated variables) avoids having to test for intertrait correlations and removing correlated traits.

Despite the possibility of problems that can be encountered when dealing with sex, age, and intertrait correlations, nonmetric traits are not necessarily doomed to these biases. Hanihara et al. (1998 b) and Hanihara and Ishida (2001 a, b, c, d, e) tested for sex and age differences, and interobserver error in their 20 nonmetric trait samples. Luckily, they discovered that there was little to no sex or age biases in any of their 81 samples from global populations. Their work was one of the most expansive of its kind and its results give hope that most traits are not affected by these variables.

Craniometrics and Nonmetrics

Both craniometrics and nonmetrics have been demonstrated to be under some sort of genetic control. Concordance of the two types of data is sometimes expected (Richtsmeier et

al. 1984). Thus, authors have used craniometrics in conjunction with nonmetrics to analyze biological distances (Bondioli et al. 1986; Corruccini 1972; Droessler 1981; El-Najjar 1978; Ishida and Dodo 1997; Reichs 1984; Rightmire 1972; Sciulli 1990; Sciulli and Schneider 1985; Wijsman and Neves 1986), cranial discrete traits with dental metrics (Christensen 1998), dental metrics with dental nonmetrics (Matsumura and Hudson 2005) or dental metrics simultaneously with dental nonmetrics (Bedrick et al. 2000) with meaningful results. Alternatively, research has indicated that in some cases there are similarities between the two types of data, and in others there are differences (e.g. Jantz 1970 who found both similarities and differences). Therefore, anthropologists are divided in opinion as to whether the two types of data sources coincide well. To illustrate why this is the case, a short review of the evidence will be presented.

In 1974, Corruccini tested the differences between craniometrics and nonmetrics on the Terry collection. He deduced that if the different types of data are treated the same way, similar results will be produced. Later, Corruccini (1976) applied univariate and multivariate statistics to craniometrics and nonmetrics and concluded that the data are correlated. Similarly, Ossenberg (1977) concluded that her nonmetric biodistance results were consistent with metric analysis of the same population.

Conversely, Rightmire (1972) concluded that nonmetric data yields different results than metric data. Yet, he postulated that nonmetric data could be used in conjunction with other forms of data to explain population structure. As in Rightmire (1972), the nonmetric data from Ishida and Dodo's (1997) study of the populations of the Pacific Rim directly contradicted the metric data from the same populations. Due to the disparity between the

results, Ishida and Dodo (1997) called for more research into how the two types of data affect one another. Although nonmetric and metric data do not necessarily produce the same results, neither one should be eliminated and labeled as useless in anthropological investigations because of the wealth of information they can provide.

Biological Distance

Biological distance (or biodistance) is one of the main statistical components of quantitative population genetics methodology. It can aid in revealing population structure through estimation of the degree of relatedness between two or more populations or subpopulations. Morton (1975) defined biodistance as a function of kinship estimates, which allows for exploration of biological relationships. Biological data can be explored much in the same way as genetic data, because as Fox et al. (1996) discovered, there is a significant relationship between genetic and biological data. Moreover, Relethford (1994) concluded that genetic data and phenotypic quantitative data coincide well, which supports the use of phenotypic data for estimating population relationships.

Biological distance can utilize nonmetric data for estimation of population relationships. Besides nonmetrics, biological distances have been ascertained from genetic data (genetic distances) (Mateus Pereira et al. 2005; Nei 1972), craniometrics (Fox et al. 1996; Hemphill 1999; Howells et al. 1966; Jantz 1973; Mackey 1977; Neves and Pucciarelli 1991), and coordinate data (McKeown 2000). However, because the focus of this dissertation is on discrete variables, this section will focus on nonmetric biological distance

methodology. Furthermore, because of the sheer number of biodistance papers, explanations of specific biodistance studies will be constrained to significant and highly representative papers that illustrate important biological distance concepts.

Berry and Berry (1967) conducted the first cranial nonmetric biological distance study in anthropology, on several populations. In their paper, the authors demonstrated that biodistance estimated with MMD could detect relationships among different populations. Their results indicated that both discrete traits and biological distance detected an underlying genetic component and the phenotypic data were a reflection of the genotype (like Relethford 1994). Other researchers followed Berry and Berry's (1967) example (e.g. Hanihara et al. 2003; Prowse and Lovell 1996) and discrete trait biological distance studies have become a useful tool in investigations of population relationships. Because biodistance can answer questions relating to population structure and archaeological, cultural, and linguistic evidence, it is a useful anthropological tool that will be a significant part of this dissertation. However, there are drawbacks in its methodology. Wijsman and Neves (1986) elaborated on the potential cons of biodistance on nonmetrics. In their study of Sao Paulo blacks, whites, and mulattos, Wijsman and Neves (1986) realized that their 31 nonmetric traits were not good indicators of population relationships. Thus, the authors warned about selection of appropriate nonmetric traits for biodistance studies. If proper trait selection is conducted following the guidelines set forth in previous sections of this chapter, the issue Wijsman and Neves (1986) encountered will be avoided.

A variety of information about populations and their practices can be deduced by utilizing biodistances, such as migration information, post-marital residence patterns, how

cemeteries are arranged, and factors uncovered in bioarchaeological investigations. Migration theories, which dominated the subdiscipline in the past, used biodistance to establish migratory patterns. However, migration theories have begun to lose their popularity (Adams et al. 1978) because they oversimplify biological situations. Anthony (1990) asserted their utility when used properly in archaeology, a statement that is applicable to physical anthropology, as well. For example, Matsumura and Hudson (2005) conducted an example of good research that employed biodistance for exploration of migration theories. In their study, Matsumura and Hudson (2005) substantiated the theory that 2 separate migrations into South East Asia occurred, beginning in the Neolithic. Despite its decrease in use, as Matsumura and Hudson (2005) demonstrate, there are times when migration is a plausible conclusion and should be explored.

Biological distance studies have also been used to illuminate post-marital residence patterns (e.g. Lane and Sublett 1972). In this type of analysis, sexes are separated and statistics are run on each sex across samples (e.g. only data from males are input into biodistance statistics to calculate biological distances across groups). The sex that is not biologically similar to other groups in the biological distance analysis and is not biologically similar to other sex of the same group, are the non-migratory sex. Post-marital residence patterns studies posit that the mobile sex is the sex that is different from the other sex in the same group, but who is similar to a sex in another group.

Lane and Sublett (1972) was the first paper to report results from incorporating biodistance as an estimator of post-marital residence patterns. Subsequent studies have built upon this original methodological framework. Lane and Sublett (1972) applied MMD to

nonmetrics, separating by sex, in multiple mortuary populations of the Allegheny Seneca. By examining each sex individually, the authors determined the females were leaving their communities and living with their husband's community (patrilocality). Lane and Sublett (1972) proposed using local populations as the unit of analysis, in order to capture the patterns of mobility. Furthermore, they concluded that the probability of closely related family members presenting the same trait is greater than distantly related individuals. Other nonmetric studies (Birkby 1982; Bondioli et al. 1986; Spence 1974; Stefan 1999) also deduced postmarital residence patterns from biodistance analyses. However, biodistance utilizing genetic data was not able to detect these types of patterns (Aguiar and Neves 1991), which may be due to the inability to properly test for some post-marital residence patterns (e.g. bilocality). For example, Schillaci and Stojanowski (2003) concluded that bilocality was the most likely post-marital residence pattern at Pueblo Bonito. However, testing for bilocality is not feasible; construction of the null hypothesis for testing bilocality is impossible.

Another manner in which biological distance has been utilized, is in the determination of burial plots within a cemetery. Birkby (1982) examined Grass Hopper Pueblo individuals for nonmetric traits and established that there were different social units in the cemetery. Kinship units, or familial areas, have also been detected (Bondioli et al. 1986) using nonmetrics and biodistance in graves from Abruzzo, Italy. The work of Birkby (1982) and Bondioli et al. (1986) can assist in interpretations of burial customs to be extrapolated to cultural practices.

Biological distance analyses can also contribute to bioarchaeological investigations. For example, Buikstra (1980) employed biological distance in her study of seven mound groups of the lower Illinois River Region. Using mean measure of divergence (MMD) as an estimator of biological distance, she determined the patrilocal postmarital residence pattern of the groups (similar to the work done in Lane and Sublett 1972), and discovered significantly different MMD scores among the mound samples. The interpretation of a significant MMD score indicates that populations are very different, and the amount of difference makes them appear to be two different populations, and not two different groups from the same population. Buikstra (1980) postulated that the significant scores were probably due to geographic isolation of some of the groups, which would prevent gene flow and encourage genetic drift. She also hypothesized that social rules and/or customs may have also prevented gene flow from occurring between groups. Because of the power of MMD and its ability to estimate limited aspects of population structure, she tested the groups across temporal changes during a large cultural shift that occurred from 400-600 A.D. Buikstra (1980) did not detect significant changes in biological data across this time period. Her overall work established that there was biological continuity underlying a major cultural shift in the lower Illinois River region.

Although biodistance studies can answer many questions about population structure, Relethford (1999) warned that biodistance is ill-suited to addressing modern humans origins questions. He effectively demonstrated that accumulated ancestry changes over time in a population. Thus, the greatest similarity of populations is not necessarily within a population (e.g. among samples), because the largest population dominates the accumulated ancestry.

As an example, Relethford (1999) pointed out that biological distances calculated from many traits on modern fossils will be more similar to earlier samples from Africa than to samples from the same geographic area. Relethford (1999) suggested that researchers should pay special attention to small biodistances associated with large sample sizes and interpret these distances as a function of population size.

Scholars have calculated biodistance, using nonmetric traits, by applying Mean Measure of Divergence (e.g. Berry and Berry 1967), Mahalanobis D^2 (Godde 2009a; Irish 2005; Ishida and Dodo 1997; Konigsberg 1990; Konigsberg et al. 1993), and discriminant analyses (e.g. Byrd and Jantz 1994 ; Jantz and Owsley 2001; Rightmire 1970). MMD and Mahalanobis D^2 treat categorical data as discrete data, while estimating a biological distance score. This number can be input into principal coordinates analysis (PCO) in order to depict the relationships of the groups, graphically. Discriminant analysis, on the other hand, treats categorical data as continuous data, a procedure that will lead to biased results. The differences between MMD and Mahalanobis for discrete traits are presented, below. The most important caveat for all statistical methods is that biological distance has to be interpreted in light of population history. Affinities found between populations should make sense in light of historical contact, geographic location, and time.

Selection of statistics that adequately test the discrete trait hypothesis is important in biodistance studies. Mean measure of divergence has been the statistic most commonly used in nonmetric biological distance investigations (e.g. Berry and Berry 1967; Prowse and Lovell 1996). Mahalanobis D^2 with a tetrachoric matrix has recently been employed in nonmetric trait examinations (Godde 2009a; Irish 2005; Ishida and Dodo 1997; Konigsberg

1990; Konigsberg et al. 1993) and shows much promise for discrete trait biological distance studies. Mahalanobis D^2 with a tetrachoric matrix is a Euclidean distance and is similar to the Mahalanobis distance utilized in metric analyses. The main difference between the two Mahalanobis distances is the tetrachoric matrix, which allows for the calculation of discrete data. An example of the utility of Mahalanobis distances in biological distance analyses can be found in Bedrick et al. (2000). Bedrick and his coworkers employed Mahalanobis for both metric and nonmetric traits and applied maximum likelihood distance to the Mahalanobis scores. Their analysis was the first of its type and it was successful in using both types of data to estimate biodistance with Mahalanobis.

The Mahalanobis D^2 in metric analyses is now used to estimate F_{st}, R matrices, and other population genetics parameters (e.g. Nystrom 2006; Steadman 2001). Because Fst and R matrices assume a linear distribution, they require a statistic that meets this criterion, such as Mahalanobis D^2. Thus, Mahalanobis D^2 with a tetrachoric matrix is appropriate for the application of F_{st} and R matrices to discrete data. Conversely, MMD is not suitable for F_{st} and R matrices because its distance is measured on a curve, and therefore it is not linear and does not meet the requirements for the production of these population genetics statistics. Because Mahalanobis D^2 with a tetrachoric matrix can be utilized with population genetics statistics, it will be employed in the current study as a means to investigate Nubian population structure, by applying population genetics statistics to it.

Temporal and Spatial Analyses

Interpretations of time and space are enabled by biological distance estimates. Several models have been put forth to account for temporal and spatial influences on biological distance. Malécot (1948) introduced the isolation by distance model, which expects populations separated by great spatial distance will reflect a decreased coefficient of kinship than populations near one another. Rudan et al. (1987) agreed that the isolation by distance model exhibits the relationship of migration and spatial distance in their anthropometric investigation of Korĉula island and Pelješac peninsula.

Other studies have agreed with Malécot (1948) and a large body of work on the topic has been produced. Sciulli (1990) speculated that isolation by distance possibly influenced the population structure of the Late Archaic Ohio sample from Duff Cemetery, although it was not the only factor affecting it. Sciulli and Schneider (1985) employed both cranial metrics and nonmetrics and observed the same spatial patterning where closer populations are more related than more spatially distant populations. Furthermore, Rothhammer and Silva (1990) deduced that biological distance is correlated with spatial distance. Allelic data has also produced similar results among Italian populations, where smaller spatial distances were correlated with a higher degree of genetic similarity (Soliani et al. 1985). As a special case of Malécot's (1948) findings, Buikstra (1977) demonstrated that there is a closer affinity among groups living along rivers. If two sites are on a river, measuring the distance between the two points by calculating the distance along the river will be more accurate than calculating the distances as a straight line drawn between two points.

There are always exceptions to rules and models and the next few papers highlight exceptions to Malécot's (1948) hypothesis. Conner (1990) could not find any significant geographical patterning between Lower Illinois groups and biological distances. He asserted that fissioning or other geographical patterns may have been obscured by the effects of gene flow. Despite a grouping of two samples along the coast, Fox et al. (1996) concluded that craniometric distances were not related to geographic distances in their Iberian peninsula samples. In investigations of the Ohio Hopewell complex, Sciulli and Mahaney (1986) determined that the biological distances separating Adena samples were comparable to Archaic samples, despite the smaller spatial distances separating the Adena samples. Finally, Schillaci and Stojanowski (2005) also did not uncover a pattern of closer genetic affiliation between Tewa Pueblo samples. However, the authors reasoned this was probably due to migration masking the population structure of the Tewa.

Prior to 1990, it was assumed that there was a relatively simple pattern where biological distance was positively correlated with temporal separation between samples. In 1990, Konigsberg synthesized elements from the island model of Wright (1951), which addressed temporal separation, the unidimensional stepping-stone model (Kimura and Weiss 1964) for spatial divisions, and a migration matrix (e.g. Harpending and Ward 1982) into a model that can analyze samples of a population that are separated by space and time. The expectations from this model are that spatial distances are positively correlated with biological distances, and conversely, temporal distances are negatively correlated with biological distances. Konigsberg (1990) examined Lower Illinois Valley and Mississippi River Valley individuals for cranial nonmetric traits and produced biological distances that

were calculated from a new categorical statistic, Mahalanobis D^2 with a tetrachoric matrix. Temporal and spatial distances were generated from the groups and the median dates were used for comparison with biological distances.

Konigsberg (1990) applied Mantel tests to temporal, spatial, and biological distance matrices to determine how space has an effect on biological distance while controlling for time, and how time influences biological distance while controlling for space. As mentioned before, the results of his statistical analysis indicated that there was a positive correlation between space and biological distance and a negative correlation between time and biological distance. A positive correlation between space and biological distances is expected; the more distant two groups are, the less of a chance there is for gene flow between them (Konigsberg 1990). Alternatively, although a negative correlation between time and biological distance sounds counterintuitive at first, it makes sense because gene flow acts as a stabilizing force over time, making temporally distant samples uniform (Konigsberg 1990). These principals are not exclusive to Illinois and Mississippian populations; rather, they can be applied to other populations to explore the effects of space and time. Bedrick et al. (2000) later confirmed the results of Konigsberg (1990).

Population Genetics and Population Structure

In order to understand the importance of using a population genetics approach in estimating population structure in the Nubians, a brief explanation of some theoretical concepts in population genetics is necessary. The *in situ* hypothesis explores biological

evolution, and thus the four forces of evolution should be discussed in anticipation that the results in this dissertation will be affected by these factors. Understanding these effects will aid in interpretation of the results and an understanding of the forces driving the change or stability of a population.

Gene flow increases within group variation and decreases between group variation, whereas mutation increases the variability within a population or samples of populations. The effects of mutations can be observed among population samples separated by time and/or space. Alternatively, natural selection can manifest itself in adaptations to environments. However, if a quantitative trait has zero heritability, no further adaptation will occur because there is zero response to selection. Although specific nonmetric traits have not been identified as advantageous for survival in certain environments, their potential adaptive responses cannot be discounted. Genetic drift can obscure population relationships and structure through increasing variability between populations because certain alleles have contributed a disproportionate amount of genetic information to one of the groups. Other than gene flow, only the effects of genetic drift have been statistically modeled for phenotypic data. Relethford (1996) proposed a scaling method to contend with genetic drift's effects. Even though it is a straightforward model, it becomes difficult to apply because it requires knowing a relative effective population size, a luxury not found in archaeological populations.

Next, the approaches to population structure investigations are explored to introduce the statistical methodology of this dissertation. Relethford and Lees (1982) defined model-bound and model-free approaches to studies of population structure. Model-bound studies

seek to incorporate quantitative traits into studies of population structure, using population genetics models and estimating population genetics parameters. Relethford and Lees (1982) proposed two different types of model-bound analyses, admixture and kinship estimation. Admixture estimation aims to calculate the "admixture in hybrid populations" (Relethford and Lees 1982: 125). Kinship estimation seeks to evaluate "genetic similarity among individuals or populations" (Relethford and Lees 1982: 126).

Conversely, model-free research explores biological variation with the application of population structure models, but does not directly measure population genetics parameters. Relethford and Lees (1982) identified two types of model-free analyses, differentiation and comparative. On the one hand, differentiation studies focus to, "determine the extent of variation among groups, but not the pattern of this variation" (Relethford and Lees 1982: 117). One of the statistics used by differentiation studies is discriminant analysis. On the other hand, comparative studies, "determine the pattern of among-group variation, and then relate that pattern to other biological, demographic, and/or historical patterns" (Relethford and Lees 1982: 117). Comparative studies typically use Mahalanobis distances in their approach. Relethford and Lees (1982) point out that the two types of model-free analyses are similar; they both "deal with the effects of population structure on among-group variation" (117). Model-bound approaches strengthen the testing of biological hypotheses, such as the *in situ* hypothesis, because they seek to estimate specific population parameters (i.e. genetic similarity).

Model-free approaches usually dominate nonmetric studies (e.g. Berry and Berry 1967), with only select studies attempting to conduct model-bound methods (Haneji et al.

2007; Hanihara 2008; Herrmann 2002; Komesu et al. 2008; Konigsberg 1987; Konigsberg 1988). Metric analyses (Nystrom 2006; Scherer 2007; Schillaci and Stojanowski 2005; Tatarek and Sciulli 2000) have become more and more model-bound oriented with the adaptation of allelic population structure statistics to continuous traits (Relethford and Blangero 1990) and the advent of RMET, written by Relethford and Blangero. RMET is a statistical program, based on the Harpending and Ward (1982) model for allele frequencies. The Harpending and Ward (1982) model estimates the expected heterozygosity of a population from a mean of the populations in the area. Simply stated, Harpending and Ward (1982) showed how it is possible for larger spatial distances to produce decreases in the frequency of migration and population similarity. Under their model, populations nearer the genetic centroid will experience higher within group variation, while populations further from the genetic centroid will have less within group diversity. When heterozygosity is plotted against distance from the centroid (the diagonal elements, or r_{ii}) for each group and a regression line is fitted through the points, the outliers on either side of the regression line are interpreted as either having higher than average heterozygosity (above the regression line) or lower than average heterozygosity (below the regression line). Some model-bound nonmetric studies (Haneji et al. 2007; Hanihara 2008; Komesu et al. 2008) have applied RMET, a continuous data statistical program, to categorical data, and thus have yielded incorrect estimates of population genetics statistics.

RMET consists of the estimation of a distance matrix (Mahalanobis), an R-matrix (biased and unbiased), F_{st} (biased and unbiased), and principal coordinates analysis, among other statistics. The R-matrix is a standardized variance co-variance matrix of the dataset, F_{st}

is the proportion of genetic variance between samples out of the total, and principal coordinates analysis allows for a graphical depiction of the relationship of the groups. F_{st} can also yield other population information, such as changes in migration patterns (Konigsberg and Buikstra 1995; Relethford et al. 1997), which is valuable in determining the direction of gene flow. Relethford and Blangero (1990) also derived an analysis that describes the magnitude of gene flow within a sample. The statistical method of this dissertation strives to be model-bound by attempting to emulate the complete Relethford and Blangero (1990) approach with minor adaptations for categorical data.

Now that the background of the data and methodology of this dissertation has been summarized, the archaeological and biological evidence will be presented. Evidence from both artifacts and mortuary patterns will be described, in order to elucidate the picture of Nubian evolution that has already been projected by others. For the most part, the biological evidence will support the archaeological interpretations.

Chapter 3

Nubians

In this dissertation, the Nubian population is investigated in order to explore their population structure and apply categorical adaptations of population genetics statistics (see Chapter 1 for specific questions explored) to samples that range from the Mesolithic – Christian time periods and in space from the 1st through just below the 3rd cataract. Initial interpretations of the archaeological record, as well as the skeletal material of Nubians, focused on evidence of contact with foreign populations (e.g. Elliot Smith and Wood Jones 1910, Reisner 1910). Reisner (1910) ascribed the remnants of contact with different populations to heavy migrations or invasions and constructed his series of time periods in Nubian history around each perceived wave of population arrival. He lettered the time periods in the order they occurred; the original succession of time periods for Nubian history were designated as A-, B-, C-, D-, and X-Group (Reisner 1910). Since the inception of the categorization of time periods in Nubian history, they have been modified to reflect current interpretations of the past with new archaeological evidence. Table 1 recreates one of the

Table 1. Nubian time periods.

Time Period	Dates
Paleolithic	12,000-15,000 years BP[1]
Mesolithic	5000-11000 years BP[2]
Neolithic	5000-2700 B.C.
A-Group	3300-2800 B.C.[3]; 3400-2400 B.C.[4]
C-Group	2300-1800 B.C.[3]; 2300-1200 B.C.[5]
Kerma	1800-1200 B.C.[3]
Pan-Grave	1786-1550 B.C.[6]
Nubian Hiatus	1000 B.C. – 100 A.D.[4]
Meroitic	0 – 350 A.D.[3]
X-Group	350-550 A.D.[3]
Christian	550-1500 A.D.[3]

[1] Adams (1977)

[2] Based on Greene et al. (1967) and Hassan (1986)

[3] Nielsen (1970)

[4] Carlson and Van Gerven (1979)

[5] Carlson and Van Gerven (1979) estimates of Lower Nubia

[6] Strouhal and Jungwirth (1980)

accepted interpretations of general Nubian time periods (most time periods can also be broken down into phases). Sometimes these time periods are associated with the rise of a certain Nubian group or site (e.g. Kerma). To be consistent and categorize the results into understandable and meaningful divisions, the groups will be referred to and treated as time periods.

As archaeological thought changed and subsequent interpretations of the archaeological record were more oriented towards smooth transitions between time periods, biological anthropologists also revised their views on the skeletal material. In 1968, Adams speculated the archaeological record demonstrated that Nubian evolution was continuous and without the hypothesized interruptions of foreign peoples as was once put forth. Instead, the contact of other peoples did not necessarily permeate the hegemony of Nubians. His 1977 book synthesized the archaeological evidence and this interpretation was voiced, yet again. Consequently, Carlson and Van Gerven (1979) drew upon Adam's conclusions and adapted them for the biological data. Whether or not any of the contact with foreign peoples manifested biologically is the main subject of the *in situ* hypothesis, which is explored in this dissertation. This chapter will present the archaeological and biological evidence for Nubian evolution under the *in situ* paradigm. However, evidence that points to migration or invasion possibilities will also be mentioned.

The Archaeology of Nubia

Nubia's territory extends from Upper Egypt through Lower Sudan, stretching from the first through the sixth cataract of the Nile. As described above, throughout Nubian history the Nubians had contact with other populations, including Egyptians and Ethiopians. The similarities between Egyptian and Nubians were so striking, the social structures even resembled one another; Nubians also had kingdoms and state-level societies. Common social structure may have been due to the interaction between the two populations. Likewise, the extensive interaction between the Nubians and Ethiopians extended into the twenty-fifth Nubian kingdom; Ethiopians were the rulers of what has been referred to as the "Ethiopian dynasty" (Adams 1977). Many other populations had contact with the Nubians, including the Bedouins and Greeks.

The *in situ* hypothesis states that Nubians evolved biologically and culturally without much contribution of gene flow from outside groups (Adams 1968; Adams 1977; Carlson and Van Gerven 1979). The archaeological evidence suggests that some of the Nubian cultural transitions were smooth and not indicative of the integration of another population in the area. However, other cultural transitions yielded major shifts in artifacts, grave form, and language that suggested prolonged contact with other populations. Thus, the Nubian archaeological record is peppered with both smooth and abrupt transitions, which implies that the amount and nature of contact of outside groups varied throughout Nubian history.

The brief synopsis of the archaeological evidence below will highlight the different transitions present in the groups that are the subject of the current investigation.

The Late Paleolithic is the first time period that suggests extensive contact with other populations. Wendorf (1968) noted that there were several forms of lithic assemblages during this time and hypothesized that the great variation in assemblages was due to migrations of different peoples to the area. Wendorf's assertion, although well-substantiated, stands in high contrast to findings of homogeneity of later Nubian time periods, such as the A-Group. The Mesolithic Nubians succeeded the Late Paleolithic Nubians and the Khartoum Mesolithic Nubians appeared to have been hunter-gatherers (Edwards 2004; Trigger 1976). The Khartoum Mesolithic groups produced pottery that was well distributed in Nubia and which dates to 5,000 – 6,000 B.C. (Trigger 1976). Conversely, the Khartoum Neolithic Nubians probably domesticated goats and sheep (Trigger 1976). The pottery of the Khartoum Neolithic appears to have evolved from the Khartoum Mesolithic (Trigger 1976). The early Neolithic groups are: Post-Shamarkian, Khartoum Variant, Abkan and Qadan. Their pottery and other artifacts are plentiful, but the skeletal material has remained elusive (Nordström 1972).

The A-Group is a Neolithic Nubian cultural horizon who was uniform geographically and temporally (Nielsen 1970). The A-Group subsistence strategies were more diverse than previous groups as they practiced pastoralism, agriculture, hunting, and fishing (Nielsen 1970). Egyptian military expeditions to the area probably coincided with the end of the A-Group time period (Nielsen 1970). Authors have postulated that a later group, the C-Group, may have evolved from the A-Group (Nielsen 1970). However, Nielsen (1970) pointed out a

large gap of time between the end of the A-Group and the beginning of the C-Group, despite the cultural continuity between the two groups. A third time period, the B-Group, was postulated to have existed between the A- and C-Groups (Reisner 1910), but current work has established that the B-Group is not a true Nubian time period (Smith 1966). Adams (1977) drew upon previous work from other archaeologists and presented evidence that the relative poverty of the B-Group graves implied they were actually the lower class A-Group, rather than a new population migrating to the area or a change in time periods. Even with the gap between the A-Group and the C-Group, the smooth transition between these two cultures exemplifies the continuity that has been detected in the Nubian archaeological record.

The C-Group survived as a Nubian culture, despite the extensive Egyptian contact that occurred from military expeditions and occupation (Nielsen 1970). Adams (1964) suggested that at the end of the time period, the C-Group left Lower Nubia because of the receding water levels that made agricultural efforts difficult. The abandonment of Lower Nubia accounts for the disappearance of the C-Group from the archaeological record. The overlapping Kerma time period, in contrast, yielded ceramics that are similar to the C-Group (Trigger 1976) and implies cultural continuity between the two groups. The ceramics were so similar that archaeologists have erroneously attributed ceramics from the Kerma period to the C-Group (Trigger 1976). Furthermore, agriculture continued with the Kermites, who also employed pastoralism. Adams (1984) interprets the evidence from the Kerma site as remnants of a chiefdom:

> The tombs at Kerma, unlike those in Egypt, proclaim a chiefdom rather than a state, that is, a society in which authority has been formally consolidated only in the hands of the ruler, an in which there is as yet no hierarchical differentiation of power and wealth. The royal tombs, although concentrated in a single zone in the Kerma

> necropolis, occur side by side with common burials, and they are quantitatively rather than qualitatively distinct from their neighbors. (Adams 1984).

Despite commonalities in pottery, the individuals from Kerma demonstrated an increasingly complex social structure from the preceding C-Group (Trigger 1976). An interesting feature, Pan-graves (shallow, pan-shaped graves), have been dated to the Kerma time period through careful examination of the burials (Adams 1977). Adams (1977) agrees with other scholars that these represent the Pan-Grave culture, which is a separate Nubian group that existed during the Kerma period, and were not a part of the C-Group or Kerma cultures. Thus, at this time, three separate Nubian cultures existed throughout Nubia.

The next Nubian group to occupy Lower Nubia was the Meroites, a state level society, who returned to the area after a long hiatus, approximately 1,000 years later (Adams 1977; Nielsen 1970). Adams (1968) and Nielsen (1970) speculated whether or not the population that moved into Lower Nubia after the hiatus was actually Nubian. Adams (1968, 1977) stated that the cultural continuity between the Meroites and other Nubians implied that the Meroites were a Nubian group returning to Lower Nubia after abandonment of the area. The only cultural difference he noted was the appearance of the as of yet undeciphered Meroitic written language. Conversely, Nielsen (1970) contended the Meroites were a combination of Nubians from other areas of Nubia and possibly peoples from the western deserts and Kordofan. The Meroites practiced agriculture, which is consistent with a smooth evolution in subsistence strategies from the Kerma culture. Furthermore, the large amount of trade that began with Kerma was maintained with the Meroites (Edwards 2004). Imports from other areas were found mainly amongst grave goods (Edwards 2004). Moreover, the

results of the cranial nonmetric study of Godde (2009a) supported the notion that the Meroites were a Nubian population returning to the area.

Cultural continuity may have continued with the X-Group, who were very similar to the Meroites. In fact, Nielsen (1970) contended, "there is no abrupt break with the Meroitic traditions" (20) in the X-Group. Adams (1977) presented evidence that suggested cultural continuity between the Meroites and X-Group; pottery, iron spears, arrowheads, and tools were similar between the two groups. This evidence has led other scholars to conclude that the Meroites evolved into the X-Group, who transitioned into the Christians (Adams 1977). However, Nielsen (1970) also noted that some artifacts suggested the X-Group was a mixture of the different populations living in the area, including the Blemmyes, Nobatae, and any other foreign peoples who migrated to the area during the Meroitic period (Nielsen 1970). The Christian time period followed the X-Group with an uninterrupted cultural evolution (Adams 1977; Nielsen 1970), which is especially apparent in the slow changes in ceramics (Adams 1977). Evidence from two Christian cemeteries, whose skeletal remains will be utilized in this study, have suggested that both the mainland and island Kulubnarti groups were probably practicing agriculture and pastoralism as their main subsistence strategies (Adams et al. 1999).

The archaeological record has preserved both the homogenous and heterogeneous aspects of Nubian history. Despite the slow continuous evolution of artifacts, evidence of contact with foreign peoples persisted in the archaeological record (Adams 1977). However, this evidence was not necessarily indicative of migration or invasion hypotheses (Adams 1977). Mortuary archaeological and biological investigations will supplement the existing

archaeological evidence. Because the changes across Nubian history are not completely smooth, it is necessary to utilize statistics that estimate population variation and to sample groups that are representative of as much time and space as possible. This type of research design will elucidate the subtle aspects of population structure. The mortuary and biological evidence will assist in interpretations of archaeological evidence across smooth and abrupt transitions.

Mortuary Archaeology of Nubia

The burial practices of Nubians reflect change over time and will be interpreted in relation to the archaeological and biological data, taking a cultural historical approach. The Mesolithic Nubians are the earliest time period included in this dissertation. As will be presented in Chapter 4, the Mesolithic groups were hunter-gatherers and, consequently, their burials reflect a less complex social structure. The number of individuals interred in burials varied between one and two and the bodies were placed in flexed position, for the most part (Greene et al. 1967).

A-Group and C-Group burials were rather similar to one another, characterized by round, oval, or an occasional rectangular shape (Nielsen 1970). Frequently A-Group burials were used for more than one consecutive burial (Nielsen 1970). Initially, the bodies were inserted into the grave in a flexed position and subsequent burials were either placed on top of the first burial, with a layer of sediment in between, or the original individual was moved to the side of the grave to make room for the second individual (Nielsen 1970). Grave goods

were abundant in the A-Group burials (Adams 1977). The cultural remnants include jewelry and pottery that were manufactured either in Nubia or in Egypt (Adams 1977). These grave goods have only been found in A-Group burials and their purpose in everyday life is unknown (Adams 1977). Additionally, at Tunqala West, tumuli were created with stone, and included a stone offering, and probably stelae (Adams 1977).

C-Group burials occasionally boast standing flat slabs and usually present with a round superstructure of stones on the perimeter of the pit (Nielsen 1970). Like the A-Group, the bodies are usually flexed and burial pits were reused for subsequent interment of other individuals (Nielsen 1970). Although these burial customs are quite similar, they can be distinguished when found in the same cemetery by their subtle differences (e.g. superstructure differences). The similitude of these burial customs lends support to the notion of cultural continuity between these two groups. Another indication of cultural continuity over later times was the trend of placing some sort of marker over a burial, which began with the C-Group and continued through the Christian time period (Adams et al. 1999).

The mortuary archaeology from the period of time between the A-Group and the Christians supports Nubian homogeneity and the *in situ* hypothesis. However, there is one exception between the A-Group and Christians. The time period that succeeded the C-Group, Kerma, has produced graves that are consistent with three different cultures (Nielsen 1970). The Pan-Grave culture appeared around the time of the Kermites and was named because of their use of shallow, oval graves (Adams 1977). Archaeologists have found pan-graves amongst both C-Group and Kerma burials that are distinct from both the C-Group and

Kerma burials (Adams 1977). In addition to the Pan-Grave culture, Pharonic burials were also found during the Kerma time period in separate cemeteries from the Kerma and Pan-Grave individuals. Nielsen (1970) noted similarities between individuals from Kerma and Pharonic burials, despite the many prior studies Nielsen cited that concluded from the archaeological evidence that the Pharonic burials were actually Egyptians.

The increased complexity in the Kerma time period was also evident in their burial customs. The tombs consisted of pits filled with a body and grave goods (Trigger 1976). Within the tumuli, rulers were placed supine on beds of stone (Trigger 1976). Accessory graves were found surrounding chambers where presumed rulers were interred (Trigger 1976).

The X-Group utilized the same burial areas as the Meroites, making distinguishing between the two groups difficult (Nielsen 1970). Meroitic tombs were usually constructed of rectangular shaped burial chambers (Zabkar and Zabkar 1982) and the individuals were placed extended (Nielsen 1970). Meroitic burials are usually oriented east to west (Zabkar and Zabkar 1982). The X-Group built tombs similar to those created by the Meroites and sometimes X-Group burials were found in the same burial complexes as the Meroites, but the X-Group left the Meroitic burials undisturbed (Nielsen 1970). These X-Group tombs may have shafts that led to end or side chambers (Nielsen 1970). Additionally, X-Group tombs can be set off by a flat superstructure (Nielsen 1970). The bodies were placed in one of two positions: 1. flexed, or 2. extended and supine (Nielsen 1970). Opposite from the Meroites, the X-Group placed their graves north to south (Zabkar and Zabkar 1982). Like the X-Group, the Christians also buried their dead in the same cemeteries as the preceding time

period. However, unlike the X-Group, the Christian tombs are "simple narrow shafts," a.k.a. "slot graves" (Nielsen 1970: 122). Bodies were placed supine in the grave with few, if any grave goods (Nielsen 1970).

For the most part, the evolution of Nubian burials was smooth and reflected an increased complexity in design, which parallels the increased complexity of their social structure. The mortuary data is consistent with the archaeological data, presented above, that demonstrates a slow evolution over time within the Nubians (despite evidence of contact with other populations). The biological data will support these archaeological data.

The Biological Data

This section presents the biological data ordered by data type (e.g. cranial metrics), rather than by Nubian time period (as in the archaeology). The earliest research published on Nubian biological affinities focused on racial typologies and the Nubians' place within them. The early partitioning of time periods was based on the precept that any changes in the population were due to replacement or migration from other populations (e.g. Batrawi 1945, 1946; Elliott Smith and Wood Jones 1910, Reisner 1919). Van Gerven et al. (1973) attempted to present a different paradigm with which to study Nubian biological data. Van Gerven and his coworkers suggested using a biocultural approach that combines patterns of mortality, skeletal growth, and pathology for assessing biological data. Later, Carlson and Van Gerven (1979) synthesized their views on Nubian biological evolution with the archaeological record (and Adams 1968, 1977) and deduced that the Nubians biologically

evolved *in situ*. Since that time, most scholars conduct biological studies of Nubians within the *in situ* theoretical framework.

In order to detect *in situ* development, Carlson and Van Gerven (1979) put forth evidence of homogeneity among Nubian groups and concluded that homogeneity is indicative of *in situ* change. A corollary of their precept is that if Nubian groups are biologically distant (e.g. large biological distances) from other populations, then *in situ* evolution is inferred. Conversely, biological diffusion, or biological changes due to contact with other populations will manifest itself in the heterogeneity of a population. A related concept indicates that if Nubians are similar to another population with known contact, then biological diffusion may be one of the causes.

Cranial metrics have mostly contributed to the biological knowledge base of Nubian evolution. Mukherjee et al. (1955) conducted a metric analysis of Jebel Moya crania and found that they were morphologically distinct from other Nubian and African groups. Irish and Konigsberg (2007) reassessed dental discrete traits from the crania involved in Mukherjee et al. (1955) and confirmed Mukherjee et al.'s (1955) original findings. According to the authors, there is little evidence that suggests Jebel Moyans were not Nubians, despite their uniqueness. In 1977, Van Gerven et al. investigated the change in craniofacial variation over time through the Meroitic, X-Group, and Christian time periods at Kulubnarti. A trend in facial reduction was apparent in the samples, a trend found in several metric analyses on Nubian data. The facial reduction was later confirmed by Carlson and Van Gerven (1976) who looked at a Mesolithic sample from the Wadi Halfa, and compared it to A-Group, C-Group, Meroitic, X-Group, and Christian remains also from the Wadi Halfa.

They found the Mesolithic Nubians were ancestral to later Nubian groups and the changes over time were associated with changes in subsistence strategies. Carlson (1976) also agreed with the reduction in craniofacial complex over time and related these transformations to changes in subsistence strategies.

Van Gerven (1982) looked at craniofacial variation among Meroitic, X-Group, and Christian Nubians from the Batn el Hajar and Kulubnarti. Variation was detected in the data reflecting temporal and geographic changes. Facial size reduction was indicated in a temporal trend, while a geographic trend between lower Nubia and Kulubnarti groups became evident as groups from these areas were more similar during the Christian time period. Carlson and Van Gerven (1979) contended that most Nubian biological studies yielded results that reflected homogeneity among Nubian groups. However, Buzon (2006) contradicted those earlier studies by finding heterogeneity among the Nubians at Kerma and Tombos, especially in relation to Egyptians, who she found to be more homogeneous overall.

In addition to extensive craniofacial metric data, dental studies have also been plentiful. Greene et al. (1967) examined Mesolithic dentition from Wadi Halfa (one of the samples in this study) for both metric and nonmetric traits and determined that the nonmetric features were an interesting mixture of morphology, including shovel-shaped incisors, and numerous supernumerary cusps. Moreover, Greene and his coworkers determined the size of the Mesolithic dentition was large, greater than Skühl Neandertals. Later, Greene (1972) confirmed that tooth size decreased from Mesolithic through Christian time periods. He further interpreted homogeneity over time and space using the Meroitic, X-Group, and Christian Nubian groups (Kulubnarti), in conjunction with a Badarian Egyptian sample. In

1982, Greene also verified without an outgroup that the Meroitic, X-Group, and Christian were all similar to one another. Calcagno (1986) remeasured the Mesolithic Nubian dentition from Greene et al.'s (1967) paper and determined they were similar in size to Australian Aborigines, who have the largest modern human dentition. He also discounted Greene et al.'s (1967) comparison of Nubians to extinct hominids.

Similar continuity information has been revealed by dental nonmetrics. Johnson and Lovell (1995) detected biological continuity between the A-Group and C-group of Lower Nubia (Wadi Halfa), using MMD. Moreover, Irish (2005) also demonstrated a homogeneous distribution of Nubians from the Final Neolithic, through the Christian time periods with MMD. However, Irish (2005) asserted that after the late Pleistocene there was a population replacement that occurred some time prior to the Final Neolithic (which is supported by the lithic evidence). Turner and Markowitz (1990) examined dental discrete traits on late Pleistocene, Meroitic, X-Group, and Christian samples and found continuity over time from the Meroitic through Christian time periods. However, there was a gap between the late Pleistocene and Meroitic Nubians (prior to the continuity observed among the Meroitic, X-Group, and Christian samples), indicating to the authors that a population replacement probably occurred. Irish and Turner (1990) continued the research of Turner and Markowitz (1990) with more dental traits and additional samples and their findings were consistent with Turner and Markowitz (1990). After these two studies, Irish (1998) determined that late Paleolithic Nubians were different than most other North Africans. The differences implied to him that other North African groups did not contribute to the genetic makeup of the late Paleolithic Nubians. Irish confirmed these findings in 2000, when he noted that

Iberomaurusians and post-Pleistocene North African samples were different from Late Paleolithic Nubians.

As of yet, little has been done with cranial nonmetrics. Berry et al. (1967), Berry and Berry (1972) both used Nubian samples for their cranial nonmetric biological distance studies. However, conclusions about Nubian affinities were minimal as they were used primarily as an outgroup. Prowse and Lovell (1996) also utilized the A-Group from Wadi Halfa as an outgroup to determine the relationships among those interred in specific elite and non-elite Egyptian cemeteries. The authors observed the A-Group for both cranial and dental nonmetrics. Interestingly, they concluded that the A-Group was more similar to high status Egyptian individuals than the high-status Egyptians were to other Egyptian groups. Prowse and Lovell's conclusions fall inline with archaeological evidence that suggests great wealth of some of the A-Group burials; it is possible the elite A-Group corresponded with upper class Egyptians by pure virtue of their social status. Similar to Berry and Berry (1972), Hanihara et al. (2003) also included individuals from Kerma, Sesebi (a sample comprised of three time periods), and the islands of Hesa and Biga (Christian) in their assessment of biological relationships across the world. Conclusions about Nubians were in relation to larger geographic groups and did not pertain to the *in situ* hypothesis.

A small collection of studies actually examined Nubian affinities with cranial discrete traits. Prowse and Lovell (1995) utilized cranial nonmetrics to test the *in situ* hypothesis in A-and C-Group Nubians. Their results from MMD analysis of biological material were consistent with the *in situ* hypothesis; the A-Group and C-group were homogeneous. In metric and nonmetric analyses of Nubian crania from Sayala, Strouhal and Jungwirth (1980)

discovered that the C-Group and Pan-Grave peoples were not one homogeneous biological group. Furthermore, Strouhal and Jungwirth (1979) compared remains from Nubian cemeteries and certain graves with Roman artifacts from the Sayala burial complexes to determine who was buried at Sayala. Their metric and nonmetric analysis concluded that the Blemmyes were the individuals interred with Roman grave goods at Sayala. Thus, Sayala boasted a diverse demographic (Blemmyes, C-Group, Pan Grave), which supports the probability of biological differences between the C-Group and Pan-Grave peoples.

More recently geneticists have also contributed to the biological diffusion vs. *in situ* debate (Fox 1997). Fox (1997) examined mitochondrial DNA in a Meroitic sample and discovered sub-Saharan markers. Thus, Fox (1997) deduced there was south-north gene flow in the Nubians and in situ development was not a plausible hypothesis for Nubian biological evolution. Similarly, Krings et al. (1999) studied mitochondrial DNA in Egyptian, Nubian, and southern Sudanese samples. Their work uncovered diversity consistent with gene flow occurring in both a north-south and south-north direction in the last few thousand years. Further, they noted the gene flow from south-north was greater or happened sooner than the north-south migrations.

The biological data, for the most part, is consistent with *in situ* evolution (except for DNA). These findings imply that *in situ* evolution will probably be evident in the results of this dissertation. The next chapter will present the Nubian groups utilized in this study, which include many of the samples presented in the literature review of the biological data.

Chapter 4

Materials

The dataset utilized in this dissertation is comprised of data provided by several researchers (Dr. Tsunehiko Hanihara, Dr. Nancy Lovell, and Dr. Eugene Strouhal), in combination with data collected myself. The dataset as a whole represents seven sites and nine time periods in Nubian history (see Fig. 1 for site locations and Table 2 for time periods, site, sample sizes, and researcher). Median dates were calculated for each sample in order to select a date to use for temporal analysis (c.f. Konigsberg 1990). The methodology associated with median dates will be discussed further in the Methods chapter.

This dataset consists of samples that represent most time periods in Nubian history, as well as geographic areas that span from the first through below the third cataracts. The expansive nature of the dataset will allow for a thorough population genetics approach to interpreting Nubian population structure. Also, the samples explored here have not been analyzed together in other projects and will provide a unique insight to Nubian biological evolution. Below, the sites are described from available information. Each of these

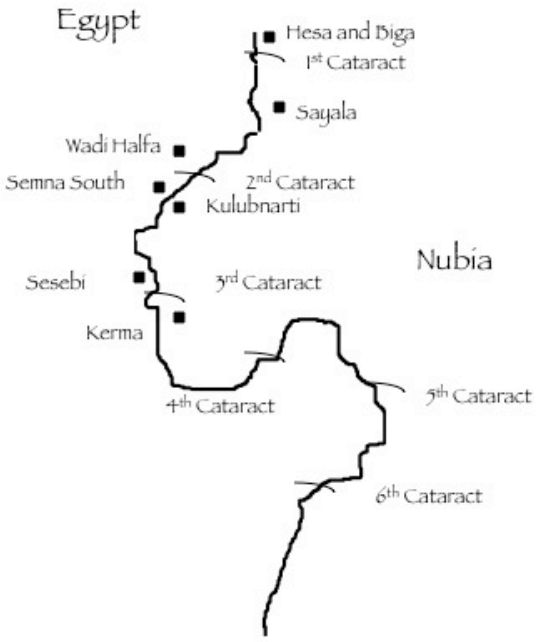

Figure 1. Map of Nubia.

Table 2. Sample information for 13 groups in this dissertation analysis

Time Period	Site	Referred as	Dates	Median Date	Sample size	Researcher	Collection Location
Mesolithic	Wadi Halfa	Mesolithic (MESO)	6050-9050 years B.C.[2]	7550 B.C.	11	Godde	CU
A-Group	South of Wadi Halfa	A-Group (AGRP)	3300-2800 B.C.[3]	3050 B.C	34	Lovell	COP
C-Group	North of Wadi Halfa	C-Group (CGRP)	2300-1800 B.C.[3]	2050 B.C.	41	Lovell	COP
C-Group	Sayala	Sayala C-Group (CGRP)	1786-1550 B.C.	1668 B.C.	20	Strouhal	KHM
Kerma	Kerma	Kerma (KERM)	1800-1200 B.C.[3]	1500 B.C.	224	Hanihara	CAM
Pan-Grave	Sayala	Pan-Grave (PANG)	1786-1550 B.C.	1668 B.C.	9	Strouhal	KHM
Meroitic	Semna South	Meroitic (MERO)	0-350 A.D.	175 A.D.	268	Godde	ASU
X-Group	Semna South	X-Group (XGRP)	350-550 A.D.	450 A.D.	28	Godde	ASU
Christian	Semna South	Semna South Christians (SEMC)	550-1500 A.D.	1025 A.D.	11	Godde	ASU
Christian	Islands of Hesa/Biga	Hesa/Biga (HABA)	543-640 A.D.	592 A.D.	139	Hanihara	CAM
Christian	Kulubnarti (mainland)	Kulubnarti Mainland (KULM)	550-800	675 A.D.	81	Godde	CU
Christian	Kulubnarti (island)	Kulubnarti Island (KULI)	550-800	675 A.D.	42	Godde	CU
Kerma, Meroitic, Christian, and unknown	Sesebi	Sesebi (SESE)	1800 B.C.-1500 A.D.	1150 A.D.	89	Hanihara	NHM
Total:					997		

University of Colorado at Boulder (CU), University of Copenhagen (COP), (KHM) Kunsthistorisches Museum Vienna, Arizona State University (ASU), University of Cambridge (CAM), Natural History Museum, London (NHM)

samples will be utilized in the population genetics analyses detailed in the next chapter.

Hesa and Biga

The Archaeological Survey of Nubia excavated the islands of Hesa and Biga, under Reisner's supervision. Temples were established on Biga during the Ptolemaic-Roman period, while Hesa was used for burials (Elliot Smith and Wood-Jones 1910). Later, a cemetery was established on Biga, as well (Elliot Smith and Wood-Jones 1910). Occupation of this site was continuous from the Ptolemaic-Roman period and on (Elliot Smith and Wood-Jones 1910). Christian burials were found in the same chambers as those from the Ptolemaic-Roman period and were distinctive from the prior burials (Elliot Smith and Wood-Jones 1910).

Kerma

Reisner excavated Kerma during 1913-1916 for Harvard University and the Boston Museum of Fine Arts. The site of Kerma yielded skeletons from the time period of the same name. Kerma was used for trade and had evidence for Egyptian occupation or influence (Collett 1933). There were many rare features of Kerma that are not seen elsewhere in Nubia. For example, Collett (1933) noted the graves of rulers included evidence of sacrificial graves accompanying them (Collett 1933). Moreover, there was also evidence of a mass sacrifice with over 300 people (Collett 1933). From this time period, burials were

found in a large earthen mound, which is also unique in Nubian history (Adams 1984). Collett (1933) conducted a study to determine the affinities of the interred at Kerma. She concluded, based on the coefficient of racial likeness, that the individuals were Egyptian. Later, Adams (1984) pointed out that the individuals at Kerma were really a culturally separate group of C-Group Nubians.

Kulubnarti

Located between the second and third cataracts of the Nile are two cemeteries from the Christian time period at the site of Kulubnarti, in the Batn-el-Hajar ("Belly of Rock"). One sample is comprised of skeletons from mainland inhabitants on the West bank of the Nile, and the other sample consists of individuals from a small island, adjacent to the mainland (Turner et al. 2007). The island was created by the effects of the Aswan High Dam; prior to its construction the island was part of the mainland (Adams et al. 1999; Kilgore et al. 1997). The island cemetery was primarily Christian, although some X-Group and Islamic burials were also detected (Adams et al. 1999). Dating the cemeteries has proven inconclusive due to inconsistencies in artifacts and surrounding structures (Adams et al. 1999), but the current dates that are reported are AD 550-800 for both (Turner et al. 2007). Social stratification has not been deciphered from grave goods, because the artifacts are relatively the same in all burials and are more consistent with Christian beliefs and principles rather than with status (Turner et al. 2007).

Sayala

At Sayala, burials from both C-Group and Pan-Grave cultures were excavated along the eastern bank of the Nile (Strouhal and Jungwirth 1980). Strouhal and Jungwirth (1980) contended the pan graves at Sayala represented the only pure Pan-Grave culture that had been discovered up to that point in time; other pan graves exhibited influences of other cultures, such as the Blemmyes. The Pan-Grave burials were located further inland than the C-Group interments (Bietak and Bauer 1966), implying differences between the C-Group and Pan-Grave groups. Strouhal and Jungwirth (1980) asserted that the Pan-Grave people were nomadic hunter-gatherers whose men may have been involved with the Egyptian army. The data from these samples were extracted from (Strouhal and Jungwirth 1980) with permission from Dr. Strouhal.

Semna South

The Semna South site represents three time periods, Meroitic, X-Group, and Christian. These remains were salvaged from the construction of the High Aswan Dam by the Oriental Institute and the University of Chicago in 1966-8. These cemeteries were located in the Batn El Hajar on the West bank of the Nile (approximately 15 miles from Wadi Halfa) (Zabkar and Zabkar 1982). North of the fort constructed at the site, all three time periods were found in the same cemetery (Zabkar and Zabkar 1982). The graves were distinct in structure, orientation, and grave goods. The Meroitic graves were oriented east-

west, the X-Group north-south, and the Christians east-west (Zabkar and Zabkar 1982). A feature of the Christian burials at Semna South that is not usually cited in the Christian mortuary archaeology literature is that the individuals were placed in an extended position and were supine (Zabkar and Zabkar 1982). The most marked feature of the Christian burials was the shrouding of the interred individuals (Zabkar and Zabkar 1982).

Scandinavian Joint Expedition to Nubia

Dr. Nancy Lovell contributed data from the A- and C-Groups unearthed in the Scandinavian Joint Expedition to Nubia (SJE) in 1963-4. The A-Group remains are from a cemetery south of Wadi Halfa, while the C-Group is from a cemetery north of Wadi Halfa (Prowse and Lovell 1995). Out of the twelve A-Group cemeteries excavated during the SJE, site 277 is the most representative of the whole (Nielsen 1970). Thus, Dr. Lovell collected discrete data on site 277, only (Prowse and Lovell 1995). The C-Group site (179) held the most numerous skeletons (Prowse and Lovell 1995).

Sesebi

The site at Sesebi yielded evidence to suggest that not only did Sethos' I reign dominate the town, but also Akhenaten, among other Egyptian Pharoahs (Blackman 1937; Fairman 1938). The town of Sesebi sat on the west bank of the Nile and was protected by fortress-like walls (Blackman 1937). The cemetery was disturbed prior to excavation and the

graves were looted (Lisowski 1952). Thus, some of the skulls were found on the surface and their original context is unknown (Lisowski 1952). The excavations unearthed remains from the Kerma, Meroitic, and Christian time periods. Unfortunately, crania from all three time periods, in addition to the unknown skulls, were lumped together in the dataset provided by Dr. Hanihara and were not designated as to which group each skull belonged. Thus, this group will be utilized for comparison purposes and will not be input into temporal and geographic analyses.

Wadi Halfa

This dissertation was fortunate enough to include several individuals from the Mesolithic. The sample was found 2.5 km inland from the Nile at Wadi Halfa (Saxe 1971). Saxe (1971) hypothesized from their burial practices that this hunter-gatherer society had some sort of social stratification. The burials were highly variable; the graves sometimes held one or two individuals, positions differed, and direction of the head was not consistent. This cemetery was permanent, which led Saxe (1971) to infer that this group of Mesolithic Nubians was sedentary and not nomadic.

The next chapter covers some initial data quality/selection procedures preparatory to the analyses focused on the seven questions and their corollaries regarding Nubian population structure. Each bias will be addressed and tested for, if applicable, and the statistical methodology will also be detailed. Finally, the methods for temporal and spatial analyses will be outlined.

Chapter 5

Methods

In this chapter, the methodology is presented which details how I will attempt to estimate population structure in Nubians, utilizing nonmetric traits. Even though there has been a push for results that support in situ evolution in Nubians, the studies that have been conducted use select subpopulations that do not represent the total Nubian temporal and spatial distribution and don't test the *in situ* hypothesis across the entire population (e.g. Greene 1982). Incorporating as many subgroups as possible, as in this dissertation, will strengthen the study because the potential variability found in the entire population can be explored. Furthermore, these samples can be combined and split to test specific hypotheses about Nubian history (see Chapter 1). This strategy will help depict Nubian biological evolution as accurately as possible. By conducting this type of analysis, the level of homogeneity present in the Nubian population can be estimated and interpreted in relation to the *in situ* hypothesis. Moreover, this study aims to move towards a more model-bound approach in discrete trait analysis.

Table 3. Traits observed, definitions, and reported narrow heritabilities of discrete traits

Discrete Traits	Original definitions of traits	Carson (2006)	Sjφvold (1984)
Accessory infraorbital foramen (AIOF)	Berry and Berry 1967; Hanihara and Ishida 2001e	0.478 ±0.251	0.062 ± 0.188
Accessory mental foramen (AMF)	De Villiers 1968; Gershenson et al. 1986; Hanihara and Ishida 2001e; Murphy 1957	-	-
Asterionic bone (ASB)	Ossenberg 1969, 1970; Hanihara and Ishida 2001b	0.196 ± 0.228	0.555 ± 0.196
Biasterionic suture (BAS)	Dodo 1974; Ossenberg 1969; Hanihara and Ishida 2001a; Hanihara and Ishida 2001c	-	-
Condylar canal patent (CCP)	Dodo 1974; Hauser and De Stefano 1989; Hanihara and Ishida 2001e	0.350 ± 0.267	0.096 ± 0.188
Condylus tertius (CT)	Dodo 1974; Hanihara and Ishida 2001d	-	-
Hypoglossal canal bridging (HGCB)	Dodo 1974; Hanihara and Ishida 2001d	undefined	0.140 ± 0.168
Jugular foramen bridging (JFB)	Dodo 1986a, b; Hanihara and Ishida 2001d	-	-
Medial palatine canal (MPC)	Dodo 1974; Hauser and De Stefano 1989; Hanihara and Ishida 2001d	-	-
Metopism (MET)	Hauser and De Stefano 1989; Hanihara and Ishida 2001c	undefined	0.344 ±0.376
Mylohyoid bridging (MHB)	Dodo 1974; Jidoi et al. 2000; Hanihara and Ishida 2001d	-	-
Occipitomastoid bone (OMB)	Dodo 1974; Ossenberg 1970; Hanihara and Ishida 2001b	undefined	-
Ossicle at lambda (OL)	Dodo 1974; Hanihara and Ishida 2001b	0.410 ± 0.245	0.238 ± 0.242
Ovale-spinosum confluence (OSC)	Dodo 1974; Hanihara and Ishida 2001c	-	-
Parietal notch bone (PNB)	Dodo 1974; Hanihara and Ishida 2001b	0.077 ± 0.176	0.152 ± 0.222
Precondylar tubercle (PCT)	Hanihara and Ishida 2001d	-	-
Supraorbital foramen (SOF)	Dodo 1974, 1987; Hanihara and Ishida 2001e	undefined	0.378 ± 0.183
Transverse zygomatic suture (TZS)*	Dodo 1974; Hanihara et al. 1998b; Hanihara and Ishida 2001c	undefined	-
Tympanic dehiscence (TD)*	Dodo 1974; Hanihara and Ishida 2001c	undefined	-

*Frequency of this trait = 0 in Carson (2006)

- Indicates Carson and/or Sjφvold did not examine heritabilities for this trait

Undefined corresponds to a zero heritability

The original set of 20 nonmetric traits (based on Hanihara et al.'s (2003) collection of traits) is listed in Table 3, with the associated sources where the traits are defined (both originally and in the Hanihara articles). Hanihara and Ishida (2001 a, b, c, d) identified four groupings of nonmetric traits, based on their developmental characteristics: 1. supernumerary ossicle varaiations, 2. hypostatic variations, 3. hyperstotic variations, and 4. vessel and nerve related variations. Supernumerary ossicles are comprised of ossicle at lambda, parietal notch bone, asterionic bone, and occipitomastoid bone. Hypostotic variations, based on Ossenberg's (1970) categorization of nonmetric traits, include tympanic dehiscence, ovale-spinosum confluence, metopism, transverse zygomatic suture vestige, and biasterionic suture. Hyperstotic traits, again based on Ossenberg (1970), were listed as medial palatine canal, hypoglossal canal bridging, precondylar tubercle, condylus tertius, jugular foramen bridging, auditory exostosis, and mylohyoid bridging. Finally, patent condylar canal, supraorbital foramen, accessory infraorbital foramen, and accessory mental foramen were categorized as vessel and nerve related variants. Auditory exostosis was removed from analysis prior to data collection as its etiology may be, in part, environmentally induced (refer to Chapter 2).

Several influences were identified in the literature review of Chapter 2 as affecting the development of nonmetric traits, namely, sex, age, and intertrait correlations. Some traits were identified as sex dependant by particular researchers in the review of trait biases. However, the suite of traits selected by Hanihara et al. (2003) were tested and determined to be only minimally affected by sex. Thus, their inclusion in this study is justified. Researchers often still test for differences between sexes when calculating biodistance, in order to verify the sexes are similar enough to be pooled for analysis. A chi-square test

(conducted in NCSS (Hintze 2006)) will be utilized to test for differences between sexes to verify they are not significantly different and do not need to be separately analyzed.

As discussed in Chapter 2, inclusion of juveniles into nonmetric samples can bias the results, as nonmetric trait development may not be complete. Thus, as Saunders (1989) suggested, only adult individuals were observed in the data collection for this dissertation. Furthermore, Hanihara et al.'s (2003) assertions that age during adulthood does not significantly affect nonmetric traits' appearance are accepted. In order to identify adults, two aging methods will be employed. Hanihara et al. (2003) utilized eruption of the third molar and fusion of the sphenooccipital synchondrosis as an adult aging technique. The current study will perform these same aging methods. Finally, the low intertrait correlations Hanihara et al. (2003) detected in their 20 nonmetric trait sample also supports the selection from these traits. Thus, the current study employs the Hanihara nonmetrics as the original group of traits from which the final set will be selected.

Interobserver error is a factor that must be addressed in any type of nonmetric study that incorporates data from multiple observers, as in the current study. None of the samples included in this dissertation were observed by more than one researcher and this research design must be addressed. There is no way to test for interobserver error when none of the skulls were examined in common among the researchers. Because all of the samples are from the same population, it may be feasible to assume the samples should have similar trait frequencies. Although there are major issues with this assumption as I am testing for intersample variation, it is probably the best way and only way to deal with this particular dataset. Thus, interobserver error was tested for across the samples, even though no samples were observed by more than one observer.

Ishida and Dodo (1990) tested interobserver differences in discrete traits and found the differences to be profound in eleven characteristics. Nine of the traits that demonstrated high interobserver error are included in the 20 nonmetric trait set from Hanihara et al. (2003): biasterionic suture, asterionic bone, occipitomastoid bone, third occipital condyle, foramen of Huschke, transverse zygomatic suture, accessory mental foramen, mandibular torus, and jugular foramen bridging. Later, Gualdi-Russo et al. (1999) examined interobserver error in asterionic bone, among others, and concluded it was not subject to high interobserver error. Instead, as Gualdi-Russo et al. (1999) demonstrated, interobserver error is not a problem if definitions for traits are clear and strictly followed, and if experienced observers are conducting the study. Finnegan and Rubison (1980) also subscribed to a similar notion; they believed that experience is important, as well. However, they still noted differences among observers (Finnegan and Rubison 1980), and thus these differences need to be tested for.

Although Ishida and Dodo (1990) asserted not combining multiple authors' data into one study, and only including traits with low interobserver error, Ishida dealt with interobserver error in a different manner in a later paper (Fukumine et al. 2004). In that article, six of the eleven traits with high interobserver error were utilized in calculations of biological distance. The justification for including these traits revolved around reducing interobserver error by employing 16 total traits. Conversely, other studies including the same author tested for interobserver error using Fisher's exact probability test (Haneji et al. 2007) to test for differences among datasets. Moreover, Komesu et al. (2008) (which includes both Ishida and Dodo) dropped three traits with high interobserver errors from subsequent analyses due to the work of Ishida and Dodo (1990), but retained other traits identified above as having high interobserver error. Due to the multitude of ways interobserver error is dealt

with, this study conducted a combination of these methods. In order to contend with interobserver error, the figures, definitions, and scoring in Hanihara and Ishida 2001 (a, b, c, d) were studied and followed as closely, as possible. Additionally, interobserver differences were tested for with a Fisher's exact test on each trait to identify potential interobserver errors for 2x2 tables (two observers) and with the adaptation to Fisher's exact test by Freeman and Halton (1951) for RxC tables (four observers), using SAS 9.1.2. Sample size was controlled for by testing the average frequencies per observer.

Intraobserver error can also affect discontinuous datasets. Molto (1979) explored intraobserver error and found it to be high in 8 of the 39 traits he tested. In this dissertation, only one of those traits is included, accessory infraorbital foramen. I argue here that accessory infraorbital foramina are not difficult to recognize and score if strict adherence to the definition is followed (similar to the argument in Gualdi-Russo et al. (1999)). Despite the initial collection of data from accessory infraorbital foramen, this trait was not used in calculations of biological distances in any of the results chapters (7-13).

Heritabilities were also a factor in trait selection. Chapter 2 presented the literature on heritability information for nonmetric traits in humans, non-human primates, and mice. Table 3 displays the heritability estimates from Carson (2006) for the original set of 20 nonmetric traits, as well as those from Sjϕvold (1984). Carson (2006) argued that selection of traits must include an assessment of heritabilites and trait selection should select those with high heritabilities. However, as was presented in Chapter 2, heritability estimates differ from population to population and from environment to environment. Thus, narrow heritabilities in one population in one place are not indicative of all populations and all places. In order to demonstrate this, the present study will select data from two sources:

nonmetric variables with high heritabilities and a mixture of nonmetric variables with low or unknown heritabilities. The selection of two types of discrete data will allow for conclusions regarding the utility of nonmetric traits with low heritability values from calculations on one population.

Dichotomy/Polychotomy

Sjϕvold (1977) suggested dichotomization of multiple categorically scored traits in order for the data to be quantified properly through statistics. Currently, most discrete traits are recorded on a present/absent scale. Hauser and De Stefano (1989) modified some traits that had been scored as binary to include multiple categories of expression. This revision to the data collection was designed to allow researchers to estimate biological information deduced from a trait distribution that is ordinal and would more closely mirror the underlying continuous nature of the data. Later, Buikstra and Ubelaker (1994) also presented a polychotomous scale of nonmetric scoring. Despite these changes, traits that are scored as polychotomous are converted to a dichotomous scale during statistical analysis, following Sjϕvold's (1977) suggestion. Recently, Carson (2006) argued that ignoring the multilevel component to nonmetric traits causes inaccurate estimates of heritabilities, and thus leads to inaccurate statistical estimates from dichotomization. Carson's (2006) conclusions were based on the properties of the multifactorial/threshold model. Wright (1934) originally suggested the threshold model for discontinuous traits. Fraser (1998) holds that the model, "postulates a continuous distribution of 'liability' to a particular defect and a threshold

separating the continuous distribution into discontinuous parts, with only those individuals falling beyond the threshold having the defect" (1263).

Carson (2006) attempted to model the underlying continuous distribution of nonmetric traits by using statistics on multi-level categorical data that were designed for continuous data. Carson (2006) recognized that her statistic choice was difficult to defend for analyzing categorical data. Categorical data estimated with continuous statistics will, in fact, yield erroneous estimates of the multiple category traits and her conclusions about the differences between dichotomous and polychotomous traits based on the statistical analysis are tentative, at best. However, her conclusion does make sense in light of categorical data analysis in general, and other authors have called for the collection of multiple categories of expression in nonmetrics for this reason (e.g. Hauser and De Stefano 1989; Buikstra and Ubelaker 1994; Hanihara and Ishida 2001 a, b, c, d).

Not many other studies have addressed statistical calculation of multiple level traits, except for Irish and Konigsberg (2007). In their study, Irish and Konigsberg (2007) investigated 19 African samples. Here, the authors assessed polychotomous traits with maximum likelihood to rank the category of association for traits within each sample and their standard deviation. Although this investigation did not calculate biological distance using a polychotomous categorical data structure, Irish and Konigsberg demonstrated that polychotomous scoring conveys meaningful biological and genetic information that differs across populations. Three of the variables in the data in this dissertation were collected with multiple categories of expression: biasterionic suture vestige, supraorbital foramen, and transverse zygomatic suture vestige. Categorical statistics designed to deal with polychotomous variables in Mahalanobis distances have not been developed yet to properly

analyze these character states. Thus, these data will be converted to binary states (present/absent) until a suitable polychotomous distance statistic is developed.

Counting Traits

Counting traits is important for statistical analysis because traits that can appear bilaterally (on bones that occur twice in the human skeleton through having both a left and a right side) need to be calculated differently than midline traits (traits that appear on bones that occur once in the human skeleton). In rare traits, there is a propensity for unilateral expression over bilateral expression (HallgrÌmsson et al. 2005). In order to account for this underlying genetic influence, specific counting methods have been put forth and tested to address the counting methodological problem, e.g. (Green et al. 1979; Korey 1980; McGrath et al. 1984; Mouri 1976; Ossenberg 1981).

Green et al. (1979) proposed a method where the observer scores the sides available (one or both) and then divides the total number by 2. Conversely, Korey (1980) asserted that asymmetry is not genetically correlated with bilateral traits. He proposed excluding unpaired sides from statistical analyses and to count traits by individual. The individual method entails calculating the number of individuals with a bilateral trait on either or both sides and dividing this total number by the number of individuals. Ossenberg (1981) put forth the side method for counting traits, where the number of left and right sides with present traits are added together and then divided by the total number of left and right sides. Her work was similar to the method suggested by Berry and Berry (1967) Moreover, Ossenberg (1981) suggested adding a correction of n/2 in the biological distance statistic. Her conclusions

were based on her assertion that bilateral traits have greater genetic influence because they are more pronounced.

McGrath et al. (1984) supported Korey's (1980) method, because they found a significant genetic correlation between side expression. It is hard to achieve a good balance when dealing with asymmetric sides. Due to his combination of archaeological techniques (random sampling) with a biological foundation, the current study will use the method identified in Konigsberg (1987; 1990), where both sides are scored for bilateral traits. If both sides are observable, random sides are selected per crania (when the trait expression is different for both sides) for statistical analysis.

Statistical Analyses

Mahalanobis D^2 with a tetrachoric matrix will be employed to estimate biological distance among the Nubians samples. It is designed for calculating biodistance from polygenic threshold traits. As discussed in Chapter 2, nonmetric traits are threshold traits and Cheverud and Buikstra (1981a), among others, have identified cranial nonmetrics as polygenic. Chapter 2 also highlighted the fact that intertrait correlations do not need to be tested for with chi-square analyses, as Mahalanobis distances account for phenotypic correlations between traits. Mahalanobis distance is sensitive to missing data in that the tetrachoric correlations are computed from observations classified as 0 or 1. Thus, scores of 9, or unobservable, cannot be properly processed. In order to account for missing values, variables with excessive amounts of missing data will be deleted. Further, individual cases that exhibit missing data will also be deleted. This may skew the results, as the sample size

is being reduced and the sample distribution artificially altered. However, if done correctly, elimination of variables will reduce the number of cases necessary to delete and the results will be negligibly skewed.

The statistic for Mahalanobis D^2 with a tetrachoric matrix (Blangero and Williams-Blangero 1991) is found in Konigsberg (1990) as follows:

$$d^2_{ij}=(z_{ik} - z_{jk})'T^{-1}(z_{ik} - z_{jk})$$

where z_{ik} is the threshold value for a particular trait frequency *k* in group *i,* and z_{jk}, is the threshold value for a particular trait frequency *k* in site *j,* and T is the tetrachoric matrix. Probit analyses generate the thresholds. Tetrachoric correlations are calculated between each set of traits and are then pooled and weighted by sample size. Thus, sample size is not an issue. The distance matrix was produced using programming provided by Dr. Konigsberg (personal communication) for Fortran 95.

After the biological distance matrix was obtained, an R matrix was computed. The R matrix is a "standardized variance co-variance matrix of the data" and can be calculated from the D^2 matrix (Konigsberg 2006: 213), utilizing several equations. First, a codivergence matrix must be estimated from the distance matrix and the data. The codivergence matrix is an estimation of the variance around the centroid and can be written as (Konigsberg 2006):

$$C=-0.5(I-1w')\ D^2\ (I-1w')'$$

where I is an identity matrix with the dimensions gxg (g is number of groups), w is a gx1 column of the relative weights of the populations, and D^2 is the distance matrix from above. Relative weights can be calculated from known census information (Relethford and Harpending 1994), but as is often the case in archaeological populations, census information is not available. Thus, the groups can be equally weighted (Relethford and Harpending 1994) where the w matrix above includes an equal proportion for each group that together will sum to one.

The codivergence matrix was next used to calculate minimum F_{st}. This F_{st} equation is (Konigsberg 2006):

$$\text{minimum } F_{st} = \frac{w' \text{diag}(C)}{2t + w' \text{diag}(C)}$$

diag (C) is the diagonal of the C matrix converted into a column vector and t is the number of traits. Minimum F_{st} reflects heritability of estimates of 1, indicating a pure genetic inheritance with no environmental influence (Relethford 1994; Relethford and Blangero 1990: 19). The F_{st} was input into calculations of the R matrix, as follows (Konigsberg 2006):

$$R = C(1-\text{minimum } F_{st})/2t$$

Heritabilties have not been totally resolved in nonmetrics (see Chapter 2), and thus a good heritability estimate for nonmetric traits has not been proposed. As a result, this study will

take the conservative approach and assume a narrow heritability estimate of 1 (Relethford 1994; Relethford and Blangero 1990: 19).

Next, this study included a modified Relethford-Blangero analysis (modified RB analysis). The Relethford-Blangero analysis calculates a multivariate extension of the Harpending and Ward (1982) model that "compares average within-group variation with that expected based on the distance of each population to the centroid" (Relethford and Blangero 2005). The Relethford-Blangero analysis estimates the amount of gene flow in the groups studied. Relethford and Harpending (1994) cite the Relethford-Blangero model for the expected average phenotypic variation of a population, as follows:

$$E(\overline{V}_{Gi}) = \overline{V}_{Gw}(1 - r_{ii})/(1 - r_0)$$

where $\overline{V}_{Gw}$ is the pooled average within-group phenotypic variation among populations, r_{ii} is the distance of population *i* to the centroid, and r_0 is F_{st} (the sum of the diagonal of the R matrix). If the expected average phenotypic variation of a population is subtracted from the observed average phenotypic variation of the same population ($\overline{V}_{Gw} - E(\overline{V}_{Gi})$), the residual is found (Relethford and Blangero 1990). The value of the residual indicates the amount of gene flow (Relethford and Blangero 1990). A value greater than the average residual can indicate a higher rate of gene flow from external populations into the population under study (Relethford and Blangero 1990). Conversely, a lower than average value can point to lesser rates of gene flow from external populations (Relethford and Blangero 1990).

The Relethford-Blangero analysis is designed for estimation from continuous data and substitution of r_{ii} and r_0 derived from categorical data will assist in categorization of the equation. Nonmetric data is discontinuous, and thus estimation of $\overline{V}_{Gw}$ must be done in a manner consistent with categorical data. The term $\overline{V}_{Gw}$ is calculated as the trace of the of the additive genetic covariance matrix (derived from the phenotypic covariance) divided by the number of traits (Relethford and Blangero 1990). A covariance matrix derived from a nonmetric dataset will still reflect a trace that measures the variance of the sample. Thus, the trace can be extracted from discontinuous variables and be processed as a measure of the variance. Harpending and Ward (1982) regression plots were created (in NCSS Hintze 2006) that fit a regression line to the plotted r_{ii} and $\overline{V}_{Gw}$ values. Except for the regression plots, the remaining statistical procedures outlined above were conducted in Cran-R (R Development Core Team 2005).

Principle coordinates analysis (PCO) was computed on the distance matrix (Gower 1966). PCO finds coordinates for the associations in the distance matrix and arranges them according to the similarity of the points. These coordinates can be plotted to depict population relationships and clustering. The eigenvectors were divided by the square root of their eigenvalue to eliminate standardization of the algorithm (Harpending and Jenkins 1973). PCO was conducted in NTSYS 2.1 by double-centering the matrix and then extracting the eigenvalues and eigenvectors. The PCO scatterplots were produced from NCSS (Hintze 2006).

Temporal and Spatial Analyses

In addition to population genetics interpretations of the data, temporal and spatial influences will also be explored. Temporal distances were generated by calculating the median date (Table 2) from the range of dates associated with the sites. The absolute value of the median dates was subtracted from one another to determine the time separating the sites. This procedure is based on Konigsberg (1990) who used median radiocarbon dates for calculation.

The groups used in this study will overlap either geographically or temporally. These overlaps create controls in the data, where individual variables become isolated. For example, if two sites are from the same time period, the possible influence time exerts onto biological distance is radically reduced because these groups existed at relatively the same times. Because time is no longer distinct between the two groups and spatial distance is still present between the sites, temporal influence is negligible and spatial influences may still be exerting strong effects on the results.

Buikstra (1977) demonstrated that there were autocorrelations along rivers where groups closer together along a river were similar, while groups further apart along the river were less similar. This is important when calculating spatial distances between sites. If two sites are on a river, measuring the distance between the two points by calculating the distance along the river will be more accurate than calculating the distances as a straight line drawn between two points. However, Konigsberg (1990) demonstrated that linear distances (straight line approach) were correlated similarly with river distances. In the current study, spatial distances will be calculated using river distances as the sites were all located along the

River Nile and travel is documented to have occurred along this waterway (Adams 1977). The River Nile is relatively straight for much of the area above the second cataract. However, the river makes a 90º turn between the second and third cataracts. Although some of the calculated river distances between sites will be relatively similar to straight-line distances, others will deviate from a straight line. In light of this, river distances are still the most appropriate manner to estimate spatial distance, but it must be recognized that some river distance approximations will be relatively analogous to straight-line distances. Each site will be located and pinpointed on a map drawn to scale. ImageJ (Abramoff et al. 2004) will be used to calculate pixel distances between the sites, along the Nile.

Temporal and spatial influences involve calculations with three-way Mantel tests (Smouse et al. 1986). A Mantel test is a statistic that tests for associations between matrices. In this study, Mantel tests will assess whether there are significant associations between spatial and biological matrices, while controlling for time. Additionally, while controlling for space, significant associations between temporal and biological matrices will also be tested. These analyses will statistically test whether biological distances increase or decrease with space and/or time, which will allow for interpretations of spatial and temporal variables on biological distances. The Mantel results can be interpreted in relation to Konigsberg's (1990) model.

The results from the application of the methodology are presented in the next eight chapters (6-13). Chapter 6 presents the trait frequencies, interobserver error, chi-square tests for the sexes, and mapping information. The succeeding chapters delve into each of the seven questions of Nubian population structure, as outlined in Chapter 1.

Chapter 6

General Results

The frequency of each of the 19 discrete traits (number of times present divided by total number of individuals on whom the trait could be scored), per sample, is listed in Table 4. It is important to mention here that unobservable scores in these samples do not just refer to fragmentation; rather, unobservable may also describe bones with excessive mummified tissue that obscure the trait under focus. Due to the excellent preservation of the remains, bone and soft tissue, most of the unobservable scores were a result of tissue covering the trait in the samples I scored. Thus, the trait frequencies reflect this scoring procedure.

The discrete traits in this dissertation were scored following the definitions presented by Hanihara et al. (2003). Therefore, the datasets scored by Dr. Hanihara and myself were consistent with present/absent and multiple category scoring. However, the data provided by Dr. Lovell and Dr. Strouhal did not reflect the same polychotomous scoring. In order to contend with this issue, the methodology that both observers utilized was reviewed in order to standardize all four datasets. Dr. Lovell's scoring for tympanic dehiscence

Table 4. Frequencies of nonmetric traits

	Mesolithic		
	K	**N**	**Frequency**
Accessory infraorbital foramen (AIOF)	0	4	0%
Accessory mental foramen (AMF)	0	7	0%
Asterionic bone (ASB)	2	11	18%
Biasterionic suture (BAS)	0	8	0%
Condylar canal patent (CCP)	0	1	0%
Condylus tertius (CT)	0	6	0%
Hypoglossal canal bridging (HGCB)	0	7	0%
Jugular foramen bridging (JFB)	0	3	0%
Medial palatine canal (MPC)	0	6	0%
Metopism (MET)	0	11	0%
Mylohyoid bridging (MHB)	1	8	13%
Occipitomastoid bone (OMB)	1	10	10%
Ossicle at lambda (OL)	0	10	0%
Ovale-spinosum confluence (OSC)	1	10	10%
Parietal notch bone (PNB)	0	11	0%
Precondylar tubercle (PCT)	1	6	17%
Supraorbital foramen (SOF)	5	11	45%
Transverse zygomatic suture (TZS)	4	11	36%
Tympanic dehiscence (TD)	1	6	17%

Table 4 continued. Frequencies of nonmetric traits

	A-Group			C-Group		
	K	**N**	**Frequency**	**K**	**N**	**Frequency**
Accessory infraorbital foramen (AIOF)	2	9	22%	9	29	31%
Accessory mental foramen (AMF)	5	31	16%	2	37	5%
sterionic bone (ASB)	2	5	40%	3	21	14%
Biasterionic suture (BAS)	0	6	0%	1	29	3%
Condylar canal patent (CCP)	2	5	40%	6	20	30%
Condylus tertius (CT)	-	-	-	-	-	-
Hypoglossal canal bridging (HGCB)	-	-	-	-	-	-
Jugular foramen bridging (JFB)	-	-	-	-	-	-
Medial palatine canal (MPC)	-	-	-	-	-	-
Metopism (MET)	0	11	0%	1	35	3%
Mylohyoid bridging (MHB)	9	30	30%	5	35	14%
Occipitomastoid bone (OMB)	-	-	-	-	-	-
Ossicle at lambda (OL)	1	11	9%	1	32	3%
Ovale-spinosum confluence (OSC)	-	-	-	-	-	-
Parietal notch bone (PNB)	0	3	0%	2	20	10%
Precondylar tubercle (PCT)	0	10	0%	3	25	12%
Supraorbital foramen (SOF)	13	31	42%	11	35	31%
Transverse zygomatic suture (TZS)	0	20	0%	0	34	0%
Tympanic dehiscence (TD)	4	22	18%	7	33	21%

Table 4 continued. Frequencies of nonmetric traits

	Sayala C-Group			Pan-Grave		
	K	**N**	**Frequency**	**K**	**N**	**Frequency**
Accessory infraorbital foramen (AIOF)	1	11	9%	0	7	0%
Accessory mental foramen (AMF)	1	17	6%	0	8	0%
Asterionic bone (ASB)	6	15	40%	2	9	22%
Biasterionic suture (BAS)	-	-	-	-	-	-
Condylar canal patent (CCP)	-	-	-	-	-	-
Condylus tertius (CT)	-	-	-	-	-	-
Hypoglossal canal bridging (HGCB)	-	-	-	-	-	-
Jugular foramen bridging (JFB)	-	-	-	-	-	-
Medial palatine canal (MPC)	-	-	-	-	-	-
Metopism (MET)	2	16	13%	0	8	0%
Mylohyoid bridging (MHB)	-	-	-	-	-	-
Occipitomastoid bone (OMB)	-	-	-	-	-	-
Ossicle at lambda (OL)	1	15	7%	1	8	13%
Ovale-spinosum confluence (OSC)	-	-	-	-	-	-
Parietal notch bone (PNB)	1	15	7%	0	8	0%
Precondylar tubercle (PCT)	0	12	0%	1	9	11%
Supraorbital foramen (SOF)	2	15	13%	1	8	13%
Transverse zygomatic suture (TZS)	-	-	-	-	-	-
Tympanic dehiscence (TD)	1	15	7%	4	8	50%

Table 4 continued. Frequencies of nonmetric traits

	Kerma			Hesa/Biga		
	K	**N**	**Frequency**	**K**	**N**	**Frequency**
Accessory infraorbital foramen (AIOF)	18	205	9%	18	129	14%
Accessory mental foramen (AMF)	10	108	9%	6	47	13%
Asterionic bone (ASB)	47	222	21%	33	133	25%
Biasterionic suture (BAS)	38	222	17%	22	132	17%
Condylar canal patent (CCP)	101	202	50%	53	134	40%
Condylus tertius (CT)	2	196	1%	2	133	2%
Hypoglossal canal bridging (HGCB)	48	206	23%	41	134	31%
Jugular foramen bridging (JFB)	59	195	30%	23	131	18%
Medial palatine canal (MPC)	30	204	15%	17	128	13%
Metopism (MET)	9	224	4%	7	138	5%
Mylohyoid bridging (MHB)	16	109	15%	8	47	17%
Occipitomastoid bone (OMB)	17	221	8%	15	133	11%
Ossicle at lambda (OL)	27	223	12%	18	134	13%
Ovale-spinosum confluence (OSC)	7	216	3%	1	137	1%
Parietal notch bone (PNB)	40	220	18%	15	135	11%
Precondylar tubercle (PCT)	17	196	9%	14	133	11%
Supraorbital foramen (SOF)	87	223	39%	61	138	44%
Transverse zygomatic suture (TZS)	17	214	8%	21	129	16%
Tympanic dehiscence (TD)	58	224	26%	14	138	10%

Table 4 continued. Frequencies of nonmetric traits

	Sesebi			Meroitic		
	K	**N**	**Frequency**	**K**	**N**	**Frequency**
Accessory infraorbital foramen (AIOF)	5	84	6%	19	256	7%
Accessory mental foramen (AMF)	1	8	13%	5	234	2%
Asterionic bone (ASB)	17	86	20%	23	262	9%
Biasterionic suture (BAS)	19	87	22%	27	265	10%
Condylar canal patent (CCP)	36	79	46%	107	238	45%
Condylus tertius (CT)	0	81	0%	1	242	0%
Hypoglossal canal bridging (HGCB)	20	81	25%	59	253	23%
Jugular foramen bridging (JFB)	22	80	28%	36	242	15%
Medial palatine canal (MPC)	8	85	9%	0	237	0%
Metopism (MET)	1	87	1%	3	265	1%
Mylohyoid bridging (MHB)	0	8	0%	2	238	1%
Occipitomastoid bone (OMB)	13	85	15%	21	263	8%
Ossicle at lambda (OL)	10	87	11%	15	254	6%
Ovale-spinosum confluence (OSC)	3	87	3%	8	262	3%
Parietal notch bone (PNB)	12	86	14%	25	265	9%
Precondylar tubercle (PCT)	8	81	10%	40	241	17%
Supraorbital foramen (SOF)	40	88	45%	78	266	29%
Transverse zygomatic suture (TZS)	11	75	15%	14	236	6%
Tympanic dehiscence (TD)	14	87	16%	33	264	13%

Table 4 continued. Frequencies of nonmetric traits

	X-Group			Christian		
	K	**N**	**Frequency**	**K**	**N**	**Frequency**
Accessory infraorbital foramen (AIOF)	1	25	4%	1	10	10%
Accessory mental foramen (AMF)	1	25	4%	0	10	0%
Asterionic bone (ASB)	4	26	15%	1	11	9%
Biasterionic suture (BAS)	1	26	4%	0	11	0%
Condylar canal patent (CCP)	11	27	41%	3	11	27%
Condylus tertius (CT)	0	26	0%	0	11	0%
Hypoglossal canal bridging (HGCB)	5	25	20%	2	11	18%
Jugular foramen bridging (JFB)	3	25	12%	2	11	18%
Medial palatine canal (MPC)	0	22	0%	0	10	0%
Metopism (MET)	0	24	0%	0	11	0%
Mylohyoid bridging (MHB)	0	25	0%	0	10	0%
Occipitomastoid bone (OMB)	2	26	8%	0	11	0%
Ossicle at lambda (OL)	1	25	4%	1	11	9%
Ovale-spinosum confluence (OSC)	1	26	4%	1	11	9%
Parietal notch bone (PNB)	2	26	8%	1	11	9%
Precondylar tubercle (PCT)	7	26	27%	1	11	9%
Supraorbital foramen (SOF)	4	25	16%	1	11	9%
Transverse zygomatic suture (TZS)	3	26	12%	1	10	10%
Tympanic dehiscence (TD)	4	26	15%	3	11	27%

Table 4 continued. Frequencies of nonmetric traits

	Kulubnarti (mainland)			Kulubnarti (island)		
	K	**N**	**Frequency**	**K**	**N**	**Frequency**
Accessory infraorbital foramen (AIOF)	4	79	5%	0	41	0%
Accessory mental foramen (AMF)	0	74	0%	2	38	5%
Asterionic bone (ASB)	9	81	11%	4	42	10%
Biasterionic suture (BAS)	1	78	1%	1	38	3%
Condylar canal patent (CCP)	51	77	66%	22	39	56%
Condylus tertius (CT)	0	79	0%	0	38	0%
Hypoglossal canal bridging (HGCB)	9	77	12%	8	35	23%
Jugular foramen bridging (JFB)	13	74	18%	2	37	5%
Medial palatine canal (MPC)	2	78	3%	4	32	13%
Metopism (MET)	1	81	1%	1	42	2%
Mylohyoid bridging (MHB)	4	73	5%	0	38	0%
Occipitomastoid bone (OMB)	4	80	5%	3	42	7%
Ossicle at lambda (OL)	8	81	10%	1	42	2%
Ovale-spinosum confluence (OSC)	3	80	4%	1	41	2%
Parietal notch bone (PNB)	3	81	4%	5	42	12%
Precondylar tubercle (PCT)	28	78	36%	8	38	21%
Supraorbital foramen (SOF)	29	81	36%	14	41	34%
Transverse zygomatic suture (TZS)	9	77	12%	4	40	10%
Tympanic dehiscence (TD)	20	72	28%	15	40	38%

and supraorbital foramen were both converted solely to a present/absent scale; this modification eliminated the degree of expression of the foramina, and instead, measured only the complete manifestation of the trait. Hauser and DeStefano (1989) recommend this change because they claim that complete expression of the foramina properly reflects the underlying genetic components.

The trait frequencies were examined across samples to determine which traits had low frequencies among the samples (<10% as in Jantz (1970)) and should be removed from further analysis. Jantz (1970) retained traits with low frequencies that appeared to have the power to discriminate between samples. His procedure was also followed in this dissertation and the traits that were retained for analysis will be mentioned in each of the remaining chapters, below. Condylus tertius, metopism, and mylohyoid bridging were removed from the analysis completely due to their low frequencies across samples (Table 4).

Medial palatine canal was dropped from analysis due to discrepancies in recording between Dr. Hanihara and myself. Interobserver error among the remaining 15 traits was tested for with Fisher's exact tests and the results are presented in Tables 5 and 6. Three discrete traits had significant interobserver error at the .05 level: accessory mental foramen, biasterionic suture, and supraorbital foramen. Both accessory mental foramen and biasterionic suture were eliminated from subsequent analyses. However, upon closer examination across the samples, sample size appeared to have played a role in the supraorbital foramen results. I recalculated the Fisher's exact tests across the observers,

Table 5. Fisher's exact test for interobserver error across all observers

Trait	p-value
SOF	<.0001 *
TD	0.2208

* significant at the .05 level

Table 6. Fisher's exact test for interobserver error between Hanihara and Godde

Trait	p-value
AIOF	0.2828
AMF	0.0287 *
ASB	0.7264
BAS	0.0001*
CCP	0.5673
HGCB	0.401
JFB	0.0734
OL	0.1262
OMB	0.3106
OSC	0.4448
PCT	0.2278
PNB	0.1123
TZS	1

* significant at the .05 level

separating by sample and sample size. The samples with sizes <30 were tested separately from the samples with sizes >30, with only one exception. The Mesolithic sample's frequencies were more inline with the large sample sizes, and thus I lumped the Mesolithic sample into the large sample size cohort. To examine the effects of the Mesolithic sample, I removed it completely from Fisher's exact tests. When the Fisher's exact tests were recomputed, the trait was no longer significant (Table 7). Although the tests split along sample size did not test among all observers per sample size, there was overlap among the observers, indicating that interobserver error was most likely low among all observers.

In some cases, the number of traits available after trait selection procedures were low (<4). It is general practice in biodistance studies (both metric and nonmetric) to select models with the most variables so that a large of amount of variation will be represented by the results. The nature of some of the samples in this study (highly fragmentary) prevented the assessment of biological distance on more than two variables. In estimates of phenotypic distance, more variables are more representative of the actual variation. However, restriction as a result of fragmentation limited the number of variables that could be utilized in this dissertation.

Sex differences were tested within each sample, except for Sesebi, to ensure pooling of the samples was warranted (Table 8). Sex differences were not tested in the Sesebi sample due to its mixed nature; if there were sex differences as a result of postmarital residence patterns, they would have been undetectable because there was no separation between each group. The sex differences overall were minimal and the incidence was only five times across samples and traits. Thus, the sexes were safely pooled for further analyses.

Table 7. Supraorbital foramen broken down by sample size

Samples	Observers	p-value
XGRP, SEMC, PANG, SAYC	Godde, Strouhal	0.5377
MERO, KULM, KULI, AGRP, CGRP, KERM, HABA,SESE	Godde, Hanihara, Lovell	0.2336
MESO, MERO, KULM, KULI, AGRP, CGRP, KERM, HABA,SESE	Godde, Hanihara, Lovell	0.1457

Table 8. Sex differences by group

	AIOF	AMF	ASB	BAS	CCP	HGCB	JFB	OL
MESO	0.0000	0.0000	0.6850	0.0000	0.0000	0.0000	0.0000	0.0000
AGRP	0.1515	0.8442	0.3613	0.0000	0.3613	-	-	0.7401
CGRP	0.7837	0.3673	0.3681	0.2921	0.4924	-	-	0.5150
SAYC	0.5157	0.3405	0.6752	-	-	-	-	0.5224
PANG	0.0000	0.0000	0.3914	-	-	-	-	0.6862
KERM	0.1611	0.8052	0.0786	0.0342 *	0.9081	0.5658	0.4761	0.6348
MERO	0.2166	0.9184	0.7685	0.9997	0.4792	0.7936	0.3692	0.9223
XGRP	0.2881	0.3268	0.0441 *	0.3451	0.0719	0.0698	0.6915	0.3656
SEMC	0.1967	0.0000	0.4279	0.0000	0.8982	0.6576	0.4974	0.1653
KULI	0.0000	0.8778	0.8406	0.3875	0.0411*	0.4756	0.3629	0.2655
KULM	0.8230	0.0000	0.3974	0.8382	0.4584	0.1699	0.5363	0.9223
HABA	0.5577	0.2084	0.0035 *	0.0181 *	0.0810	0.5082	0.4649	0.5912

* significant at the .05 level

- trait not scored

0 zero trait frequency

Table 8 continued. Sex differences by group

	OMB	OSC	PCT	PNB	SOF	TZS	TD
MESO	0.6905	0.7881	0.7408	0.0000	0.3808	0.0000	0.6242
AGRP	-	-	0.0000	0.0000	0.7272	0.0000	0.6463
CGRP	-	-	0.2258	0.8809	0.5971	0.0000	0.7432
SAYC	-	-	0.1990	0.6035	0.7181	-	0.2690
PANG	-	-	0.5708	0.0000	0.6862	-	0.1025
KERM	0.0658	0.4602	0.2772	0.8718	0.6159	0.7056	0.1951
MERO	0.9400	0.9843	0.7940	0.3203	0.8063	0.6386	0.2019
XGRP	0.9096	0.3451	0.1166	0.1730	0.4222	0.3850	0.3562
SEMC	0.0000	0.1653	0.1653	0.1653	0.1653	0.3894	0.8982
KULI	0.6673	0.3468	0.3347	0.4798	0.1981	0.4529	0.2506
KULM	0.6018	0.8837	0.7064	0.8822	0.6737	0.9935	0.8624
HABA	0.5765	0.4779	0.3089	0.2534	0.4189	0.2725	0.4507

* significant at the .05 level

- trait not scored

0 zero trait frequency

The map that was constructed to scale for time and space calculations utilized information from site reports, journal articles, books, and other maps in order to exactly identify the geographic location of each of the sites (Fig. 2). The only exceptions are the A- and C-Groups of which the only site information available was north and south of Wadi Halfa. Thus, both of these samples were calculated from Wadi Halfa, as exact locations are unknown. The map pixel distances and temporal distances are tabulated in Table 9.

The following chapters will present the results and discussion from each of the population structure hypotheses in Chapter 1. Each one is organized into results and discussion portions. Specifically, Chapter 7 will address the *in situ* hypothesis and demonstrate the applicability (or lack there of) of the hypothesis across all samples available in this dissertation, as well as with two reduced sample datasets.

Figure 2. Map drawn to scale of each of the sites. Adapted from Adams (1977).

Table 9. Temporal and spatial distances. Temporal distances among the groups are reported in years in the upper triangle while the spatial distances are reported in pixels in the lower triangle

	KULI	KULM	MESO	CGRP	AGRP	PANG	SAYC	HABA	KERM	XGRP	MERO	SEMC
KULI	0	0	2225	2725	3725	2343	2343	83	2175	225	500	350
KULM	0	0	2225	2725	3725	2343	2343	83	2175	225	500	350
MESO	219	219	0	5500	4500	5882	5882	8142	6050	8000	7725	8575
CGRP	219	219	0	0	1000	382	382	2642	550	2725	2225	3075
AGRP	219	219	0	0	0	1382	1382	3642	1550	3500	3225	4075
PANG	2004	2004	677	677	677	0	0	2260	168	2118	1843	2693
SAYC	2004	2004	677	677	677	0	0	2260	168	2118	1843	2693
HABA	1834	1834	1708	1708	1708	265	265	0	2092	142	417	433
KERM	650	650	2289	2285	2285	7802	7802	7973	0	1950	1675	2525
XGRP	150	150	50	50	50	1643	1643	1953	1447	0	275	575
MERO	150	150	50	50	50	1643	1643	1953	1447	0	0	850
SEMC	150	150	50	50	50	1643	1643	1953	1447	0	0	0

Chapter 7

Complete Nubian Population Structure

As introduced in previous chapters of this dissertation, Nubian population structure has come under much scrutiny in regards to the effects of gene flow on its various groups. If in situ evolution is the main mechanism for biological change in Nubians, it should be readily apparent in analyses run on all samples in the population. This chapter will interpret the results of the statistical analyses associated with the *in situ* hypothesis about Nubian population structure as a whole; all, or most of the groups, are analyzed in conjunction with one another to explore population structure across all samples.

Results

Only two discrete traits (supraorbital foramen and tympanic dehiscence) were common among all groups, had a frequency greater than 10% among the samples, and were not subject to interobeserver biases. Modified Relethford-Blangero analyses proceeded on this dataset. Modified Relethford-Blangero analyses were not possible with datasets

containing a larger number of variables as some samples had zero frequencies of traits and reliable covariance matrices could not be produced for those specific samples.

The hypothesis regarding complete Nubian population structure was tested in three manners: 1. with all 13 samples, 2. without the mixed sample of Sesebi, and 3. with a reduction in samples from the same time periods so that only one time period is represented in the dataset, despite the availability of multiple samples from the same time period. Sesebi was removed due to the nature of the sample; a sample with combined groups may not yield an accurate depiction of population structure. A reduced dataset was generated and analyzed to eliminate some of the minutia of the large number of samples included in this project. The representative sample for time periods with multiple samples was selected by choosing the sample with the largest sample size. The distance matrices for the three manners in which this hypothesis was explored are in Tables 10, 11, and 12. The tetrachoric correlations used to produce the Mahalanobis distances are in Appendix A. The three matrices contain similar distance information about the samples. Specifically, Pan-Grave and Sayala C-Group were the most biologically distant groups from one another across the three analyses.

Principal coordinates analysis was performed and the resulting data plots are presented in Figs. 3, 4, and 5. The first two principal coordinates accounted for 100% of the variation in all three datasets (the high variation is a result of only analyzing two traits). All three plots depict relatively the same information; the Nubians samples appear to cluster together. There is little evidence of a clinal distribution, except for the position of the Meroites, X-Group, and Semna South Christians, all from the site of Semna South; these three samples clustered together in the analyses of all samples and all of the samples except

Table 10. Mahalanobis D^2 distances among all Nubian samples.

	KULI	KULM	MESO	CGRP	AGRP	PANG	SAYC	SESE	HABA	KERM	XGRP	MERO	SEMC
KULI	0.00												
KULM	0.11	0.00											
MESO	0.51	0.42	0.00										
CGRP	0.78	0.75	0.49	0.00									
AGRP	1.22	1.15	0.77	0.50	0.00								
PANG	1.14	1.17	1.52	1.91	2.29	0.00							
SAYC	2.16	2.13	1.81	1.38	1.08	3.29	0.00						
SESE	1.04	0.95	0.53	0.64	0.48	1.97	1.55	0.00					
HABA	0.31	0.20	0.26	0.68	1.02	1.26	2.05	0.77	0.00				
KERM	0.86	0.76	0.68	1.16	1.29	1.27	2.37	0.84	0.61	0.00			
XGRP	0.79	0.68	0.40	0.83	0.91	1.53	2.00	0.48	0.49	0.37	0.00		
MERO	0.99	0.92	1.04	1.53	1.74	0.87	2.82	1.32	0.87	0.49	0.84	0.00	
SEMC	0.71	0.62	0.21	0.40	0.57	1.72	1.63	0.35	0.46	0.78	0.43	1.19	0.00

Table 11. Mahalanobis D^2 distances among all samples, except Sesebi

	KULI	KULM	MESO	CGRP	AGRP	PANG	SAYC	HABA	KERM	XGRP	MERO	SEMC
KULI	0.00											
KULM	0.11	0.00										
MESO	0.51	0.42	0.00									
CGRP	0.78	0.74	0.49	0.00								
AGRP	1.21	1.15	0.77	0.50	0.00							
PANG	1.14	1.16	1.51	1.91	2.28	0.00						
SAYC	2.16	2.12	1.81	1.38	1.08	3.28	0.00					
HABA	1.04	0.95	0.53	0.64	0.48	1.96	1.55	0.00				
KERM	0.31	0.20	0.25	0.68	1.02	1.26	2.04	0.77	0.00			
XGRP	0.86	0.76	0.68	1.16	1.29	1.26	2.37	0.84	0.62	0.00		
MERO	0.79	0.68	0.40	0.83	0.91	1.52	2.00	0.48	0.49	0.37	0.00	
SEMC	1.06	0.99	1.08	1.57	1.77	0.92	2.85	1.33	0.93	0.49	0.86	0.00

Table 12. Mahalanobis D^2 distances of Nubian samples without multiple time periods represented

	MESO	CGRP	AGRP	PANG	SAYC	HABA	KERM	XGRP	MERO
MESO	0.00								
CGRP	0.29	0.00							
AGRP	0.46	0.49	0.00						
PANG	1.75	1.86	2.21	0.00					
SAYC	1.48	1.34	1.07	3.20	0.00				
HABA	0.39	0.66	0.48	1.90	1.53	0.00			
KERM	0.53	0.67	0.99	1.22	1.99	0.75	0.00		
XGRP	0.91	1.17	1.27	1.23	2.34	0.82	0.63	0.00	
MERO	0.57	0.85	0.91	1.48	1.97	0.47	0.49	0.37	0.00

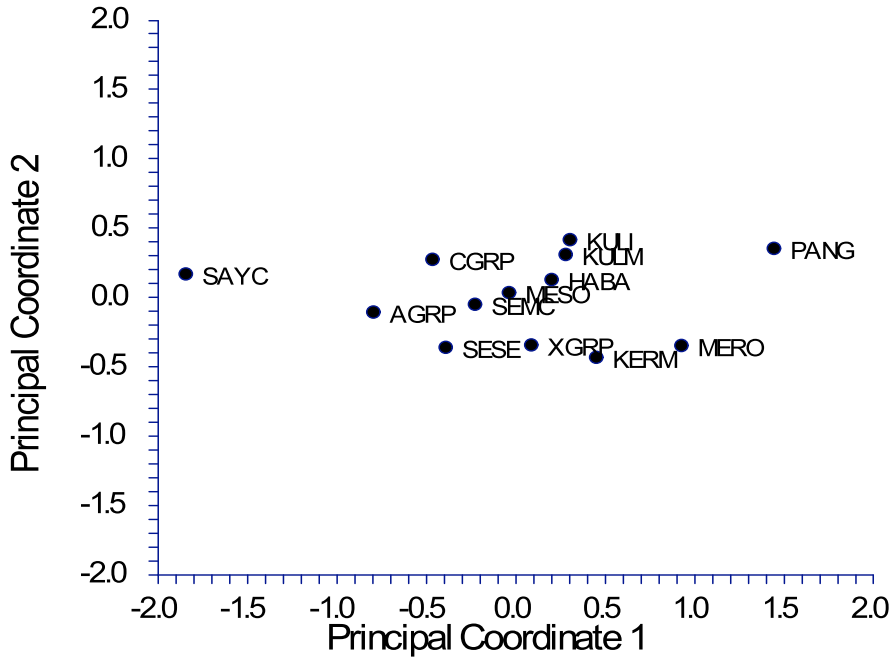

Figure 3. PCO plot of all Nubian samples

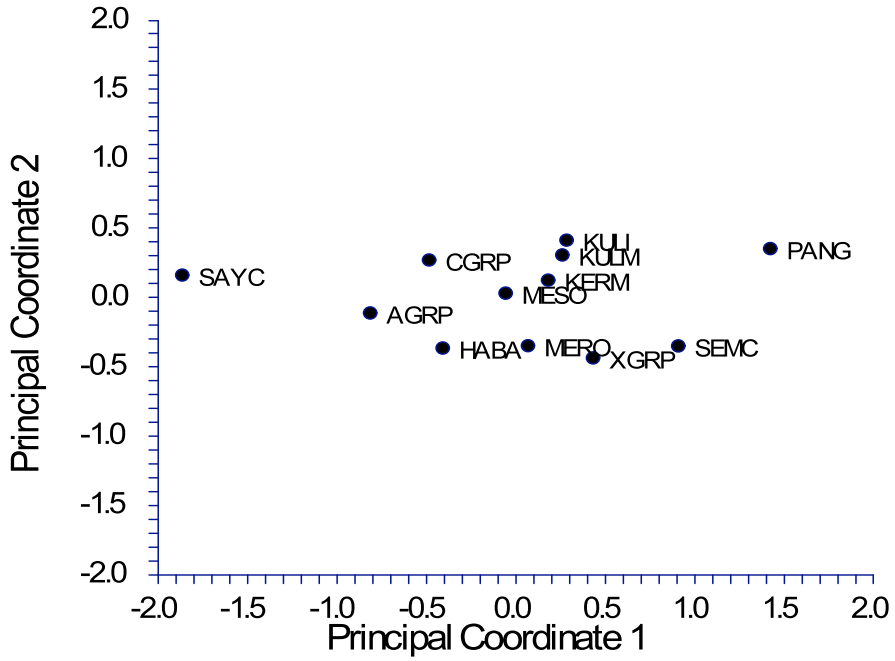

Figure 4. PCO plot of all samples except Sesebi

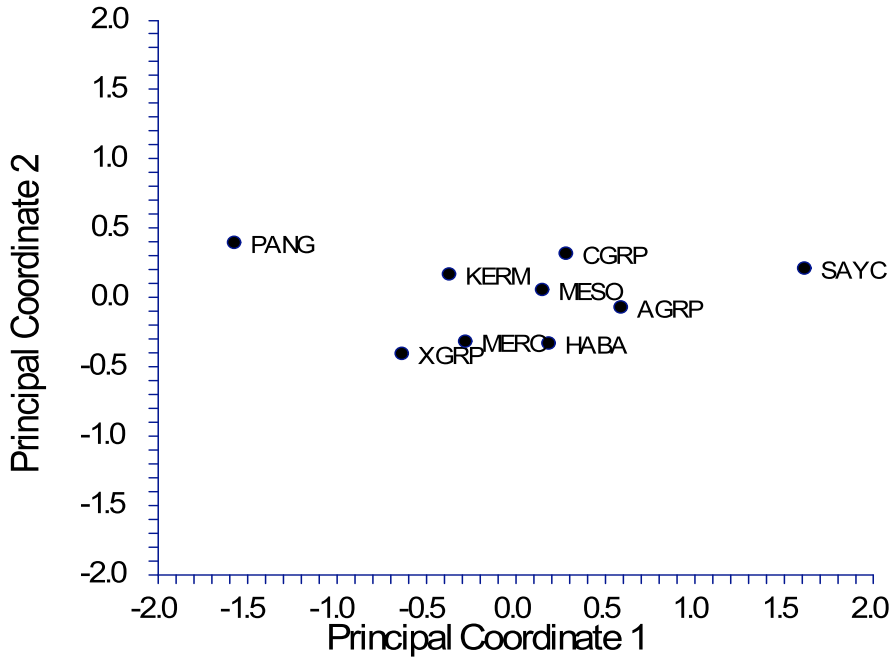

Figure 5. PCO plot of the reduced dataset

Sesebi. However, a temporal distribution is not evident. The 3-way Mantel tests confirm that there is no significant correlation overall between biological distance and space controlling for time (r=0.11207, p=0.7178) and for biological distance and time controlling for space (r =-0.08398, p=0.3421) in the pooled sample of all of the groups except for Sesebi. Likewise, significant correlations were lacking in the reduced sample (biological distance with space: r= -0.06680, p=0.3909; biological distance with time: r=- 0.31270, p=0.1372). Mantel tests were not conducted on the dataset with Sesebi because of its sample composition.

Population structure statistics continued with construction of C and R matrices. The C and R matrices, as well as the covariance matrices for each sample are reported in Appendix A. The results from the modified Relethford-Blangero analysis can be found in Tables 13, 14, and 15, along with the final sample sizes used in all statistical analyses relevant to this chapter's hypothesis. Regression plots support the information in the modified RB analysis (Figs. 6, 7, 8), except for the samples with the closest to average variance; the average variance samples fell just over the line onto the incorrect side. The incorrect placement of these samples may be due to their close proximity to the average and the regression line's inability to place those samples on the correct side. The residuals across all three datasets indicate the same pattern for gene flow: the rates of extraregional geneflow hovered around the average.

Table 13. Modified Relethford-Blangero analysis on all Nubian samples

Sample	Sample Size	r_{ii}	$\overline{V}_{Gw}$	$E(\overline{V}_{Gi})$	Residual ($\overline{V}_{Gw} - E(\overline{V}_{Gi})$)
MESO	6	0.0410	0.2333	0.1975	0.0358
AGRP	20	0.1167	0.1868	0.1820	0.0048
CGRP	33	0.0827	0.2121	0.1890	0.0231
PANG	7	0.2350	0.2143	0.1618	0.0525
SAYC	13	0.3097	0.1538	0.1422	0.0116
KERM	219	0.0470	0.2102	0.1963	0.0139
XGRP	23	0.0900	0.1344	0.1875	-0.0531
MERO	248	0.0603	0.1583	0.1936	-0.0353
SEMC	12	0.1438	0.1545	0.1764	-0.0219
KULI	39	0.0752	0.2362	0.1905	0.0457
KULM	73	0.0621	0.2236	0.1932	0.0304
HABA	134	0.0803	0.1656	0.1894	-0.0238
SESE	88	0.0488	0.1934	0.1959	-0.0025

Fst= 0.0752

Average $\overline{V}_{Gw}$ =0.1905

Average residual= 0.01

Table 14. Modified Relethford-Blangero analysis on all Nubian samples except Sesebi

Sample	Sample Size	r_{ii}	$\overline{V}_{Gw}$	$E(\overline{V}_{Gi})$	Residual ($\overline{V}_{Gw}$ - $E(\overline{V}_{Gi})$)
MESO	6	0.0448	0.2333	0.2046	0.0287
AGRP	20	0.1190	0.1868	0.1887	-0.0019
CGRP	33	0.0862	0.2121	0.1957	0.0164
PANG	7	0.2254	0.2143	0.1659	0.0484
SAYC	13	0.3072	0.1538	0.1484	0.0054
KERM	219	0.0467	0.2102	0.2042	0.0060
XGRP	23	0.0865	0.1344	0.1956	-0.0612
MERO	248	0.0610	0.1583	0.2011	-0.0428
SEMC	12	0.1451	0.1545	0.1831	-0.0286
KULI	39	0.0729	0.2362	0.1985	0.0377
KULM	73	0.0603	0.2236	0.2012	0.0224
HABA	134	0.0839	0.1656	0.1962	-0.0306

Fst= 0.1116

Average $\overline{V}_{Gw}$ =0.1903

Average residual= 0

Table 15. Modified Relethford-Blangero analysis on reduced Nubian samples

Sample	Sample Size	r_{ii}	$\overline{V}_{Gw}$	$E(\overline{V}_{Gi})$	Residual ($\overline{V}_{Gw}$ - $E(\overline{V}_{Gi})$)
MESO	6	0.0459	0.2333	0.1992	0.0341
AGRP	20	0.0827	0.1868	0.1915	-0.0047
CGRP	33	0.0692	0.2121	0.1943	0.0178
PANG	7	0.2548	0.2143	0.1555	0.0588
SAYC	13	0.2566	0.1538	0.1552	-0.0014
KERM	219	0.0679	0.2102	0.1946	0.0156
XGRP	23	0.1040	0.1344	0.1870	-0.0526
MERO	249	0.0634	0.1583	0.1955	-0.0372
HABA	134	0.0610	0.1656	0.1960	-0.0304

Fst=0.1117

Average $\overline{V}_{Gw}$ =0.1854

Average residual=0

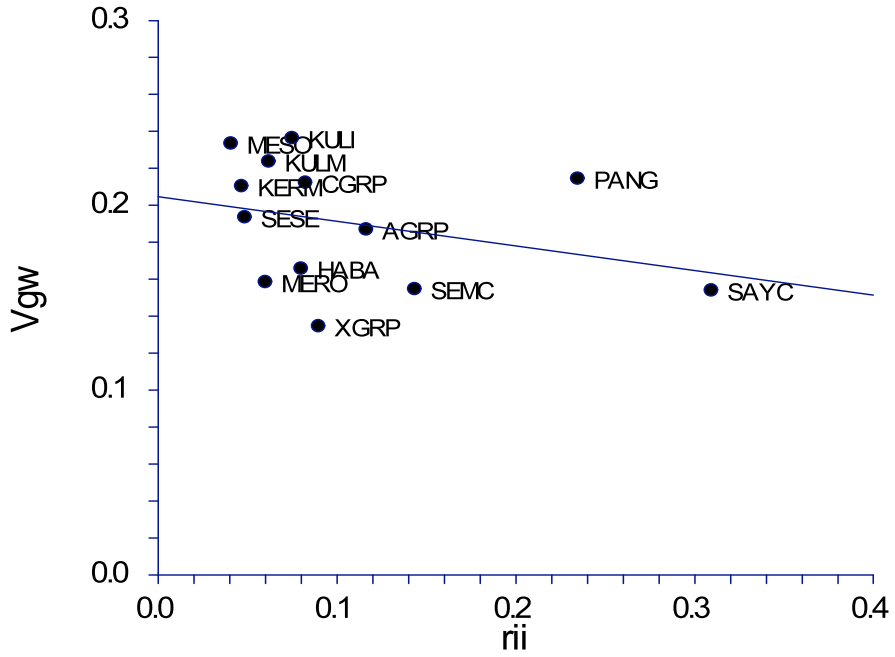

Figure 6. Regression plot of modified RB analysis for all Nubian groups

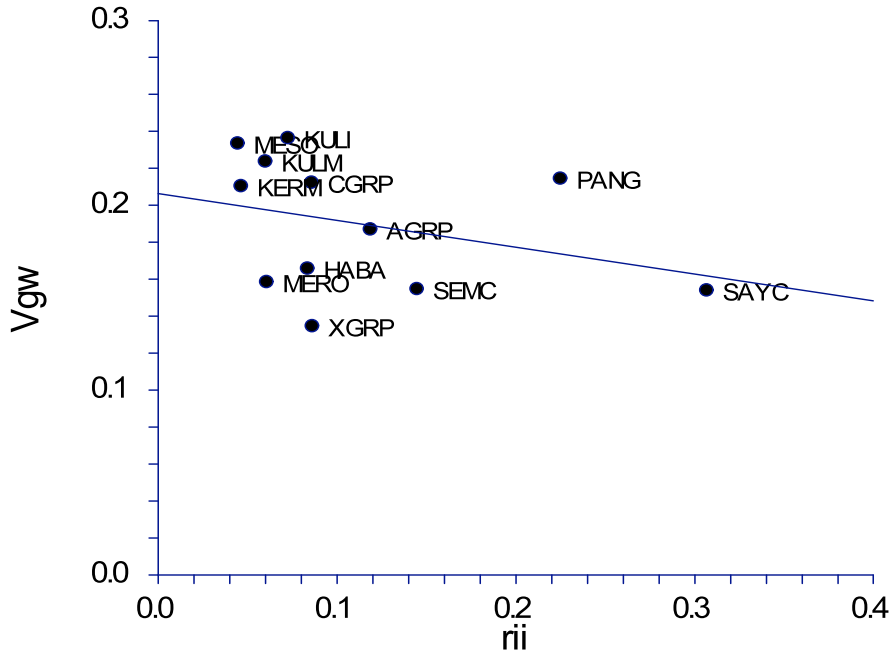

Figure 7. Regression plot of modified RB analysis for all Nubian groups, except Sesebi

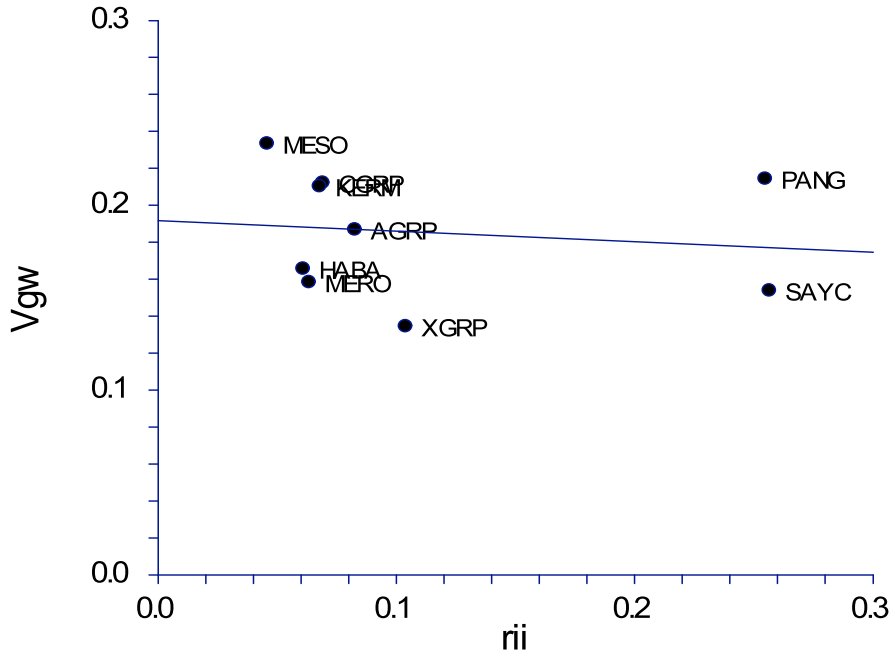

Figure 8. Regression plot of modified RB analysis for reduced dataset

The F_{st}, or variation among the groups, ranged from 0.0753 to 0.1116. These values are rather high in comparison to F_{st} estimates in documented non-admixed and admixed Irish samples in Relethford and Blangero (1990), which range from 0.02 in non-admixed to 0.05 in admixed samples. Furthermore, comparison to Jorde's (1980) appraisal of F_{st} estimates of major population groups across the literature puts the Nubian estimates inline with estimates derived from continental groupings. Removal of the mixed Sesebi sample resulted in an increase in F_{st} among the samples. However, the reduced Nubian dataset had a very similar F_{st} value to the dataset with only Sesebi eliminated.

Discussion

In order to understand what the results indicate about population structure, one must realize the forces affecting the differences among groups. There are three potential variables that could have influenced the results in the modified Relethford-Blangero analysis: 1. mutation, 2. extraregional gene flow, and 3. random genetic drift. Mutation and random genetic drift may have minimally influenced the results here, as the three time periods at Semna South all clustered together. Thus, there may have been some isolation by distance. The amount of isolation was small, though, because the Semna South samples also clustered with the rest of the Nubian samples in the analysis.

Two factors presumably affected the results in the biological analyses: population size and the mixed nature of the Sesebi sample. As stated in Chapter 2, estimates of biological distance can be obscured by long-term large effective population size. Conclusions based on population size cannot be put forth because population estimates are

not available from these Nubian samples as they are archaeological and no census exists. Alternatively, Sesebi's influence on F_{st} estimates may be a product of its composition; it is a pooled sample of crania from 3 groups. Sesebi's presence in the all sample dataset reduced F_{st} estimates to an artificially lower number. Thus, the results from the all sample analysis are not weighted highly in exploring the *in situ* hypothesis.

The clustering of the Nubian groups is rather heterogeneously spread across the principal coordinates axes and is indicative of an overall heterogeneous pattern. This diverse pattern is also observed in the temporal and spatial patterning. As is demonstrated in the high separation of the Pan-Grave and Sayala C-Group samples (both from the Sayala site), the clustering has little indication of temporal or spatial patterning (except for Semna South). These findings are not consistent with the *in situ* hypothesis, which states that Nubians groups are homogeneous. However, the results here agree with Buzon (2006), who also detected heterogeneity in the Nubian population when they were compared to her more homogeneous Egyptian samples.

In addition to the pattern of clustering suggesting that *in situ* biological evolution is not the most likely culprit for Nubian biological evolution, the hypothesis negation is further substantiated by the F_{st} values in Nubians; the F_{st} estimates were rather high in comparison to another population with a documented rate of gene flow (Irish) and various other major population groups. However, the modified RB analysis resulted in residuals that were all near average. Although at first glance this distribution of the residuals indicates average extraregional gene flow. However, I suggest this indicates that the gene flow levels amongst these groups were *high* (as found in F_{st}), but this high level was *average* among the groups. Previous biological studies have dismissed the possibility of gene flow greatly affecting the

A-Group, C-Group (Prowse and Lovell 1995), and Meroites (Carlson 1976; Godde 2009a; Greene 1972; Greene 1982; Van Gerven 1982; Van Gerven et al. 1977), but the results here (F_{st} and modified RB) suggest that high extraregional gene flow amongst all of the Nubian groups is a distinct possibility.

In order to support the validity of the statistical analyses, population history must be examined as it relates to the samples possessing high variation. The Mesolithic, A-Group, C-Group, both Sayala samples, both Kulubnarti Christian samples, and Hesa/Biga are from sites situated in Upper Egypt, near Egyptian occupation. The potential for gene exchange with the Egyptians is greater in these geographic positions. In fact, the A-Group was found to be biologically similar to high status Egyptians (Prowse and Lovell 1996). Moreover, there is archaeological evidence of Egyptian military expeditions during the A-Group and for extensive contact between the Egyptians and C-Group (Nielsen 1970). Nubian sites further outside of Egypt have also yielded evidence of contact with other populations.

Extraregional gene flow is a distinct possibility in the Kerma and Semna South sites. The individuals from Kerma have been identified as Egyptian (Collett 1933) and later as Nubian (Adams 1984) due the complex nature of the site (many Egyptian artifacts and customs) and the difficulty in interpreting the remains buried there. Kerma was also a major trade center and regular Egyptian contact is documented in historical and archaeological contexts. High levels of gene flow in the Meroites at Semna South are also expected. During the Meroitic period, the social structure was state-level and trade flourished along the Nile, much like Kerma. This allowed for extensive contact with foreign peoples and may have incited extraregional gene flow into the Meroites, as well as the individuals from Kerma. Cultural remains of the X-Group (also at Semna South) have yielded artifacts from

several other populations, including the Nobatae and Blemmyes (Nielsen 1970). In summation, the individuals from Kerma and Semna South have been documented both archaeologically and historically, as having adequate opportunity for extraregional gene flow.

The high rate of gene flow in the Mesolithic Nubians is consistent with Irish (2005), Irish and Turner (1990), and Turner and Markowitz (1990) who stated that some sort of population replacement occurred in the Nile Valley some time after the Paleolithic, but prior to the A- and C-Groups. Based on the results here, the proposed population replacement probably occurred prior to the Mesolithic and most likely during the Paleolithic. Wendorf (1968) concluded that several populations had migrated into Nubia, based on the multiple forms of lithic assemblages he uncovered. Thus, the biological evidence of extraregional gene flow is supported by the archaeological evidence of migration of foreign peoples to the area.

Strouhal and Jungwirth (1980) identified the Pan-Grave people as a separate, non-Nubian group inhabiting Sayala. Their skeletal analysis supported the unique mortuary practices of the Pan-Grave people; the mortuary evidence suggested the Pan-Graves were created by a foreign people in Sayala. The PCO plots do not identify the Pan-Grave sample as non-Nubian; rather, they suggest the Pan-Grave people were distantly related to Nubians, as their separation from other Nubian groups is small. The modified Relethford-Blangero analysis also detected this underlying relationship; the Pan-Grave people had similar residuals in the modified Relethford-Blangero analysis, indicating a level of gene flow that was average in relation to the other Nubian samples. One question arises in light of these results: were the Pan-Grave people a different class of C-Group Nubians? The PCO plot implies the Pan Grave people were probably part of the Nubian population, which supports

the notion they were another class of C-Group Nubians. Thus, the Pan-Grave people may actually be a special group of Nubians with unique mortuary practices, rather than a foreign people.

The C-Group, also at Sayala, lies on the fringes of the large cluster in the PCO analysis. This positioning is surprising, as another C-Group sample from Lower Nubia was also present in the PCO and biodistance investigations and the Sayala C-Group did not cluster near it. The Sayala C-Group may have clustered at the edge of the groups due to its unique social position; other populations occupied the same site during the same time period and may have contributed their genetic information to the Sayala C-Group (Strouhal and Jungwirth 1979). Yet, the Sayala C-Group still maintained some of their Nubian biological identity (as evidenced in their clustering with other Nubian groups), presumably through social customs and taboos that may have limited extraregional gene flow from occurring dramatically among those populations. The modified RB residual was average, which is indicative of the high level of variation found in the Nubian dataset and also verifies that the Sayala C-Group was subject to similar levels of gene flow as the remaining Nubian groups. Interestingly, the Mahalanobis distances display a high level of differentiation between the Sayala C-Group and Pan-Grave peoples, who also occupied Sayala. Even though both the Pan-Grave people and the Sayala C-Group people appear to be Nubian, they were highly different from one another, which is consistent with the results of Strouhal and Jungwirth (1979). The relationship among the Sayala C-Group, Pan-Grave people, and Wadi-Halfa C-Group further substantiates the suggestions that the C-Group at Sayala may have experienced some sort of isolation by distance (perhaps from social practices). The isolation may have a product of differing social classes between the C-Group and Pan-Grave peoples; class may

have dictated marriage patterns among the C-Group and Pan-Grave peoples. However, without archaeological evidence to support this notion, this conclusion is tentative and must be treated as such.

Even though the regression plot places the Sayala C-Group above the regression line (indicating it had higher than average gene flow) in the analysis with all 13 samples, the modified RB residual places the Sayala C-Group in the average gene flow category. The conflicting results may be a product of the Sayala C-Group's variance and residual values; they are the closest to the average in the all samples analysis. The regression line may not be picking up on the slightly greater than average values; rather, it is only placing the sample near the regression line because it is near the average.

A major factor in these results is small sample size and the distribution of traits associated with it. The Mesolithic, A-Group, Pan-Grave, Sayala C-Group, X-Group, and Semna South Christian samples all numbered under 30. Although the small samples were probably a random selection of the individuals from that group, they are still not necessarily representative of the greater population. Furthermore, the limited number of variables available across the Nubian samples may have hindered the results. However, because these are archaeological samples, exclusion based on sample size and availability of variables is not justified, and instead these results should be treated with caution.

The next few chapters explore similar analyses, but they are performed on isolated portions of the Nubian population. Each chapter includes samples that are relevant to the six other hypotheses introduced in Chapter 1. The succeeding chapter will examine Nubian population structure from Mesolithic – C-Group to answer questions regarding a population

replacement and the biological affinities of the groups occupying Lower Nubia before and after the 100-year hiatus between the A- and C-Groups.

Chapter 8

Change Over Time from Mesolithic – C-Group

Irish (2005), Irish and Turner (1990), and Turner and Markowitz (1990) proposed that a population replacement occurred in Nubia sometime after the Paleolithic. Evidence for this hypothesis came in the form of low levels of variation in Paleolithic Nubians and high levels of variation in A- and C-Groups. The preceding chapter also detected a similar trend; the Mesolithic sample had lower than average gene flow, while the A- and C-Groups from Wadi-Halfa region boasted higher than average gene flow. Chapter 7's results led to the conclusion that the population replacement hypothesis is supported and its timing was narrowed from between the Paleolithic and A-Group to between the Mesolithic and A-Group (probably during the Neolithic). This chapter will focus specifically on the relationships between the Mesolithic Nubians and the succeeding A- and C-Groups, in an effort to focus on the possibility of a population replacement after the Paleolithic and to explore the effects of the small hiatus (100 years) between the A- and C-Groups.

Results

Much like the preceding chapter, two traits (supraorbital foramen and tympanic dehiscence) were scored in all the samples, had high frequencies, and were present in all samples. The biological distances are tabulated in Table 16 and their tetrachoric correlations are in Appendix B. Of all of the samples, Sayala C-Group was the most distantly related to the Mesolithic sample. The first two principal coordinates accounted for 100% of the variation in the dataset and were plotted in Figure 9. The scale of the scatterplot reveals a large amount of variation among the groups, especially along the second principal coordinate. The samples cluster loosely together, with the Sayala C-Group separated from the other three samples. From the scatterplot, there appears to be no spatial cline in the distribution of the samples and Mantel tests confirm the geographic distribution findings ($r=0.4359$, $p=0.9064$) of the scatterplot. However, neither the plot nor the Mantel tests demonstrate that there is a significant correlation of time and biological distance ($r=0.0827$, $p= 0.24511$).

C matrices and R matrices were constructed for processing through modified RB analysis and are listed along with the covariance matrices in Appendix B. The modified RB analysis revealed a similar patterning among the Nubian samples; the residuals all fell near the average (Table 17). The regression plot (Figure 10) does not flag any of the samples as outliers, which also supports the visual assessment of the residuals. The final sample sizes for each group are also listed in Table 17. The F_{st} value among the 4 samples was lower than the F_{st} calculated among all or most of the samples in the preceding chapter. This smaller

Table 16. Mahalonobis D^2 distances among Mesolithic - C-Group

	MESO	CGRP	AGRP	SAYC
MESO	0.00			
CGRP	0.33	0.00		
AGRP	0.41	0.48	0.00	
SAYC	1.06	0.94	0.69	0.00

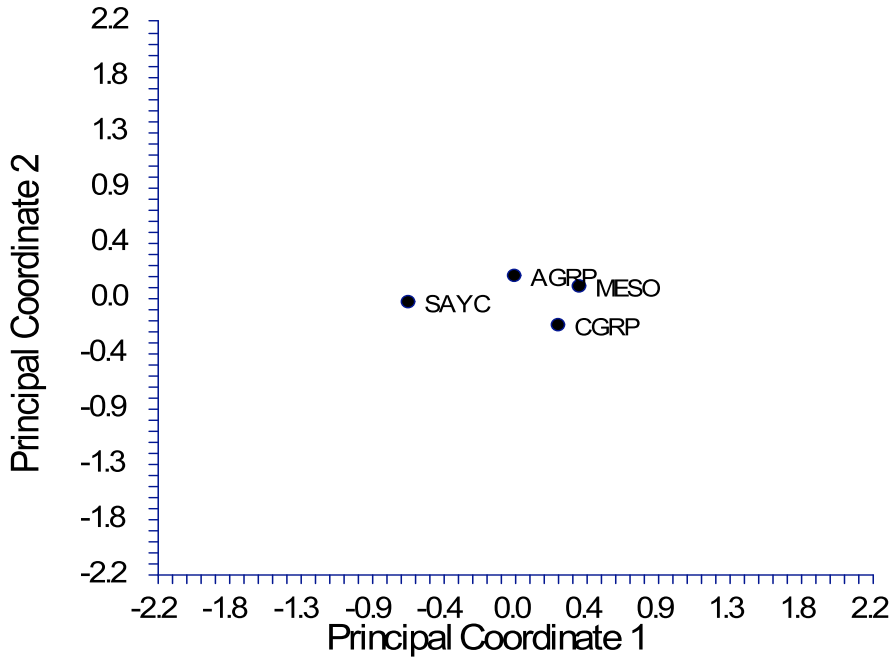

Figure 9. PCO plot of Mesolithic - C-Group

Table 17. Modified Relethford-Blangero analysis on Mesolithic - C-Group samples

Sample	Sample Size	r_{ii}	$\overline{V}_{Gw}$	$E(\overline{V}_{Gi})$	Residual ($\overline{V}_{Gw}$ - $E(\overline{V}_{Gi})$)
MESO	6	0.0492	0.2333	0.1969	0.0364
AGRP	20	0.0414	0.1868	0.1986	-0.0118
CGRP	33	0.0378	0.2121	0.1993	0.0128
SAYC	14	0.0770	0.1538	0.1912	-0.0374

Fst= 0.0513

Average $\overline{V}_{Gw}$ =0.1965

Average residual=0

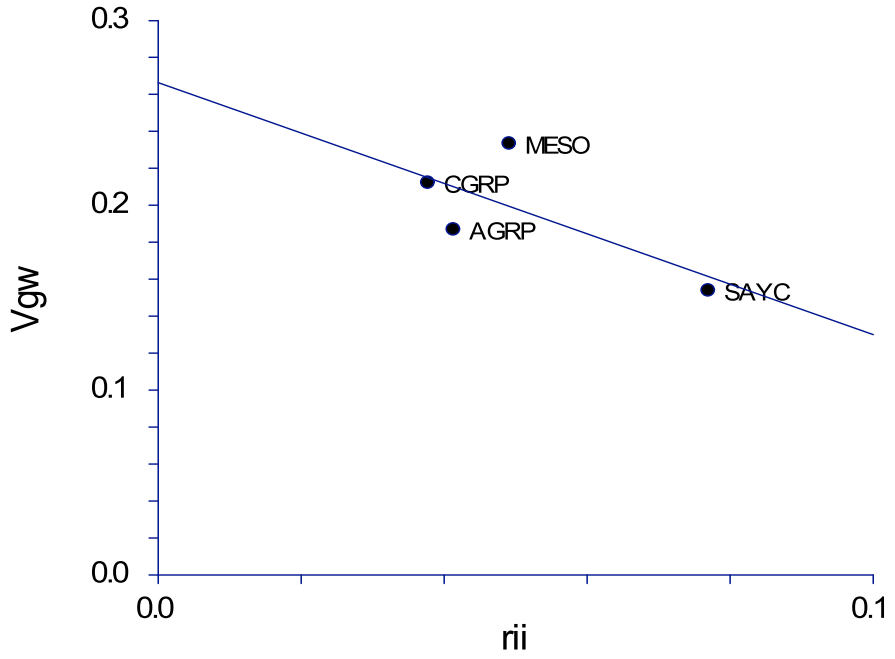

Figure 10. Regression plot of modified RB analysis for Mesolithic – C-Group samples

number is more consistent with the F_{st} from the documented admixed sample of Irish (Relethford and Blangero 1990).

Discussion

The population genetics statistics applied to the biological data of the Mesolithic, A-Group, C-Group, and Sayala C-Group revealed a pattern that is consistent with the previous chapter and prior research (Irish 2005; Irish and Turner 1990; Turner and Markowitz 1990); a high level of variation and gene flow appears to have been maintained among the Mesolithic and Wadi-Halfa A- and C-Groups. Furthermore, the mortuary archaeology is reminiscent of this same relationship; the A- and C-Group burials were similar, yet distinctly different from the Mesolithic. However, it cannot be discounted that the A- and C-Group burials were probably reflective of a more complex social structure that had slowly evolved after the Mesolithic. Irish (2005) postulated that the change among these groups was related to a population replacement in Nubia after the Paleolithic Nubian groups. Like Chapter 7, the results here support Irish's assertions; the high level of variation indicates that a population replacement probably occurred prior to the Mesolithic (during the Paleolithic?). However, the Sayala C-Group's distinctiveness in the PCO plot complicates Irish and others' population replacement contention. Two possiblities are implied by the Sayala C-Group: either, 1. a different population replacement occurred in the Sayala region, or 2. the Sayala C-Group was subject to isolation by distance, which prevented gene flow from the invading population that exchanged genetic material with the Wadi Halfa groups. Both alternatives are probable, but the second seems the most likely.

The Mesolithic, A-Group, and C-Group are the most closely related through biological distances, while the Sayala C-Group are biologically distant from the other three. The similarities among the Mesolithic, A-Group, and C-Group (as evidenced in the Mahalanobis distances and PCO) may be a result of their occupation of the same geographic area, Wadi Halfa and would also account for the isolation of the C-Group at Sayala. The modified RB residuals were all average, and when coupled with the large F_{st} value, they indicate that there was a large amount of variation present among the samples (as evidenced in the F_{st}). Moreover, the average residuals indicate that the genetic information among the four groups was similar, and perhaps, the Sayala C-Group experienced less of the extraregional gene flow that affected the Wadi Halfa groups. Thus, this evidence suggests the supposed population replacement may have drastically affected the Wadi Halfa A- and C-Groups, but not nearly as drastically in the Sayala C-Group. Because they were not affected by a population replacement, the Sayala C-Group should have the smallest modified RB residuals, as is true (see Table 17).

A hiatus of lower Nubia is detectable in the archaeological record between the A- and C-Groups (Nielsen 1970). Their Mahalanobis D^2 distance is small in relation to others in the matrix and implies the A- and C-Group were most likely related. The PCO plot also supports this. The various forms of biological evidence here do not indicate a population replacement ended the hiatus; rather, individuals descended from the A-Group who vacated Lower Nubia probably returned as the C-Group. The biological results coincide well with the archaeological record (both artifact and mortuary), which did not detect a new population formed by the C-Group.

The higher rate of presumed gene flow evident in the A- and C-Group samples may have been due to their geographic proximity to Egyptian groups and the resulting opportunity for gene flow. The Sayala C-Group were at a site occupied by three different populations (Roman and Blemmyes, in addition to the Nubians) and their opportunity for gene flow with the population exchanging genetic material with the Wadi Halfa groups may have been reduced versus the A- and C-Groups, depending on the customs and social rules of the Sayala populations.

Unfortunately, in situ biological development is not completely indicated across the Mesolithic through C-Group time periods, as indicated by evidence of a population replacement and/or gene flow with other population(s). Although there appears to be a high level of heterogeneity within the Nubians (as evidenced in the F_{st} here and in previous chapters), the variation does not isolate particular groups from the rest of the samples, indicating the heterogeneity does not partition out specific groups. In short, the heterogeneity among these samples does not support the *in situ* hypothesis. However, the *in situ* hypothesis cannot be discounted for later groups based on this analysis alone. Only further testing of the *in situ* hypothesis with later groups will support or negate it for the population.

Subsequent chapters of this dissertation will address the *in situ* hypothesis further by breaking down the history of the people of Nubia into manageable, meaningful portions that allows for further hypothesis testing. The results here are tentative, as small sample sizes plagued this dataset, and therefore this study should be interpreted cautiously. Next, the affinities among the groups spanning from the Mesolithic through the Kerma time period are explored to assess the relationship of three contemporary Nubian groups.

Chapter 9

Change over time Mesolithic – Kerma

In Nubian history, there were times when multiple Nubian groups co-existed across the landscape. Most notably, the C-Group, Pan-Grave people, and individuals from Kerma overlapped in time, but not in space. The Pharonic group probably existed at this time as well, but their biological identity is in question with their most likely affinity being Egyptian (Nielsen 1970). The C-Group and Pan-Grave people were restricted to areas above the second cataract, whereas the individuals from Kerma were located below the third cataract (Edwards 2004). Despite the spatial isolation among the contemporary groups, the archaeological and historical documentation of extensive trade and foreign contact, and the heterogeneity of the individuals from Kerma (Buzon 2006), the artifacts suggest the Kerma people were Nubians (Adams 1984). In order to understand the relationships among the three overlapping Nubian groups, and to confirm their biological affinity, Mesolithic and A-Group samples were also included in biological distance analyses to incorporate the component of biological evolution over time for a better insight into biological change.

Results

Again, only two discrete traits met the criteria necessary for a complete population genetics analysis among these particular samples: supraorbital foramen and tympanic dehiscence. Mahalanobis distances (Table 18) were greater in this dataset than the previous dataset (Mesolithic – C-Group). Inclusion of the Pan-Grave sample introduced higher biological distance scores than the previous chapter. In particular, the highest biological distance was between the Pan-Grave people and Sayala C-Group (as in Chapter 7). The other biodistances >2.0 were also associated with those two groups. The pooled tetrachoric matrix can be found in Appendix C.

Principal coordinates yielded a plot where the groups all clustered together, for the most part (Fig. 11). Mantel tests did not uncover any significant temporal trends (r= -0.39108, p=0.1642), nor was a temporal component is evident in the scatterplot. The four samples (Pan-Grave, C-Group, Sayala C-Group, Kerma) from the three overlapping groups should have clustered together if a temporal trend is present. Likewise, spatial trends could not be identified in the plot or by Mantel tests (r= -0.07079, p= 0.4197). This depiction of the relationships among these groups incorporates 100% of the variation between the first two principal coordinates.

Both C and R matrices are located in Appendix C with the covariance matrices for each sample. Modified RB analysis (Table 19, Fig. 12) generated from these matrices again yielded values that were all near the average. The regression plot also displays this

Table 18. Mahalanobis D^2 distances among Mesolithic-Kerma

	MESO	CGRP	AGRP	PANG	SAYC	KERM
MESO	0.00					
CGRP	0.29	0.00				
AGRP	0.47	0.50	0.00			
PANG	1.79	1.89	2.25	0.00		
SAYC	1.50	1.37	1.08	3.25	0.00	
KERM	0.55	0.67	1.01	1.24	2.02	0.00

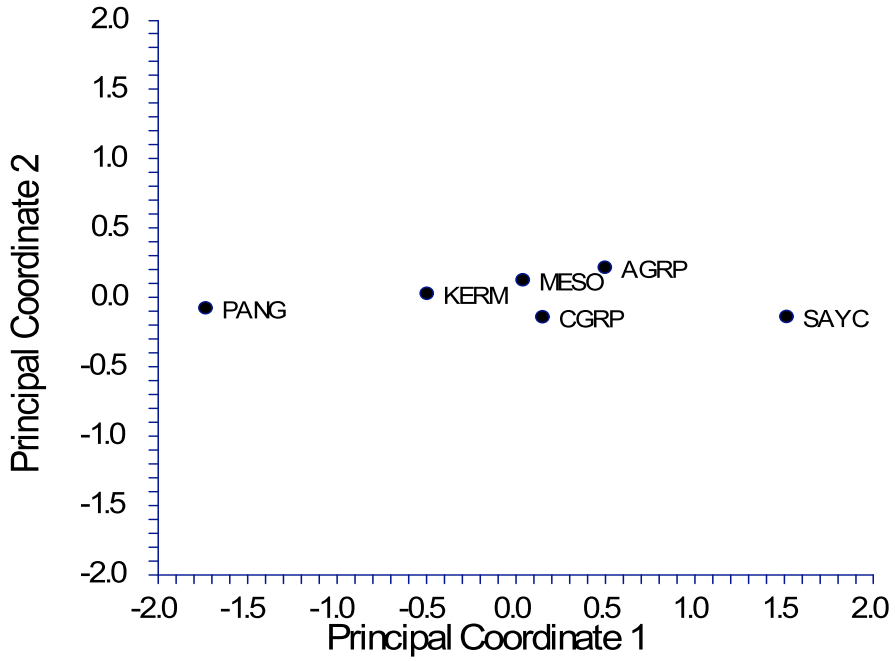

Figure 11. PCO plot of Mesolithic – Kerma samples

Table 19. Modified Relethford-Blangero analysis on Mesolithic-Kerma samples

Sample	Sample Size	r_{ii}	$\overline{V}_{Gw}$	$E(\overline{V}_{Gi})$	Residual ($\overline{V}_{Gw}$ - $E(\overline{V}_{Gi})$)
MESO	6	0.0468	0.2333	0.2189	0.0144
AGRP	20	0.0733	0.1868	0.2128	-0.0260
CGRP	33	0.0512	0.2121	0.2178	-0.0057
PANG	7	0.2606	0.2143	0.1698	0.0445
SAYC	13	0.2161	0.1538	0.1800	-0.0262
KERM	224	0.0798	0.2102	0.2113	-0.0011

Fst= 0.1213

Average $\overline{V}_{Gw}$ = 0.2018

Average residual = 0

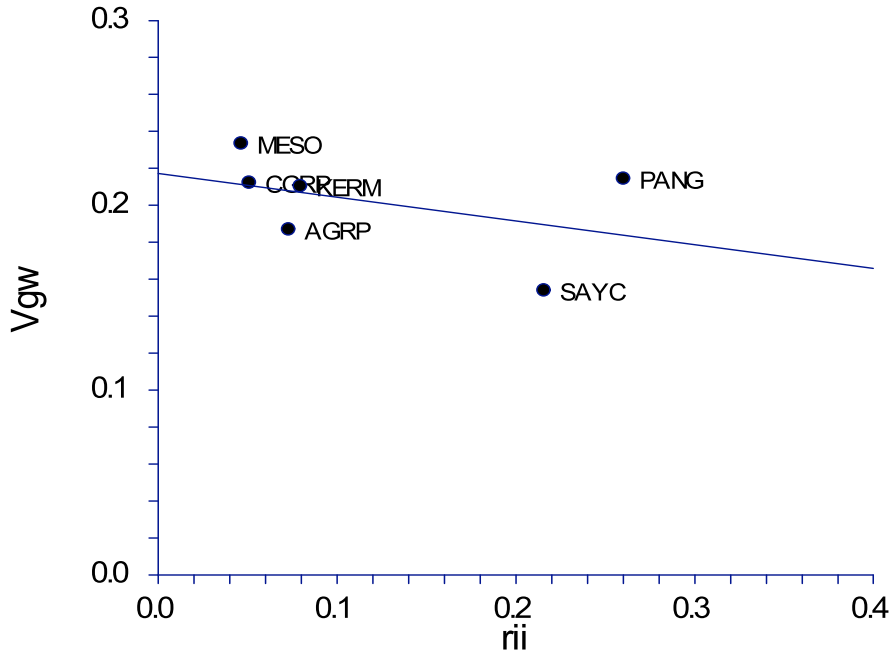

Figure 12. Regression plot of modified RB analysis for Mesolithic – Kerma samples

Information. As was the case in previous chapters, a few samples did not fall on the correct side of the regression line; the C-Group and A-Group values were plotted directly on the regression line, even though their residuals indicate they should fall below the line. The overall F_{st} value was greater than the Mesolithic-C-Group analysis and the analyses of complete Nubian groups, which indicates there was a larger level of variation among these samples.

Discussion

From the PCO scatterplot above, it is evident that the Pan-Grave, Kerma, and C-Group Nubians were probably three different Nubian groups occupying various and overlapping areas across Nubia. None of the three groups were biologically isolated in the scatterplot; rather, they all appear to comprise one large cluster along with the Mesolithic and A-Group Nubians. The points on the scatterplot are spread widely across a large range in the axes. Thus, based on the position of the samples in PCO, the samples are relatively heterogeneous. The Pan-Grave people are not completely separate from the rest of the samples, and thus are probably not a different population as others have maintained (Strouhal and Jungwirth 1979). However, the large disparity between the Pan-Grave people and Sayala C-Group supports the differentiation that Strouhal and Jungwirth (1979) observed.

Although the biological distance scores suggest that the Pan-Grave people were biologically distinct from the Sayala C-Group, the Pan-Grave people were biologically similar to the C-Group from Wadi-Halfa. Moreover, the Pan-Grave people were more closely related to the C-Group, than the A-Group and more closely related to the individuals

from Kerma than to any of the other samples in this analysis. The postulation that the Pan-Grave people were possibly Blemmyes coming from the Western desert (Strouhal and Jungwirth 1980) are not supported in this analysis. The close affiliation of the Pan-Grave people and the individuals from Kerma suggest some sort of relationship between those two groups. Kerma was a major trade center and attracted many different populations (Collett 1933). The Pan-Grave people may have been a fissioning group from the Kerma people who learned different burial practices from the exchange of ideas and culture at Kerma. The Kerma people also maintained unique mortuary practices (Collett 1933), which supports the idea that Kerma may have been the source for learning new and different mortuary treatment of remains. Kerma's strategic position also explains the higher levels of gene flow present in the sample. These higher levels support the findings of Buzon (2006) who noted heterogeneity in the individuals from Kerma.

Interestingly, all of the samples had average gene flow in the modified RB analysis. The average amount of gene flow in the Mesolithic sample, in combination with the high level of variation in this analysis, is consistent with the hypothesis that a population replacement occurred during the Paleolithic, and as established in previous chapters, also supports the archaeological evidence. This hypothesis is further substantiated by the average levels of gene flow in the A-Group and C-Group, suggesting that the population replacement took place prior to the A- and C-Group. The Sayala C-Group's average gene flow is consistent with the population replacement hypothesis. Based on the average modified RB residual associated with the Pan-Grave people also from the same site, the Pan-Grave people cannot be partitioned out as a separate population. In PCO the Pan-Grave sample clusters slightly outside of the other Nubian samples, but does not suggest assignment to a separate

population. The modified RB analysis (along with the biodistance scores) supports the PCO results; the Pan-Grave people were probably another group of Nubians who were culturally distinct, with different mortuary practices, but who were not biologically distinct.

Lack of significant correlations among biological, spatial, and temporal distances does not mean that geographic position did not contribute to the relationships observed among the samples. The C-Group and the A-Group are located in Lower Nubia, near Egypt. Contact with Egypt may have been frequent and contributed to the variation in these groups. In fact, as mentioned in previous chapters, Prowse and Lovell (1996) found upper class Egyptians to be more biologically similar to the A-Group than other Egyptians. However, the Sayala C-Group and the Pan-Grave people were also located near Egyptian occupation, but the several other populations at their site may have prevented gene flow between the Egyptians and themselves (as a result of social customs?). The distinctiveness of the Pan-Grave people, as is suggestive from their mortuary remains, may have enabled them to maintain their biological distinctiveness through cultural isolation.

The dominant hypothesis about Nubian biological evolution, the *in situ* hypothesis, is not supported by the results here. The nature of the clustering is rather widespread, which coincides with the findings that there is a high level of variation among these samples. Heterogeneity, according to Carlson and Van Gerven (1979) is indicative of biological diffusion, rather than in situ biological evolution. Thus, biological diffusion most likely occurred early in Nubian history (as indicative of the results in this chapter). However, as will be investigated in the following chapter, in situ evolution may have occurred after this time.

Chapter 10

Were the Meroites Nubian?

One of the most interesting aspects of Nubian population history is the prolonged hiatus (approximately 1,000 years) of Lower Nubia between the Kerma and Meroitic time periods. Some authors have speculated that the returning people were not Nubian (Nielsen 1970); rather, they were a new population. Yet, others find the biological data solely supports a Nubian Meroitic affinity (Carlson 1976; Godde 2009a; Greene 1972; Greene 1982). The archaeological evidence also supports the Meroites' Nubian affiliation (Adams 1968; Adams 1977). However, the linguistic evidence is hard to explain as the Meroites brought with them a new written language to the area (Adams 1977). Except for Godde (2009a), biological affinities of the Meroites were not explored using groups that immediately predate the hiatus. Even with the incorporation of a sample from before the hiatus, Godde (2009a) did not include groups that extend back further in Nubian evolution, such as the C-Group or Pan-Grave samples in her analysis. None of the analyses on this subject utilized population genetics statistics, either. Thus, this chapter contributes new information about the hiatus and Nubian population structure by utilizing more samples

predating the hiatus, as well as applying a population genetics approach to estimating gene flow.

Results

Four discrete traits met the criteria for the population structure analysis in this chapter: asterionic bone, ossicle at lambda, supraorbital foramen, and tympanic dehiscence. The largest biological distance falls between the Pan-Grave and Sayala C-Group samples (Table 20), similar to results in previous chapters. Interestingly, the Kulubnarti mainland sample and the Kerma sample have the smallest biological distance score, indicating a high level of similarity. The tetrachoric correlations used to generate the biological distance score are located in Appendix D.

The mainland Kulubnarti sample was plotted next to the Kerma sample in PCO, which is consistent with the biodistance findings above (Fig. 13). Two of the four Christian samples (Kulubnarti mainland and island) were biologically similar to Kerma, as were both Christian groups. Moreover, the samples in this study formed one large cluster. The largest biological distance was between the Pan-Grave people and Sayala C-Group and this relationship is manifest in the positioning of the two samples in the PCO plot. This picture of the relationships among the samples is provided for with principal coordinates accounting for 88% of the variation. Some spatial and temporal trends are apparent in this plot, as the Semna South and Kulubnarti samples clustered together. However, Mantel tests were not

Table 20. Mahalanobis D^2 distances among C-Group – Christian samples for examination of Meroitic affinities

	KULI	KULM	CGRP	PANG	SAYC	HABA	KERM	XGRP	MERO	SEMC
KULI	0.00									
KULM	0.73	0.00								
CGRP	1.49	1.55	0.00							
PANG	1.61	1.26	2.71	0.00						
SAYC	2.47	2.56	1.08	3.62	0.00					
HABA	1.38	1.17	0.95	2.08	1.75	0.00				
KERM	0.89	0.55	1.37	1.36	2.28	0.79	0.00			
XGRP	0.94	1.17	1.63	1.74	2.51	1.12	0.98	0.00		
MERO	0.97	0.72	1.39	1.69	2.42	0.88	0.77	0.86	0.00	
SEMC	1.36	1.00	2.26	1.01	3.24	1.54	1.09	1.15	0.94	0.00

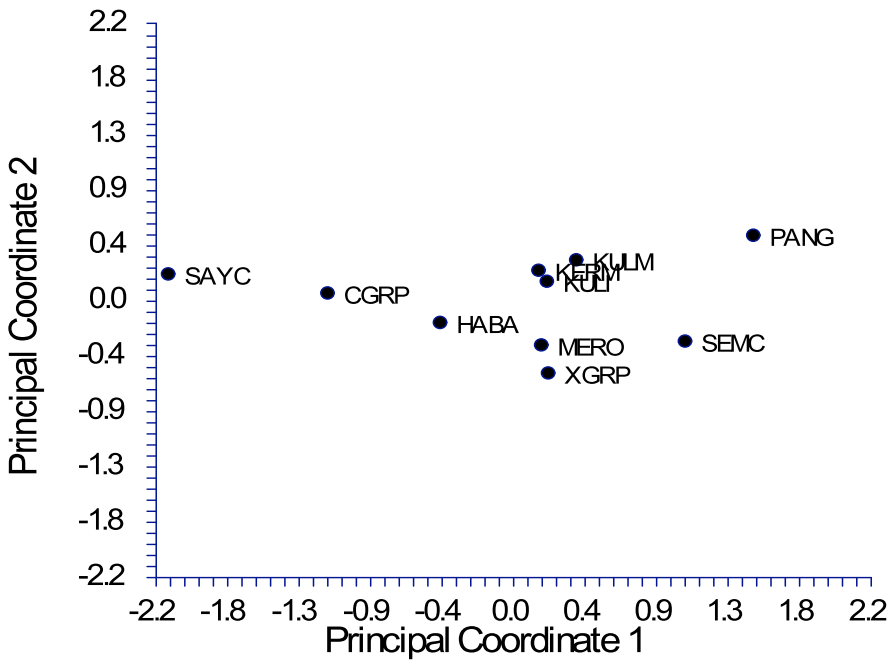

Figure 13. PCO plot of groups used to identify the biological affinities of the Meroites

significant for temporal or spatial clines (spatial: r= 0.05933, p= 0.6135; temporal: r= 0.18920, p= 0.9185). The C, R, and covariance matrices are provided in Appendix D. The modified RB analysis utilized the R matrix to calculate the expected within group variance. From these statistics, it is apparent that again, that all of the samples experienced extraregional gene flow that was similar to the average (Table 21, Fig. 14). The F_{st} for the entire dataset is both larger and smaller than prior chapters in this dissertation. It is inline with the F_{st} calculated among all 13 of the Nubian samples and displays a high level of variation among these groups.

Discussion

The Meroites clustered near the other Semna South samples, as well as Hesa/Biga. Although the groups that the Meroites clustered with succeeded the Meroitic time period at Semna South, the Meroites were still part of the larger cluster, which incorporated samples from time periods prior to the Nubian hiatus. The Meroites consistently display close biological affiliations in the biological distances. Moreover, the Meroitic RB residual is inline with the remaining residuals in this chapter, demonstrating that the Meroites did not experience greater than average gene flow in comparison with other Nubian groups. Thus, this biological evidence indicates that the Meroites were indeed a returning Nubian group to Lower Nubia after a lengthy desertion. The biological evidence is also consistent with the archaeological evidence (mortuary patterns and artifacts) of cultural continuity among the Meroites and X-Group (Adams 1977). Furthermore, I agree with Adams' (1977) assessment

Table 21. Modified Relethford-Blangero analysis on Meroitic affinities

Sample	Sample Size	r_{ii}	$\overline{V}_{Gw}$	$E(\overline{V}_{Gi})$	Residual ($\overline{V}_{Gw}$ - $E(\overline{V}_{Gi})$)
CGRP	17	0.0892	0.1360	0.1329	0.0031
PANG	7	0.1197	0.1786	0.1264	0.0522
SAYC	13	0.1756	0.1218	0.1268	-0.0050
KERM	219	0.0388	0.1714	0.1479	0.0235
XGRP	23	0.0623	0.1156	0.1442	-0.0286
MERO	246	0.0454	0.1120	0.1468	-0.0348
SEMC	12	0.0794	0.1227	0.1416	-0.0189
KULI	39	0.0591	0.1481	0.1447	0.0034
KULM	73	0.0463	0.1557	0.1467	0.0090
HABA	134	0.0573	0.1575	0.1450	0.0125

Fst=0.0773

Average $\overline{V}_{Gw}$ = .1419

Average residual=0.0016

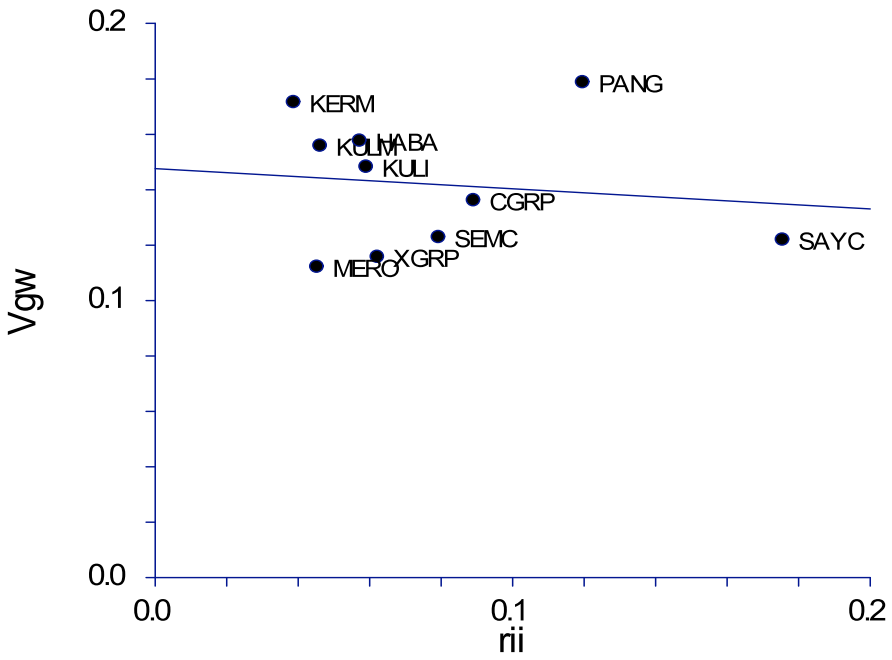

Figure 14. Regression plot of modified RB residuals for Meroitic affinities

of the Meroitic language; it was most likely developed by the Meroites during their hiatus from Nubia, rather than brought to the area by a foreign population.

The modified RB analysis, when interpreted in relation to F_{st}, revealed a high level of gene flow among the samples in this dataset. Further, all of the groups experienced similar levels of gene flow, as indicated by near average modified RB residuals. This is not surprising, considering the results in prior chapters of this dissertation; the Nubian population appears to be rather heterogeneous with all groups experiencing similar levels of gene flow.

The F_{st} indicates the level of variation among these samples is high and supports previous chapters' results where the Nubian samples contain a high level of variation. The manner in which the data plotted along the first axis in PCO also suggests heterogeneity within this dataset, as it depicts the samples as being widespread, yet similarly related. The scatterplot of the principal coordinates analysis speaks volumes about the *in situ* hypothesis and how it applies to the groups in this chapter; the samples were clustered loosely, with no outliers. Thus, the *in situ* hypothesis appears to be negated by the patterning in this analysis and among these groups. These results are consistent with previous chapters in this dissertation and furthers the trend of evidence for biological diffusion.

The next chapter functions similarly to this chapter; it tries to identify the biological affinities of the X-Group. Samples that predate and postdate the X-Group will be examined. In turn, interpretations of the archaeological material will be interpreted in relation to the results of the biological analyses.

Chapter 11

Who was the X-Group?

The X-Group was originally thought to have represented a combination of several populations, including the Blemmyes and Nobatae (Nielsen 1970). This population composition was evidenced in the artifacts the X-Group left behind (Nielsen 1970). Subsequent interpretations of artifacts have suggested that the X-Group were actually the next stage in Nubian cultural evolution, after the Meroites (Adams 1977). The more recent biological evidence has pointed towards biological continuity within the X-Group (Carlson 1976; Greene 1972; Irish 2005; Irish and Turner; 1990; Turner and Markowitz 1990; Van Gerven 1982; Van Gerven et al. 1977), which is consistent with artifact and mortuary continuity. However, the biological evidence was based on interpretations from cranial metrics and dental nonmetrics and did not include the scope or breadth of the samples in this study. Moreover, this study focuses on the two groups that immediately precede the appearance of the X-Group in the archaeological record (individuals from Kerma and the Meroites), as well as the time period succeeding the X-Group (Christian). This chapter will

provide a more in-depth analysis of the biological affinities of the X-Group in an effort to contribute to the biological evidence from other skeletal data.

Results

Nine variables were common among all of the Nubian samples (Kerma, X-Group, Meroitic, Semna South Christians, Kulubnarti island and mainland, and Hesa/Biga) and met the criteria outlined in previous chapters: asterionic bone, biasterionic suture, hypoglossal canal bridging, occipitomastoid bone, ossicle at lambda, parietal notch bone, supraorbital foramen, transverse zygomatic suture, and tympanic dehiscence. As evidenced in Table 22, the biological distances were smaller in this analysis than in the previous chapter, with only one biological distance exceeding 2.0 (Semna South Christians vs. Kerma). Moreover, the Kerma and Meroitic samples featured the smallest biological distance with a 0.85 value between them. The pooled tetrachoric matrix used to generate the biological distance matrix can be found in Appendix E.

The scatterplot produced by principal coordinates analysis (Fig. 15) revealed one large heterogeneous cluster inherent in this dataset. Two samples are potential outliers, however, and surprisingly the samples are the Semna South Christians and Hesa/Biga. Together, principal coordinates one and two account for 67% of the variation. While this is not a great amount of variation, it still depicts more than half of the variability to be found among these samples.

Table 22. Mahalanobis D^2 distances among Kerma – X-Group samples for examination of X-Group affinities

	KULI	KULM	HABA	KERM	XGRP	MERO	SEMC
KULI	0.00						
KULM	1.10	0.00					
HABA	1.71	1.65	0.00				
KERM	1.35	1.53	1.05	0.00			
XGRP	0.95	1.26	1.58	1.44	0.00		
MERO	1.27	1.44	1.11	0.85	1.33	0.00	
SEMC	1.70	1.42	2.03	1.69	1.57	1.60	0.00

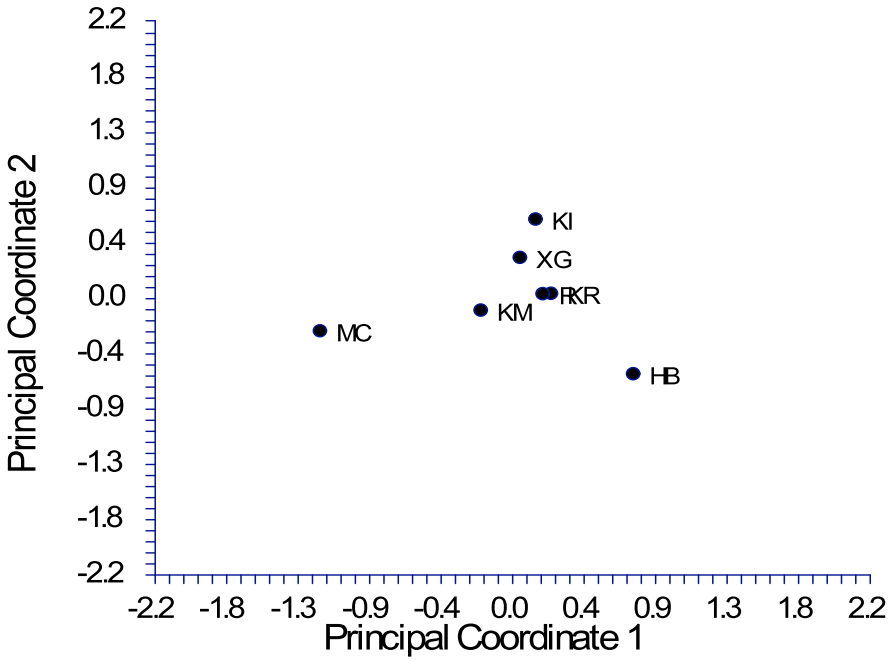

Figure 15. PCO plot of groups used to identify the biological affinities of the X-Group. The samples are designated by abbreviations: Kulubnarti island (KI) and mainland (KM), X-Group (XG), Kerma (KR), Meroitic (MR), Semna South Christians (MC), Hesa/Biga (HB).

Like previous chapters and analyses in this dissertation, no significant correlations were found between biological distance and space (r=-0.1043, p= 0.34 26), and biological distance and time (r= -0.0489, p= 0.4334). The scatterplot also reveals the lack of spatial and temporal clines.

In order to conduct the modified RB analysis, C, R, and covariance matrices were generated and can be found in Appendix E. The modified RB residuals were all around average (Table 23). The regression plot (Figure 16) supports this finding, as no samples were outliers to the regression line (which would have indicated a significantly higher or lower than average level of gene flow). Significantly, the F_{st} among these groups is quite low, lower than F_{st} information reported in previous chapters. However, it is greater than the level of documented non-admixed Irish, but it is still lower than the level of documented admixed Irish (Relethford and Blangero 1990).

Discussion

The X-Group falls neatly inline with other Nubian groups in the PCO scatterplot above. Specifically, they clustered with both Kulubnarti Christian samples, Kerma, and the Meroites. This grouping is not unexpected; the Kulubnarti samples represent the time period directly after the X-Group and the Meroites and Kerma are the two time periods directly preceding the X-Group. This relationship may be reflective of a continuing succession of biological evolution. However, the X-Group did not cluster with the Semna South Christians, who are from the same site (as also evidenced

Table 23. Modified Relethford-Blangero analysis on X-Group affinities

Sample	Sample Size	r_{ii}	$\overline{V}_{Gw}$	$E(\overline{V}_{Gi})$	Residual ($\overline{V}_{Gw} - E(\overline{V}_{Gi})$)
KERM	194	0.0243	0.1596	0.1343	0.0253
XGRP	21	0.0328	0.1156	0.1331	-0.0175
MERO	209	0.0277	0.1124	0.1338	-0.0214
SEMC	11	0.0579	0.1222	0.1296	-0.0074
KULI	30	0.0305	0.1406	0.1334	0.0072
KULM	65	0.0326	0.1251	0.1331	-0.0080
HABA	125	0.0439	0.1534	0.1316	0.0218

Fst= 0.0357

Average $\overline{V}_{Gw}$ = .1327

Average residual=0

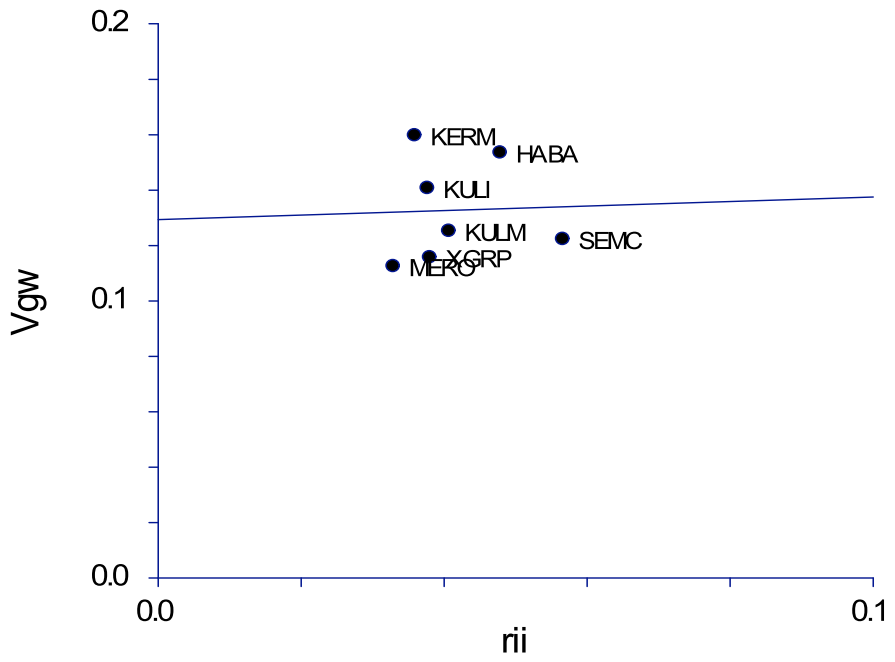

Figure 16. Regression plot of modified RB analysis for X-Group affinities

in non-significant Mantel tests). Thus, the X-Group seems to have evolved from the individuals from Kerma and the Meroities, and continued to evolve into the peoples represented in the Christian sample. Or, these results may actually be an artifact of sample size; the X-Group sample numbered less than 30 and was probably not completely representative of the actual group.

Despite the differences between the X-Group and the Semna South Christian sample, the X-Group biological distances indicate they are closely related to the rest of the Nubian samples. The modified RB residuals and regression plot, when interpreted in relation to the F_{st}, indicate that the moderately high level of variation among these groups is maintained across all the samples and no samples have experienced greater or less than average gene flow at this average level. When examining all of the statistical analyses as a whole, the results indicate that the X-Group were probably comprised of Nubians, although the high level of variation indicates they were subject to similar levels and composition of gene flow as the rest of the groups. The archaeological evidence agrees with this conclusion; artifacts from the Nobatae and Blemmyes have been uncovered during the X-Group (Nielsen 1970). Furthermore, the slight differences in X-Group mortuary practices (side chambers) may have been a result of the evolution of Nubian mortuary practices. However, the conclusions about the biological data are based solely on the dataset here, and may not be reflective of other X-Group samples and other comparisons of X-Group samples.

In regards to the *in situ* hypothesis, the results from the modified RB analysis indicate the genetic composition of the X-Group sample in this study is not entirely consistent with *in situ* biological evolution. The Mahalanobis and PCO results still portray a close affinity of the X-Group with other Nubian samples, while the high level of variation and the average

residuals indicate that higher levels of extraregional gene flow were maintained by the X-Group. This analysis again illustrates the Nubian population as a whole is rather heterogeneous.

Departing from the types of questions investigated so far in this dissertation, Chapter 12 will investigate change over time at one specific site, Semna South. Although the three samples investigated in Chapter 12 have been utilized in previous analyses in this dissertation, they have not been compared only to one another. Partitioning out these samples should highlight the biological relationships among the groups over their occupation at Semna South.

Chapter 12

Change Over Time: Semna South

Fortunately the 13 samples in this dissertation allowed for investigations into changes over time at a particular site. Semna South is a fort that was occupied by each of the successive groups: the Meroites, X-Group, and Christians. The three samples from the three succeeding time periods at Semna South should provide the means for a suitable analysis to look at the effects of time, while isolating for space (at least in theory), and for investigations into the heterogeneous nature of the Nubians, in general. Focusing on these three samples should also illuminate the already complex nature of the X-Group, in a very different fashion. This decomposition of the samples will also serve to explore the X-Group's biological affinities with the Meroites (who they are thought to have descended from) and the Christians (their supposed descendants) to deduce whether or not the X-Group truly was a product of in situ biological evolution.

Results

The Semna South samples yielded 8 acceptable traits for biological distance estimates: condylar canal patent, hypoglossal canal bridging, tympanic dehiscence, jugular foramen bridging, suprorbital foramen, transverse zygomatic suture, ossicle at lambda, and asterionic bone. The lowest biological distance occurs between the X-Group and Meroites, while the largest is found between the X-Group and Semna South Christians (Table 24). The tetrachoric matrix used to generate the biological distances can be found in Appendix F.

The first two principal coordinates were found to represent 100% of the variation. Figure 17 is the scatterplot produced from the plotting of these two factors. The X-Group and Meroites cluster closer together than either does to the Semna South Christians. As a result, a temporal cline is not readily apparent and cannot be confirmed by Mantel tests, which were run on temporal distances only because of lack of spatial distances (r=0.84212, p=0.5000). I have chosen to report Mantel test results here and it is important to realize that a significant p-value is not possible with this dataset; the maximum number of permutations is six, and thus the smallest possible p-value is 0.1667.

The C, R, and covariance matrices from population genetics statistics are located in Appendix F. The modified RB analysis indicates that the Semna South Christians are the most admixed of the three samples and the other two are roughly average (Table 25). The regression plot does not indicate the Semna South Christians are more admixed. This may be a product of the number of points on the graph; only three points were fit to the regression

Table 24. Mahalanobis D^2 distances among Semna South samples.

	XGRP	MERO	SEMC
XGRP	0.00		
MERO	0.95	0.00	
SEMC	2.01	1.92	0.00

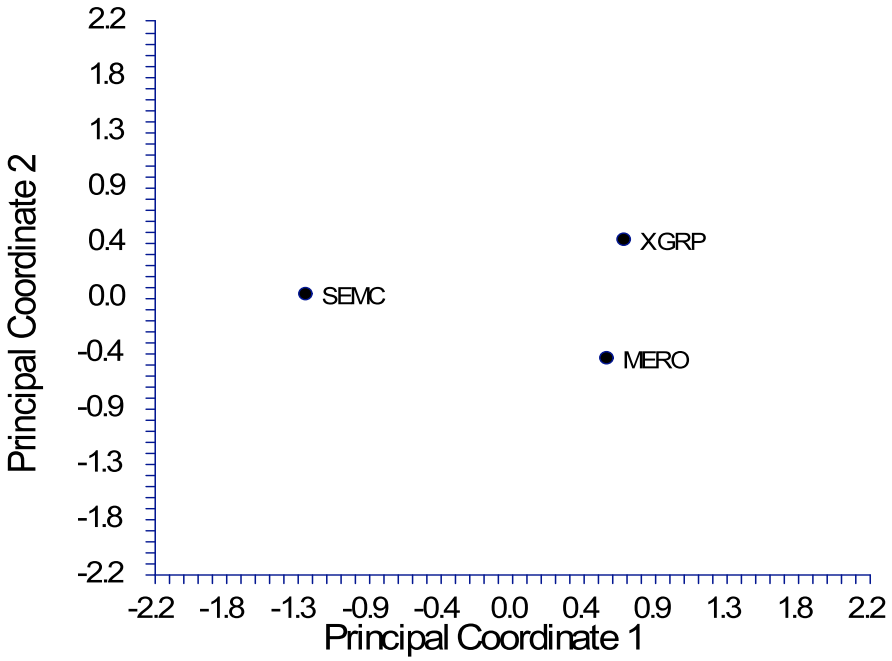

Figure 17. PCO plot of Semna South affinities

Table 25. Modified Relethford-Blangero analysis on Semna South samples

Sample	Sample Size	r_{ii}	$\overline{V}_{Gw}$	$E(\overline{V}_{Gi})$	Residual ($\overline{V}_{Gw}$ - $E(\overline{V}_{Gi})$)
XGRP	20	0.0268	0.1474	0.2098	-0.0624
MERO	196	0.0251	0.1337	0.2102	-0.0765
SEMC	11	0.0465	0.3444	0.2055	0.1389

Fst = .0328

Average $\overline{V}_{Gw}$ = .2085

Average residual = 0

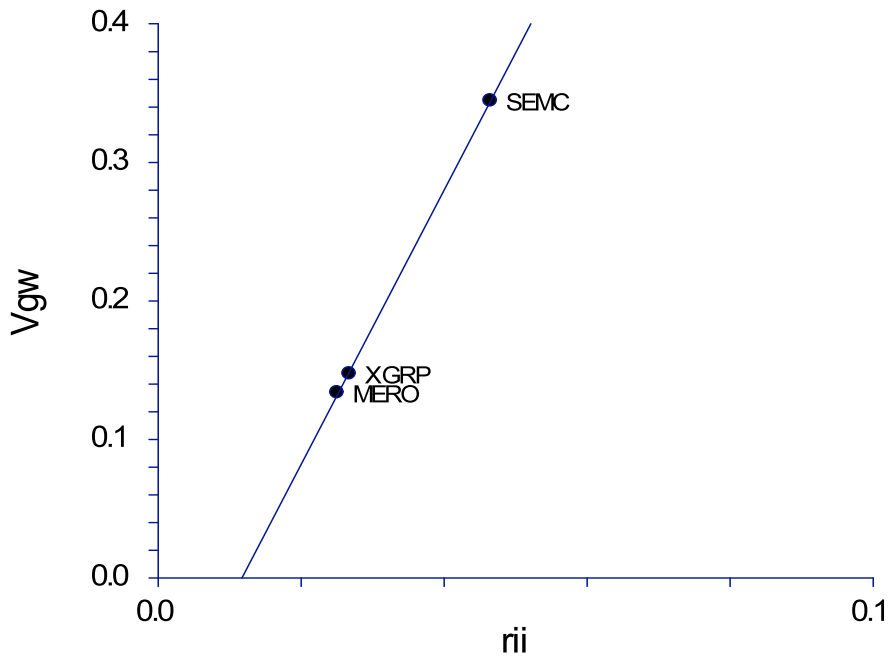

Figure 18. Regression plot of modified RB analysis on Semna South

line and the line was fit by the regression algorithm to cross all three points. The F_{st} is the smallest one calculated in this dissertation, indicating a lower rate of variation among these particular samples. However, like the previous chapter, it is still higher than documented admixed Irish.

Discussion

The results of this analysis indicate a relatively homogeneous change over time at Semna South. The biological distances demonstrate the relationship among the Semna South samples is more homogeneous than other population structure analyses in this dissertation. The lack of significant temporal associations shows the Semna South samples were not evolving in a linear fashion. Moreover, other forces (e.g. gene flow) were probably affecting the samples as well, specifically in the X-Group.

The modified RB analysis indicates the Meroites and X-Group had average gene flow, while the Semna South Christians had greater than average. The X-Group has been postulated to be comprised of foreign peoples (see Chapter 11), so it is surprising that the Semna South Christians experienced a higher rate of gene flow than the X-Group. The modified RB analysis, as well as the PCO and distance analyses, suggest that a smooth biological evolution among the three successive samples probably did not occur. Rather, these results are consistent with some gene flow from foreign populations occurring within the Semna South Christians.

Despite the indication that the Semna South Christians were not a homogeneous Nubian group, there is no evidence to suggest that the Semna South Christians were purely

made up of foreign peoples. In prior chapters, the Semna South Christians clustered well with other Nubian samples, indicating they were, for the most part, Nubian. However, the Nubian population also maintains a high level of heterogeneity, which is probably indicative of other Nubian samples having a similar composition to the Semna South Christians; the Nubian samples in this paper were also formed with genetic contribution from other populations that were similar to Semna South.

The population structure interpretations in this analysis must be tempered by sample size; two of the samples numbered less than 30. These small groups may have skewed the results. Elimination of these two samples, or avoidance of a Semna South analysis was not justified as archaeological populations are usually faced with the same issues. As with previous chapters, *in situ* evolution is not indicated by these results, which is particularly evident in the high rate of variation and the distinction of the Semna South Christians as an outlier in PCO and with a higher than average residual in the modified RB analysis.

The following chapter is structured close to this one; it also looks at change, but instead of across time, it will look at change across space. Similar methods will be used to investigate spatial influences. Moreover, the next chapter represents the final results chapter of this dissertation.

Chapter 13

Change Across Space: The Christians

Four of the thirteen samples featured in this dissertation have been dated to the Christian time period (Hesa/Biga, Kulubnarti island and mainland, and Semna South Christians). These sites are distributed across Lower Nubia and can allow great insight into the effects of space due to the short amount of time separating them. This chapter will focus on analyzing the effects across space while time is mostly controlled for.

Results

Nine traits were used to construct the distance matrix: hypoglossal canal bridging, condylar canal patent, tympanic dehiscence, jugular foramen bridging, suprorbital foramen, transverse zygomatic suture, ossicle and lambda, parietal notch bone, and asterionic bone. The results from the distance matrix (Table 26) indicate the Semna South Christians were the

Table 26. Mahalanobis D^2 distances among Christian samples.

	KULI	KULM	HABA	SEMC
KULI	0.00			
KULM	1.35	0.00		
HABA	1.61	1.77	0.00	
SEMC	2.25	2.26	2.12	0.00

most differentiated from the rest of the samples (similar to Chapter 12), as detectable in their high biological distance scores. Not unexpectedly the two Kulubnarti samples are the most related in the distance matrix. The tetrachoric correlations used to calculate these biological distances are tabulated in Appendix G.

Principal coordinates analysis detected the same pattern of relationships as in previous chapters; the Kulubnarti samples clustered together, while the Hesa/Biga and Semna South Christian samples clustered individually (see Fig. 19). The scatterplot was formed with 84% of the variation represented between the two axes (principal coordinates 1 and 2). There appears to be a spatial cline in the scatterplot (both Kulubnarti samples cluster together), but Mantel tests did not detect this pattern (r= -0.22149, p= 0.1351). Predictably, no temporal distributions were found in the data (r= 0.93360, p= 0.9576).

Modified RB analyses followed PCO and incorporated C, R, and covariance matrices for their calculations (Appendix G). All of the samples maintained average residuals across the modified RB analysis (Table 27, Fig. 20). The F_{st} among these samples is the second lowest in this dissertation, indicating the variation among these samples is relatively low. However, the F_{st} is still high in comparison to major population groups (Jorde 1980) and a documented non-admixed Irish sample (Relethford and Blangero 1990).

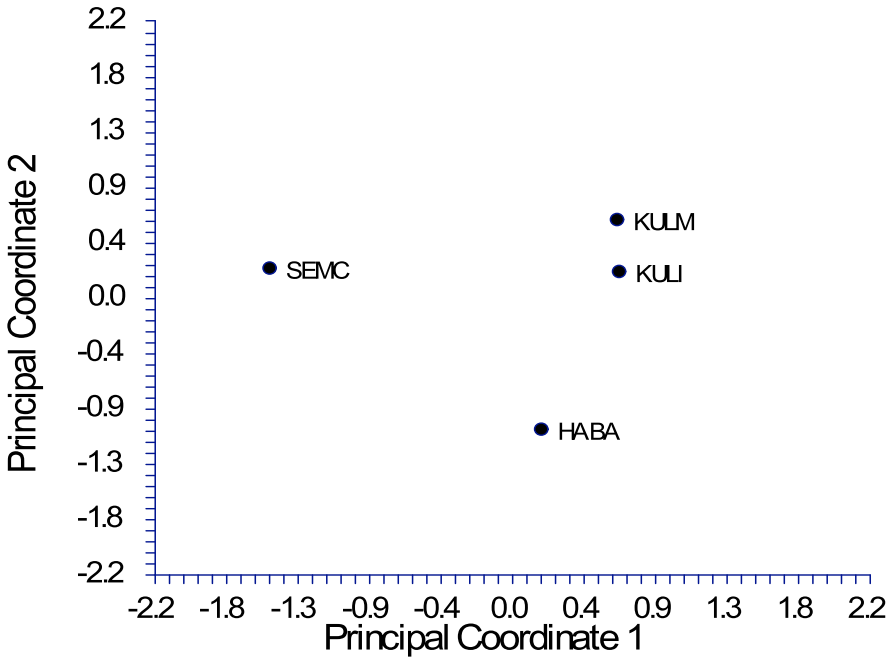

Figure 19. PCO plot of the relationships among Christian samples

Table 27. Modified Relethford-Blangero analysis on Christian samples

Sample	Sample Size	r_{ii}	$\overline{V}_{Gw}$	$E(\overline{V}_{Gi})$	Residual ($\overline{V}_{Gw}$ - $E(\overline{V}_{Gi})$)
SEMC	11	0.0506	0.1346	0.1433	-0.0087
KULI	29	0.0317	0.1481	0.1462	0.0019
KULM	63	0.0339	0.1363	0.1458	-0.0095
HABA	123	0.0355	0.1619	0.1456	0.0163

Fst=0.0379

Average $\overline{V}_{Gw}$ = 0.1452

Average residual=0

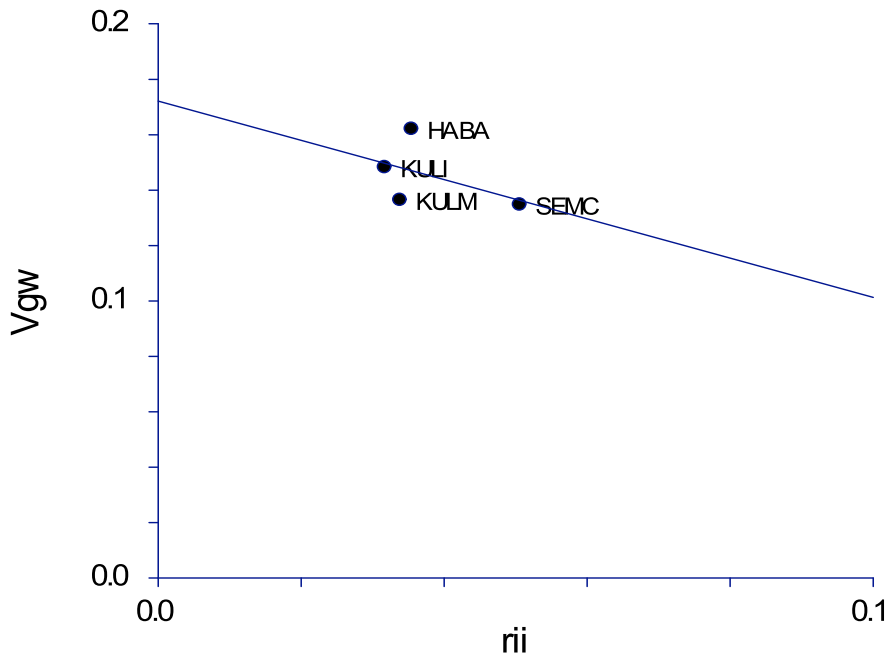

Figure 20. Regression plot of modified RB analysis on Christians

Discussion

Although the spatial patterning was not significant through Mantel tests, the PCO plot suggests that space was a factor in these results. Both Kulubnarti samples clustered together, while the Hesa/Biga and Semna South Christians formed their own clusters. The Semna South Christians were the most distinct among these samples, and this may be indicative of the introduction of foreign genes into this group (which is consistent with Chapter 12). Chapter 12 illustrated that biological continuity between the Semna South Christians and other Semna South groups was limited, suggesting some gene flow had occurred with the Christians. Genetic drift may be a significant factor in the results as the Kulubnarti Christians were the earliest inhabitants at Kulubnarti and did not have an opportunity to evolve from prior groups at that site. Furthermore, the two Kulubnarti samples clustered together, also implying spatial isolation with those two groups. Hesa/Biga's sites were occupied by Nubians through several time periods (Elliot Smith and Wood-Jones 1910) and their genetic composition may have been affected by random gentic drift, as well.

The modified RB analysis detected the same patterns as previous chapters; the residuals were all near average. When the modified RB analysis is framed with the F_{st} results, the average residuals indicate the maintenance of a higher rate of gene flow across the populations. The modified RB analysis, F_{st}, PCO, and biodistance results all agree that these samples were homogeneous relative to the other Nubian population structure analyses in this dissertation, but still heterogeneous overall. In regards to the *in situ* hypothesis, these samples don't support the precepts of its theoretical construct; the level of heterogeneity is not consistent with the *in situ* hypothesis. Furthermore, the biological distinctiveness of the

samples is reflective of alternate evolutionary factors at work. The Semna South Christians' biological distinctiveness could be a product of extraregional gene flow, while genetic drift and mutation may have been operating in Hesa/Biga, and the Kulubnarti samples.

The following chapter concludes this dissertation and summarizes the overall findings and results from the seven questions on Nubian population structure. The population structure conclusions will be placed into an overall context and in the *in situ* theoretical framework. An appraisal of the methodology is also covered.

Chapter 14

General Conclusions

The investigation into the *in situ* hypothesis in this dissertation highlights the complex nature of Nubian biological evolution. The current skeletal biological hypothesis regarding evolution in Nubians indicates they evolved in situ with little contribution from gene flow. Although a high level of variation is expected, as this is an interpopulation study, the amount of variation found exceeds the variability that should have been present. Thus, the results in this dissertation do not support in situ biological evolution; population replacement and gene flow seem likely throughout Nubian history. The results in this dissertation coincide well with the DNA results, which indicate bi-directional migrations and the presence of gene flow. Specifically, biological evolution in Nubians was mainly defined by high periods of gene flow, combined with lower levels (as evidenced in F_{st}). Despite the skeletal findings of genetic exchange between populations with Nubians, the conclusions here are not meant to detract from Nubian identity. Identity can be extrapolated from archaeological remains, in conjunction with skeletal analyses. This dissertation concludes that Nubian identity should

remain Nubian as gene flow probably served to diversify the Nubian population, rather than to destroy it.

The results of the last two chapters are particularly important evidence of biological diffusion. Chapter 12 reviewed biological changes over three time periods at one location and detected lower levels of variation than other analyses in this dissertation. Likewise, Chapter 13 investigated four contemporary samples from various locations along the Nile with similar results; drastically lower levels of variation than Chapters 7-11 were extracted. Both of these chapters show that variation at a specific site or a certain time was far less, implying that changes from extraregional gene flow were occurring over time and across Nubia (which is more inline with bidirectional migrations).

The key to understanding why the skeletal data has been mainly supportive of in situ biological evolution is partially in the manner in which the studies were constructed; each project either only focused on select groups that did not allow for detection of gene flow, or on the entire population (which obscures the results). As this dissertation demonstrated, when the Nubian population is broken down into a series of hypotheses coinciding with archaeological observations regarding possible gene flow opportunities, differing levels of gene flow can be detected. Examining the entire population at once masks the potential information that can be found.

The modified RB analysis was successful in detecting population structure in the Nubian population. The residuals were interpreted in relation to PCO, biodistances, and F_{st} and are not meant to be analyzed without those other statistical components; the modified RB analysis should be viewed as a tool to support and interpret the remaining statistical analyses. The main evidence that supports the utility in the modified RB analysis is that the results in

this dissertation coincide well with DNA research on the same subject. Furthermore, the results are also consistent with the archaeological evidence. This dissertation also partially puts Carson's (2006) narrow heritability estimates into its proper context; heritabilities will differ across environments and populations, and the results from one population in one environment are not necessarily reflective of how discrete traits behave. This dissertation effectively employed discrete traits and uncovered relationships that were consistent with other biological data with known heritability rates (e.g. DNA). Thus, this dissertation demonstrates discrete traits are still useful in biological distance and population genetics analyses.

The lack of spatial associations in this dissertation is highly unusual in these contexts. However, attributes of the Nile may be responsible for the lack of spatial correlations. The Nile is inhospitable to boats or sea-faring crafts as it is marked frequently by dangerous rapids. Moreover, the river is split into a series of cataracts, which are natural formations of rock that make the river nearly impassable at these points. Sheer cliffs also accompany the river, making traveling along the riverside difficult. It is a possibility that travel along the Nile did not occur on the riverbanks, nor did it take place along a straight line from point of origin to destination. Rather, people moving to destinations along the Nile may have followed it for short or long periods, and then traveled away from the river for a distance, and later returned to it.

This dissertation attempted to apply a population genetics approach to discrete trait analysis. Admittedly, this methodology can be improved upon (such as adding heritability estimates when suitable heritability estimates can be calculated) and as it stands it is a solid foundation for future research. Moreover, most of the results were produced from at least

one small sample size or a limited number of variables, and thus the interpretations may be biased by this issue. However, it does demonstrate how bioarchaeological studies that are plagued by small sample sizes can generate valuable and meaningful information from scant biological material. Furthermore, its similarity to DNA results suggests the methodology is detecting the genotype from the phenotypic data.

BIBLIOGRAPHY

Abramoff M, Magelhaes P, and Ram S. 2004. Image processing with ImageJ. Biophotonics International 11:36-42.
Adams W. 1968. Invasion, diffusion, evolution? Antiquity 42:194-215.
Adams W. 1977. Nubia: corridor to Africa. Princeton: Princeton University Press.
Adams W. 1984. The first colonial empire: Egypt in Nubia, 3200-1200 B.C. Comp Stud Soc Hist 26:36-71.
Adams W, Adams N, Van Gerven D, and Greene D. 1999. Kulubnarti III: the cemeteries. Oxford: The Sudan Archaeological Research Society.
Adams W, Van Gerven D, and Levy R. 1978. The Retreat From Migrationism. Ann Rev Anthropol 7:483-532.
Aguiar G, and Neves W. 1991. Postmarital residence and within-sex genetic diversity among the Urubu-Ka'apor Indians, Brazil Amazon. Hum Biol 63:467-488.
Alt K, Pichler S, Vach W, KlÌma B, Vlcek E, and Sedlmeier J. 1997. Twenty-five thousand-year-old triple burial from DolnÌ Vestonice: An ice-age family? Am J Phys Anthropol 102:123-131.
Anthony D. 1990. Migration in archeology: the baby and the bathwater. Am Anthropol 92:895-914.
Arriaza B, Merbs C, and Rothschild B. 1993. Diffuse idiopathic skeletal hyperostosis in Meroitic Nubians from Semna South, Sudan. Am J Phys Anthropol 92:243-248.
Ascenzi A, and Balistreri P. 1975. Aural exostoses in a Roman skull excavated at the "Baths of the Swimmer" in the ancient town of Ostia. J Hum Evol 4:579-584.
Batrawi A. 1945. The racial history of Egypt and Nubia. The Journal of the Royal Anthropological Institute of Great Britain and Ireland 75:81-101.
Batrawi A. 1946. The racial history of Egypt and Nubia: Part II. The racial relationships of the ancient and modern populations of Egypt and Nubia. The Journal of the Royal Anthropological Institute of Great Britain and Ireland 76:131-156.
Bedrick E, Lapidus J, and Powell J. 2000. Estimating the Mahalanobis distance from mixed continuous and discrete data. Biometrics 56:394-401.
Berry A. 1975. Factors affecting the incidence of non-metrical skeletal variants. J Anat 120:519-535.
Berry A, and Berry R. 1967. Epigenetic variation in the human cranium. J Anat 101:361-379.
Berry A, and Berry R. 1972. Origins and relationships of the ancient Egyptians. Based on a study of non-metrical variations in the skull. J Hum Evol 1:199-208.
Berry A, Berry R, and Ucko P. 1967. Genetical change in Egypt. Man 2:551-568.
Bietak M, and Bauer K. 1966. Ausgrabungen in Sayala-nubien 1961-1965: Denkmäler der C-gruppe und der Pan-gräber-kultur. Wien: Österreichische Akademie der Wissenschaften, Philosophisch-Historische Klasse, Denkschriften 92 = Berichte des Österreichischen Nationalkomitees der UNESCO-Aktion für die Rettung der Nubischen Altertümer 3.
Birkby W. 1982. Biosocial interpretations from cranial nonmetric traits of Grasshopper Pueblo skeletal remains. In: Longacre W, Holbrook S, Graves M, and Agenbroad L, editors. Multidisciplinary research at Grasshopper Pueblo, Arizona. Tucson: University of Arizona. p 36-41.

Blackman A. 1937. Preliminary Report on the Excavations at Sesebi, Northern Province, Anglo-Egyptian Sudan, 1936-37. J Egypt Archaeol 23:145-151.
Blangero J, and Williams-Blangero S. 1991. Estimating biological distances from dichotomous threshold traits. Am J Phys Anthropol Suppl 12:51-52.
Bondioli L, Corruccini R, and Macchiarelli R. 1986. Familial segregation in the iron age community of Alfedena, Abruzzo, Italy, based on osteodental trait analysis. Am J Phys Anthropol 71:393-400.
Buikstra J. 1977. Biocultural dimensions of archeological study: a regional perspective. In: Blakely R, editor. Biocultural adaptation in prehistoric America. Athens,: University of Georgia Press. p 67-84.
Buikstra J. 1980. Epigenetic Distance: A Study of Biological Variability in the Lower Illinois River Region. In: Browman D, editor. Early Native Americans: Prehistoric Demography, Economy, and Technology. New York: Mouton Publishers. p 271-299.
Buikstra J, and Ubelaker D. 1994. Standards for data collection from human skeletal remains. Fayetteville: Arkansas Archaeological Survey.
Buzon M. 2006. Health of the non-elites at Tombos: Nutritional and disease stress in New Kingdom Nubia. Am J Phys Anthropol 130:26-37.
Byrd J, and Jantz R. 1994. Osteological Evidence for Distinct Social Groups at the Leavenworth Site. In: Owsley D, and Jantz R, editors. Skeletal Biology in the Great Plains. Washington: Smithsonian Institution Press. p 203-218.
Calcagno J. 1986. Dental reduction in post-pleistocene Nubia. Am J Phys Anthropol 70:349-363.
Carlson D. 1976. Temporal variation in prehistoric Nubian crania. Am J Phys Anthropol 45:467-484.
Carlson D, and Van Gerven D. 1979. Diffusion, Biological Determinism, and Biocultural Adaptation in the Nubian Corridor. Am Anthropol 81:561-580.
Carson E. 2006. Maximum likelihood variance components analysis of heritabilities of cranial nonmetric traits. Hum Biol 131:169-180.
Cheverud J. 1981. Variation in highly and lowly heritable morphological traits among social groups of Rhesus Macaques (Macaca mulatta) on Cayo Santiago. Evolution 35:75-83.
Cheverud J, and Buikstra J. 1981a. Quantitative genetics of skeletal nonmetric traits in the rhesus macaques on Cayo Santiago. I. Single trait heritabilities. Am J Phys Anthropol 54:43-49.
Cheverud J, and Buikstra J. 1981b. Quantitative genetics of skeletal nonmetric traits in the rhesus macaques on Cayo Santiago. II. Phenotypic, genetic, and environmental correlations between traits. Am J Phys Anthropol 54:51-58.
Cheverud J, and Buikstra J. 1982. Quantitative genetics of skeletal nonmetric traits in the rhesus macaques of Cayo Santiago. III. Relative heritability of skeletal nonmetric and metric traits. Am J Phys Anthropol 59:151-155.
Christensen A. 1998. Colonization and Microevolution in Formative Oaxaca, Mexico. World Archaeol 30:262-285.
Collett M. 1933. A Study of Twelfth and Thirteenth Dynasty Skulls from Kerma (Nubia). Biometrika 25:254-284.
Conner M. 1990. Population structure and skeletal variation in the Late Woodland of west-central Illinois. Am J Phys Anthropol 82:31-43.

Connor J, and Evans D. 1982. Genetic aspects of fibrodysplasia ossificans progressiva. J Med Genet 19(1):35-39.
Corruccini R. 1972. The biological relationships of some prehistoric and historic pueblo populations. Am J Phys Anthropol 37:373-388.
Corruccini R. 1974. An examination of the meaning of cranial discrete traits for human skeletal biological studies. Am J Phys Anthropol 40:425-445.
Corruccini R. 1976. The interaction between nonmetric and metric cranial variation. Am J Phys Anthropol 44:285-293.
Corruccini R, Handler J, Mutaw R, and Lange F. 1982. Osteology of a slave burial population from Barbados, West Indies. Am J Phys Anthropol 59:443-459.
Devor E. 1987. Transmission of human craniofacial dimensions. J Cran Genet Dev Bio 7:95-106.
Donlon D. 2000. The value of infracranial nonmetric variation in studies of modern *Homo sapiens*: An Australian focus. Amer J Phys Anthrop 113:349-368.
Droessler J. 1981. Craniometry and biological distance : biocultural continuity and change at the Late-Woodland - Mississippian interface. Evanston, Ill.: Center for American Archeology at Northwestern University. xvi, 253 p.
Edwards D. 2004. The Nubian past. London: Routledge Taylor & Francis Group.
El-Najjar M. 1978. Southwestern physical anthropology: Do the cultural and biological parameters correspond? Am J Phys Anthropol 48:151-157.
El-Najjar M, and Dawson G. 1977. The effect of artificial cranial deformation on the incidence of wormian bones in the lambdoidal suture. Am J Phys Anthropol 46:155-160.
Elliot Smith G, and Wood-Jones F. 1910. The archaeological survey of Nubia: report for 1907-1908, volume II, report on human remains. Cairo: National Printing Department.
Fairman H. 1938. Preliminary Report on the Excavations at Sesebi (Sudla) and 'Amarah West, Anglo-Egyptian Sudan, 1937-8. J Egypt Archaeol 24:151-156.
Finnegan M, and Rubison R. 1980. The assessment and analysis of interobserver error in non-metric cranial studies. Am J Phys Anthropol 52:226.
Fox C. 1997. mtDNA analysis in ancient Nubians supports the existence of gene flow between sub-Sahara and North Africa in the Nile Valley. Ann Hum Biol 24:217-227.
Fox C, Gonz·lez MartÌn A, and Vives Civit S. 1996. Cranial variation in the Iberian Peninsula and the Balearic Islands: Inferences about the history of the population. Am J Phys Anthropol 99:413-428.
Fraser F. 1998. Some Underlooked Properties of the Multifactorial/Threshold Model. The American Journal of Human Genetics 62(5):1262-1265.
Frayer D. 1988. Auditory exostoses and evidence for fishing at Vlasac. Curr Anthropol 29:346-349.
Fukumine T, Hanihara T, Nishime A, and Ishida H. 2004. Nonmetric cranial variation of early modern human skeletal remains from Kumejima, Okinawa and the peopling of the Ryukyu Islands. Anthropol Sci 114:141-151.
Godde K. 2004. A measure of biological distance in Nubians: a look at intrapopulation variation. Sacramento: California State University, Sacramento.

Godde K. 2006. Auditory exostoses found in Meroitic Nubians at Semna South: implications for subsistence strategies and/or social practices. Am J Phys Anthropol Suppl 129:92.
Godde K. 2009a. Who were the Meroites? A biological investigation into the Nubian post-hiatus group. Intl J Osteoarchaeol in press.
Godde K. 2009b. An examination of proposed causes of auditory exostoses. Intl J Osteoarchaeol in press.
Gottlieb K. 1978. Artificial cranial deformation and the increased complexity of the lambdoid suture. Am J Phys Anthropol 48:213-214.
Gower J. 1966. Some distance properties of latent root and vector methods used in multivariate analysis. Biometrika 53:325-338.
Green R, Myers Suchey J, and Gokhale D. 1979. The statistical treatment of correlated bilateral traits in the analysis of cranial material. Am J Phys Anthropol 50:629-634.
Greene D. 1972. Dental anthropology of early Egypt and Nubia. J Hum Evol 1:315-324.
Greene D. 1982. Discrete dental variations and biological distances of Nubian populations. Am J Phys Anthropol 58:75-79.
Greene D, Ewing G, and Armelagos G. 1967. Dentition of a Mesolithic population from Wadi Halfa, Sudan. Am J Phys Anthropol 27:41-55.
Grüneberg H. 1952. Genetical studies on the skeleton of the mouse. IV. Quasi-continuous variations J Genet 51:95-114.
Gualdi-Russo E, Tasca M, and Brasili P. 1999. Scoring of nonmetric cranial traits: a methodological approach. J Anat 195:543-550.
HallgrÌmsson B, Donnabháin B, Blom D, Lozada M, and Willmore K. 2005. Why are rare traits unilaterally expressed?: Trait frequency and unilateral expression for cranial nonmetric traits in humans. Am J Phys Anthropol 128:14-25.
Haneji K, Hanihara T, Sunakawa H, Toma T, and Ishida H. 2007. Non-metric dental variation of Sakishima Islanders, Okinawa, Japan: a comparative study among Sakishima and neighboring populations. Anthropol Sci 115:35-45.
Hanihara T. 2008. Morphological variation of major human populations based on nonmetric dental traits. Amer J Phys Anthrop 136(2):169-182.
Hanihara T, Ishida H, and Dodo Y. 2003. Characterization of biological diversity through analysis of discrete cranial traits. Am J Phys Anthropol 121:241-251.
Harpending H, and Jenkins T. 1973. Genetic distance among southern African populations. In: Crawford M, and Workman P, editors. Methods and Theories of Population Genetics. Albuquerque: University of New Mexico Press. p 177-199.
Harpending H, and Ward R. 1982. Chemical systematics and human evolution. In: Nitecki M, editor. Biochemical aspects of evolutionary biology : proceedings of the Fourth Annual Spring Systematics Symposium, held at the Field Museum of Natural History, Chicago, Illinois, May 9, 1981. Chicago: University of Chicago Press. p 213-256.
Hassan F. 1986. Chronology of the Khartoum 'Mesolithic' and 'Neolithic' and related sites in the Sudan: statistical analysis and comparisons with Egypt. Afr Archaeol Rev 4:83-102.
Hauser D, and De Stefano G. 1989. Epigenetic variants of the human skull. Stuttgart: E. Scheizerbart'sche Verlagsbuchhandlung.
Hemphill B. 1999. Biological affinities and adaptations of Bronze Age Bactrians: IV. A craniometric investigation of Bactrian origins. Am J Phys Anthropol 108:173-192.

Herrmann N. 2002. Biological affinities of archaic period populations from west-central Kentucky and Tennessee. Knoxville: University of Tennessee, Knoxville.
Hertzog K. 1968. Association between discontinuous cranial traits. Am J Phys Anthropol 29:397-403.
Hintze J. 2006. NCSS, PASS and GESS. Kaysville: NCSS.
Howells W, Angel J, Birdsell J, Brues A, Capell A, Coon C, Giles E, Hiernaux J, Karve I, Lundman B and others. 1966. Population distances: Biological, linguistic, geographical, and environmental [and comments and reply]. Curr Anthropol 7:531-540.
Humphrey L, and Scheuer L. 2006. Age of closure of the foramen of Huschke: an osteological study. Int J Osteoarchaeol 16:47-60.
Hutchinson D, Denise C, Daniel H, and Kalmus G. 1997. A reevaluation of the cold water etiology of external auditory exostoses. Am J Phys Anthropol 103:417-422.
Irish J. 1998. Diachronic and synchronic dental trait affinities of Late and Post-Pleistocene peoples from North Africa. Homo 49:138-155.
Irish J. 2000. The Iberomaurusian enigma: North African progenitor or dead end? J Hum Evol 39:393-410.
Irish J. 2005. Population continuity vs. discontinuity revisited: Dental affinities among late Paleolithic through Christian-era Nubians. Amer J Phys Anthrop 128:520-535.
Irish J, and Konigsberg L. 2007. The ancient inhabitants of Jebel Moya redux: measures of population affinity based on dental morphology. Int J Osteoarchaeol 17:138-156.
Irish J, and Turner CI. 1990. West African dental affinity of late Pleistocene Nubians: peopling of the Eurafrican-South Asian triangle II. Homo 41:42-53.
Ishida H, and Dodo Y. 1990. Interobserver error in scoring nonmetric cranial traits. J Anthrop Soc Nippon 98:403-409.
Ishida H, and Dodo Y. 1997. Cranial variation in prehistoric human skeletal remains from the Marianas. Amer J Phys Anthrop 104:399-410.
Jantz R. 1970. Change and variation in skeletal populations of Arikara Indians. Lawrence: University of Kansas.
Jantz R. 1973. Microevolutionary change in Arikara crania: A multivariate analysis. Am J Phys Anthropol 38:15-26.
Jantz R, and Owsley D. 2001. Variation among early North American Crania. Am J Phys Anthropol 114:146-155.
Johnson A, and Lovell N. 1995. Dental morphological evidence for biological continuity between A-Group and C-Group periods in Lower Nubia. Intl J Osteoarchaeol 5:368-376.
Jorde L. 1980. The genetic structure of subdivided human populations: A review. In: Mielke J, and Crawford M, editors. Current developments in anthropological genetics New York: Plenum Press. p 135-208.
Kennedy G. 1986. The relationship between auditory exostoses and cold water: A latitudinal analysis. Am J Phys Anthropol 71:401-415.
Kilgore L, Jurmain R, and Van Gerven D. 1997. Palaeoepidemiological patterns of trauma in a medieval Nubian skeletal population. Int J Osteoarchaeol 7:103-114.
Kimura M, and Weiss G. 1964. The stepping-stone model of population structure and the decrease of genetic correlation with distance. Genetics 49:561-576.

Klaric I. 2000. Population structure of the rural communities on the island of Krk (Croatia): A comparison of genetic, cultural, and geographic data. Am J Hum Biol 12:509-525.
Komesu A, Hanihara T, Amano T, Ono H, Yoneda M, Dodo Y, Fukumine T, and Ishida H. 2008. Nonmetric cranial variation in human skeletal remains associated with Okhotsk culture. Anthropol Sci 116:33-47.
Konigsberg L. 1987. Population genetic models for interpreting prehistoric intra-cemetery biological variation: Ph.D. Dissertation, Northwestern University.
Konigsberg L. 1988. Migration models of prehistoric postmarital residence. Am J Phys Anthropol 77:471-482.
Konigsberg L. 1990. Analysis of Prehistoric biological variation under a model of isolation by geographic and temporal distance. Hum Biol 62:49-70.
Konigsberg L. 2006. A post-Neumann history of biological and genetic distance studies in bioarchaeology. In: Buikstra J, and Beck L, editors. Bioarchaeology: the contextual analysis of human remains. Amsterdam: Elsevier. p 263-275.
Konigsberg L, and Buikstra J. 1995. Regional approaches to the investigation of past human biocultural structure. In: Beck L, editor. Regional approaches to mortuary analysis. New York: Plenum Press. p 191-219.
Konigsberg L, Kohn L, and Cheverud J. 1993. Cranial deformation and nonmetric trait variation. Am J Phys Anthropol 90:35-48.
Korey K. 1980. The incidence of bilateral nonmetric skeletal traits: A reanalysis of sampling procedures. Am J Phys Anthropol 53:19-23.
Krings M, Salem A, Bauer K, Geisert H, Malek A, Chaix L, Simon C, Welsby D, Di Rienzo A, Utermann G and others. 1999. mtDNA analysis of Nile River Valley populations: A genetic corridor or a barrier to migration? Am J Hum Genet 64:1166-1176.
Lane R, and Sublett A. 1972. Osteology of social organization: Residence pattern. Am Antiquity 37:186-201.
Lisowski F. 1952. A report on the skulls from excavations at Sesebi (Anglo-Egyptian Sudan). International Congress of Anthropological Ethnological Sciences.
Lundy J. 1980. The mylohyoid bridge in the Khoisan of Southern Africa and its unsuitability as a Mongoloid genetic marker. Am J Phys Anthropol 53:43-48.
Mackey J. 1977. A multivariate, osteological approach to Towa culture history. Am J Phys Anthropol 46:477-482.
Malécot G. 1948. Les Mathématiques de I'hérédité. Paris: Masson.
Manzi G, Sperduti A, and Passarello P. 1991. Behavior-induced auditory exostoses in imperial Roman society: Evidence from coeval urban and rural communities near Rome. Am J Phys Anthropol 85:253-260.
Mateus Pereira L, Socorro A, Fernandez I, Masleh M, Vidal D, Bianchi N, Bonatto S, Salzano F, and Herrera R. 2005. Phylogenetic information in polymorphic L1 and Alu insertions from East Asians and Native American populations. Am J Phys Anthropol 128:171-184.
Matsumura H, and Hudson M. 2005. Dental perspectives on the population history of Southeast Asia. Am J Phys Anthropol 127:182-209.
McGrath J, Cheverud J, and Buikstra J. 1984. Genetic correlations between sides and heritability of asymmetry for nonmetric traits in rhesus macaques on Cayo Santiago. Am J Phys Anthropol 64:401-411.

McKeown A. 2000. Investigating variation among Arikara crania using geometric morphometry: University of Tennessee, Knoxville.
Molto J. 1979. The assessment and meaning of intraobserver error in population studies based on discontinuous cranial traits. Am J Phys Anthropol 51:333-344.
Morton N. 1975. Kinship, information and biological distance. Theor Popul Biol 7:246-255.
Mouri T. 1976. A study of non-metrical cranial variants of the modern Japanese in the Kinki district. J Anthropol Soc Nippon 84:191-203.
Mukherjee R, Rao C, and Trevor J. 1955. The ancient inhabitants of Jebel Moya. Cambridge: Cambridge University Press.
Nei M. 1972. Genetic Distance between Populations. Am Nat 106:283-292.
Neves W, and Pucciarelli H. 1991. Morphological affinities of the first Americans: an exploratory analysis based on early South American human remains. J Hum Evol 21:261-273.
Nielsen O. 1970. Human remains: metrical and non-metrical anatomical variations. Säve-Söderbergh T, editor. Denmark: The Scandinavian Joint Expedition to Sudanese Nubia.
Nordström H-A. 1972. Neolithic and A-Group sites. Säve-Söderbergh T, editor. Upsala: Scandinavian University Press.
Nystrom K. 2006. Late Chachapoya population structure prior to Inka conquest. Am J Phys Anthropol 131:334-342.
Okumura M, Boyadjian C, and Eggers S. 2007. Auditory exostoses as an aquatic activity marker: A comparison of coastal and inland skeletal remains from tropical and subtropical regions of Brazil. Am J Phys Anthropol 132:558-567.
Ossenberg N. 1970. The influence of artificial cranial deformation on discontinuous morphological traits. Am J Phys Anthropol 33:357-371.
Ossenberg N. 1977. Congruence of distance matrices based on cranial discrete traits, cranial measurements, and linguistic-geographic criteria in five Alaskan populations. Am J Phys Anthropol 47:93-98.
Ossenberg N. 1981. An argument for the use of total side frequencies of bilateral nonmetric skeletal traits in population distance analysis: The regression of symmetry on incidence. Am J Phys Anthropol 54:471-479.
Perizonius W. 1979. Non-metric cranial traits: Sex difference and age dependence. J Hum Evol 8:679-684.
Prowse T, and Lovell N. 1995. Biological continuity between the A- and C-groups in lower Nubia: Evidence from cranial non-metric traits. Int J Osteoarchaeol 5:103-114.
Prowse T, and Lovell N. 1996. Concordance of cranial and dental morphological traits and evidence for endogamy in ancient Egypt. Am J Phys Anthropol 101:237-246.
R Development Core Team. 2005. R: A language and environment for statistical computing. Vienna: R Foundation for Statistical Computing.
Reichs K. 1984. Pearls or people: A biometric analysis of interregional exchange during Hopewell times. Cent Issues Anthropol 5:47-65.
Reisner G. 1910. The archaeological survey of Nubia. Report for 1907-8 Vol I: archaeological report. Cairo: Survey Department Cairo.

Reisner G. 1919. Outline of the ancient history of the Sudan, Part IV: the first kingdom of Ethiopia. Its conquest of Egypt, and its development into a kingdom of the Sudan 1100-250 B.C. . Sudan Notes and Records 2:35-67, 237-254.
Relethford J. 1999. Models, predictions, and the fossil record of modern human origins. Evol Anth 8:7-10.
Relethford J, and Blangero J. 1990. Detection of differential gene flow from patterns of quantitative variation. Hum Biol 62:5-25.
Relethford J, and Blangero J. 2005. RMET. Help File.
Relethford J, Crawford M, and Blangero J. 1997. Genetic drift and gene flow in post-famine Ireland. Hum Biol 69:443-465.
Relethford J, and Harpending H. 1994. Craniometric variation, genetic theory, and modern human origins. Am J Phys Anthropol 95:249-270.
Relethford J, and Lees F. 1982. The use of quantitative traits in the study of human population structure. Yrbk Phys Anthropol 25:113-132.
Relethford JH. 1996. Genetic drift can obscure population history: problem and solution. Hum Biol 68:29-44.
Richtsmeier J, Cheverud J, and Buikstra J. 1984. The relationship between cranial metric and nonmetric traits in the rhesus macaques from Cayo Santiago. Am J Phys Anthropol 64:213-222.
Richtsmeier J, and McGrath J. 1986. Quantitative genetics of cranial nonmetric traits in randombred mice: Heritability and etiology. Am J Phys Anthropol 69:51-58.
Rightmire G. 1970. Bushman, Hottentot and South African Negro crania studied by distance and discrimination. Am J Phys Anthropol 33:169-195.
Rightmire G. 1972. Cranial measurements and discrete traits compared in distance studies of African Negro skulls. Am J Phys Anthropol 44:263-276.
Rothhammer F, and Silva C. 1990. Craniometrical variation among South American prehistoric populations: Climatic, altitudinal, chronological, and geographic contributions. Am J Phys Anthropol 82:9-17.
Rudan P, Simic D, Smolejcic-Naran N, Bennett L, Janicijevic B, Jovanovic V, Lethbridge M, Milicic J, Roberts D, Sujoldzic A and others. 1987. Isolation by distance in Middle Dalmatia†-†Yugoslavia. Am J Phys Anthropol 74:417-426.
Saunders S. 1989. Nonmetric skeletal variation. In: Isçan M, and Kennedy K, editors. Reconstruction of life from the skeleton. New York: Alan R. Liss. p 95-108.
Saunders S, and Popovich F. 1978. A family study of two skeletal variants: Atlas bridging and clinoid bridging. Am J Phys Anthropol 49:193-203.
Sawyer D, Gianfortune V, Kiely M, and Allison M. 1990. Mylohyoid and jugular foramen bridging in Pre-Columbian Chileans. Am J Phys Anthropol 82:179-181.
Sawyer D, and Kiely M. 1987. Jugular foramen and mylohyoid bridging in an Asian Indian population. Am J Phys Anthropol 72:473-477.
Saxe A. 1971. Social dimensions of mortuary practices in a Mesolithic population from Wadi Halfa, Sudan. Am Antiquity 36:39-57.
Scherer A. 2007. Population structure of the classic period Maya. Am J Phys Anthropol 132:367-380.
Schillaci M, and Stojanowski C. 2003. Postmarital residence and biological variation at Pueblo Bonito. Am J Phys Anthropol 120:1-15.

Schillaci M, and Stojanowski C. 2005. Craniometric variation and population history of the prehistoric Tewa. Am J Phys Anthropol 126:404-412.
Sciulli P. 1990. Cranial metric and discrete trait variation and biological differentiation in the terminal Late Archaic of Ohio: The Duff site cemetery. Am J Phys Anthropol 82:19-29.
Sciulli P, and Schneider K. 1985. Cranial variation in the terminal Late Archaic of Ohio. Am J Phys Anthropol 66:429-443.
Scuilli P, and Mahaney M. 1986. Evidence of local biological continuity for an Ohio Hopewell complex population. Midcontinental J Archaeol 11:181-199.
Sellevold J. 1980. Mandibular torus morphology. Am J Phys Anthropol 53:569-572.
Shimada I, Shinoda K, Farnum J, Corruccini R, and Watanabe H. 2004. An integrated analysis of Pre-Hispanic mortuary practices: A middle Sican case study. Curr Anthropol 45:369-402.
Sjφvold T. 1977. Non-metrical divergence between skeletal populations. Ossa 4:1-133.
Sjφvold T. 1984. A report on the heritability of some cranial measurements and non-metric traits. In: Vark G, and Howells W, editors. Multivariate statistical methods in physical anthropology Dordrecht: Reidel. p 223-246.
Smith H. 1966. The Nubian B-Group. Kush 14:69-124.
Smouse PE, Long JC, and Sokal RR. 1986. Multiple regression and correlation extensions of the Mantel test of matrix correspondence. Syst Zool 35:627-632.
Soliani L, Lucchetti E, De Iasio S, and Conterio F. 1985. Some effects of recent migrations on similarity between biological structures of regional populations in Italy. J Hum Evol 14:709-716.
Spence M. 1974. Residential practices and the distribution of skeletal traits in Teotihuacan, Mexico. Man 9:262-273.
Standen V, Arriaza B, and Santoro C. 1997. External auditory exostosis in prehistoric Chilean populations: A test of the cold water hypothesis. Am J Phys Anthropol 103:119-129.
Steadman D. 2001. Mississippians in motion? A population genetic analysis of interregional gene flow in west-central Illinois. Am J Phys Anthropol 114:61-73.
Stefan V. 1999. Craniometric variation and homogeneity in prehistoric/protohistoric Rapa Nui (Easter Island) regional populations. Am J Phys Anthropol 110:407-419.
Stefan V, and Chapman P. 2003. Cranial variation in the Marquesas Islands. Am J Phys Anthropol 121:319-331.
Strouhal E, and Jungwirth J. 1979. Paleogenetics of the late Roman-early Byzantine cemeteries at Sayala, Egyptian Nubia. J Hum Evol 8:699-703.
Strouhal E, and Jungwirth J. 1980. Die anthropologische Untersuchung der C-Gruppen- und Pan-Graber-Skelette aus Sayala, Agyptisch - Nubien. Wien: Verlag der Österreichischen Akademie der Wissenschaften.
Tatarek N, and Sciulli P. 2000. Comparison of population structure in Ohio's late archaic and late prehistoric periods. Am J Phys Anthropol 112:363-376.
Trigger B. 1976. Nubia under the pharoahs. Boulder: Westview Press.
Trinkaus E. 1978. Bilateral asymmetry of human skeletal non-metric traits. Amer J Phys Anthrop 49(3):315-318.

Turner B, Edwards J, Quinn E, Kingston J, and Van Gerven D. 2007. Age-related variation in isotopic indicators of diet at medieval Kulubnarti, Sudanese Nubia. Int J Osteoarchaeol 17:1-25.
Turner CI, and Markowitz M. 1990. Dental discontinuity between Late Pleistocene and recent Nubians. I. Peopling of the Eurafrican-South Asian triangle. Homo 41:32-41.
Tyrrell A. 2000. Skeletal non-metric traits and the assessment of inter- and intra-population diversity: past problems and future potential. In: Cox M, editor. Human osteology in archaeology and forensic science. London: Greenwich Medical Media. p 289-306.
Van Gerven D. 1982. The contribution of time and local geography to craniofacial variation in Nubia's Batn el Hajar. Am J Phys Anthropol 59:307-316.
Van Gerven D, Armelagos G, and Rohr A. 1977. Continuity and change in cranial morphology of three Nubian archaeological populations. Man 2:270-277.
Van Gerven D, Carlson D, and Armelagos G. 1973. Racial history and bio-cultural adaptation of Nubian archaeological populations. J Afr Hist 14:555-564.
Velasco-Vazquez J, Betancor-Rodriguez A, Arnay-De-La Rosa M, and Gonzalez-Reimers E. 2000. Auricular exostoses in the prehistoric population of Gran Canaria. Am J Phys Anthropol 112:49-55.
Vitzthum V. 2003. A number no greater than the sum of its parts: the use and abuse of heritability. Hum Biol 75:539(520).
Wendorf F. 1968. The prehistory of Nubia. Dallas: Southern Methodist University Press.
Wijsman E, and Neves W. 1986. The use of nonmetric variation in estimating human population admixture: A test case with Brazilian blacks, whites, and mulattos. Am J Phys Anthropol 70:395-405.
Wright S. 1934. The results of crosses between inbred strains of guinea pigs, differing in number of digits. Genetics 19:537-551.
Wright S. 1951. The genetical structure of populations. Annals of Eugenics 15:323-354.
Zabkar L, and Zabkar J. 1982. Semna South: a preliminary report on the 1966-68 excavations of the University of Chicago Oriental Institute Expeditions to Sudanese Nubia. J Amer Research Center on Egypt 19:7-45.

APPENDIX A

Table 1A. Tetrachoric correlations for all Nubian samples

	SOF	TD
SOF	1	
TD	0.14	1

Table 2A. Tetrachoric correlations for all Nubian samples, except Sesebi

	SOF	TD
SOF	1	
TD	0.1341	1

Table 3A. Tetrachoric correlations for Nubian samples with only one time period represented

	SOF	TD
SOF	1	
TD	0.079	1

Table 4A. C matrix for all Nubian samples.

	KULI	KULM	MESO	CGRP	AGRP	PANG	SAYC	SESE	HABA	KERM	XGRP	MERO	SEMC
KULI	0.3370												
KULM	0.2530	0.2783											
MESO	0.0044	0.0212	0.1838										
CGRP	-0.0375	-0.0486	0.0318	0.3703									
AGRP	-0.1790	-0.1761	-0.0325	0.1944	0.5227								
PANG	0.1242	0.0831	-0.1392	-0.2438	-0.3554	1.0530							
SAYC	-0.2190	-0.2314	-0.1203	0.1875	0.4133	-0.4264	1.3876						
SESE	-0.1728	-0.1551	0.0065	0.0453	0.2020	-0.2781	0.1002	0.3596					
HABA	0.1206	0.1453	0.0693	-0.0506	-0.1453	-0.0001	-0.2237	-0.0986	0.2104				
KERM	-0.0607	-0.0402	-0.0443	-0.1918	-0.1812	0.0945	-0.2907	-0.0407	-0.0002	0.4031			
XGRP	-0.0918	-0.0666	0.0275	-0.0945	-0.0610	-0.1013	-0.1704	0.0756	-0.0026	0.1496	0.2699		
MERO	-0.0026	-0.0004	-0.1052	-0.2557	-0.2870	0.4135	-0.3941	-0.1576	-0.0073	0.2810	0.0366	0.6442	
SEMC	-0.0759	-0.0626	0.0969	0.0932	0.0851	-0.2240	-0.0126	0.1137	-0.0175	-0.0784	0.0289	-0.1653	0.2185

Table 5A. R matrix for all Nubian samples

	KULI	KULM	MESO	CGRP	AGRP	PANG	SAYC	SESE	HABA	KERM	XGRP	MERO	SEMC
KULI	0.0752												
KULM	0.0565	0.0621											
MESO	0.0010	0.0047	0.0410										
CGRP	-0.0084	-0.0109	0.0071	0.0827									
AGRP	-0.0400	-0.0393	-0.0073	0.0434	0.1167								
PANG	0.0277	0.0186	-0.0311	-0.0544	-0.0793	0.2350							
SAYC	-0.0489	-0.0517	-0.0268	0.0418	0.0922	-0.0952	0.3097						
SESE	-0.0386	-0.0346	0.0015	0.0101	0.0451	-0.0621	0.0224	0.0803					
HABA	0.0269	0.0324	0.0155	-0.0113	-0.0324	0.0000	-0.0499	-0.0220	0.0470				
KERM	-0.0136	-0.0090	-0.0099	-0.0428	-0.0404	0.0211	-0.0649	-0.0091	0.0000	0.0900			
XGRP	-0.0205	-0.0149	0.0061	-0.0211	-0.0136	-0.0226	-0.0380	0.0169	-0.0006	0.0334	0.0603		
MERO	-0.0006	-0.0001	-0.0235	-0.0571	-0.0641	0.0923	-0.0880	-0.0352	-0.0016	0.0627	0.0082	0.1438	
SEMC	-0.0169	-0.0140	0.0216	0.0208	0.0190	-0.0500	-0.0028	0.0254	-0.0039	-0.0175	0.0064	-0.0369	0.0488

Table 6A. C matrix for all Nubian samples except Sesebi

	KULI	KULM	MESO	CGRP	AGRP	PANG	SAYC	HABA	KERM	XGRP	MERO	SEMC
KULI	0.3284											
KULM	0.2453	0.2716										
MESO	0.0097	0.0274	0.2018									
CGRP	-0.0317	-0.0420	0.0497	0.3881								
AGRP	-0.1746	-0.1709	-0.0156	0.2104	0.5360							
PANG	0.1023	0.0624	-0.1467	-0.2512	-0.3640	1.0149						
SAYC	-0.2222	-0.2339	-0.1113	0.1961	0.4185	-0.4429	1.3831					
HABA	-0.1671	-0.1484	0.0251	0.0624	0.2175	-0.2848	0.1077	0.3775				
KERM	0.1163	0.1420	0.0788	-0.0411	-0.1369	-0.0171	-0.2232	-0.0885	0.2104			
XGRP	-0.0729	-0.0513	-0.0426	-0.1902	-0.1804	0.0705	-0.2979	-0.0375	-0.0078	0.3896		
MERO	-0.0939	-0.0677	0.0385	-0.0839	-0.0512	-0.1153	-0.1687	0.0877	-0.0003	0.1457	0.2749	
SEMC	-0.0396	-0.0345	-0.1148	-0.2666	-0.2888	0.3718	-0.4054	-0.1516	-0.0326	0.2747	0.0342	0.6532

Table 7A. R matrix for all Nubian samples except Sesebi

	KULI	KULM	MESO	CGRP	AGRP	PANG	SAYC	HABA	KERM	XGRP	MERO	SEMC
KULI	0.0729											
KULM	0.0545	0.0603										
MESO	0.0021	0.0061	0.0448									
CGRP	-0.0070	-0.0093	0.0110	0.0862								
AGRP	-0.0388	-0.0380	-0.0035	0.0467	0.1190							
PANG	0.0227	0.0139	-0.0326	-0.0558	-0.0809	0.2254						
SAYC	-0.0493	-0.0519	-0.0247	0.0436	0.0929	-0.0984	0.3072					
HABA	-0.0371	-0.0330	0.0056	0.0139	0.0483	-0.0632	0.0239	0.0839				
KERM	0.0258	0.0315	0.0175	-0.0091	-0.0304	-0.0038	-0.0496	-0.0197	0.0467			
XGRP	-0.0162	-0.0114	-0.0095	-0.0422	-0.0401	0.0157	-0.0662	-0.0083	-0.0017	0.0865		
MERO	-0.0209	-0.0150	0.0085	-0.0186	-0.0114	-0.0256	-0.0375	0.0195	-0.0001	0.0323	0.0610	
SEMC	-0.0088	-0.0077	-0.0255	-0.0592	-0.0641	0.0826	-0.0900	-0.0337	-0.0072	0.0610	0.0076	0.1451

Table 8A. C matrix for Nubian samples with no overlapping time periods

	MESO	CGRP	AGRP	PANG	SAYC	HABA	KERM	XGRP	MERO
MESO	0.2066								
CGRP	0.1123	0.3115							
AGRP	0.0602	0.0945	0.3725						
PANG	-0.2003	-0.1989	-0.3460	1.1476					
SAYC	-0.0588	0.0624	0.2297	-0.4477	1.1556				
HABA	0.0463	-0.0346	0.0833	-0.2402	-0.0518	0.2746			
KERM	-0.0098	-0.0268	-0.1559	0.1151	-0.2655	-0.0834	0.3057		
XGRP	-0.1177	-0.1945	-0.2148	0.1915	-0.3576	-0.0410	0.0715	0.4682	
MERO	-0.0388	-0.1260	-0.1235	-0.0212	-0.2662	0.0467	0.0490	0.1943	0.2857

Table 9A. R matrix for Nubian samples with no overlapping time periods

	MESO	CGRP	AGRP	PANG	SAYC	HABA	KERM	XGRP	MERO
MESO	0.0459								
CGRP	0.0249	0.0692							
AGRP	0.0134	0.0210	0.0827						
PANG	-0.0445	-0.0442	-0.0768	0.2548					
SAYC	-0.0131	0.0139	0.0510	-0.0994	0.2566				
HABA	0.0103	-0.0077	0.0185	-0.0533	-0.0115	0.0610			
KERM	-0.0022	-0.0059	-0.0346	0.0256	-0.0590	-0.0185	0.0679		
XGRP	-0.0261	-0.0432	-0.0477	0.0425	-0.0794	-0.0091	0.0159	0.1040	
MERO	-0.0086	-0.0280	-0.0274	-0.0047	-0.0591	0.0104	0.0109	0.0431	0.0634

Table 10A. Covariance matrix for Kulubnarti island sample

	SOF	TD
SOF	0.2362	
TD	0.0783	0.2362

Table 11A. Covariance matrix for Kulubnarti mainland sample

	SOF	TD
SOF	0.2283	
TD	0.0573	0.2188

Table 12A. Covariance matrix for Mesolithic sample

	SOF	TD
SOF	0.3000	
TD	0.1000	0.1667

Table 13A. Covariance matrix for C-Group sample

	SOF	TD
SOF	0.2519	
TD	-0.0009	0.1723

Table 14A. Covariance matrix for A-Group sample

	SOF	TD
SOF	0.2395	
TD	0.0026	0.1342

Table 15A. Covariance matrix for Pan-Grave sample

	SOF	TD
SOF	0.1429	
TD	-0.0714	0.2857

Table 16A. Covariance matrix for Sayala C-Group sample

	SOF	TD
SOF	0.0769	
TD	0.0064	0.0769

Table 17A. Covariance matrix for Sesebi sample

	SOF	TD
SOF	0.2502	
TD	0.0200	0.1366

Table 18A. Covariance matrix for Hesa/Biga sample

	SOF	TD
SOF	0.2491	
TD	0.0122	0.0821

Table 19A. Covariance matrix for Kerma sample

	SOF	TD
SOF	0.2271	
TD	0.0269	0.1933

Table 20A. Covariance matrix for X-Group sample

	SOF	TD
SOF	0.1502	
TD	-0.0237	0.1186

Table 21A. Covariance matrix for Meroitic sample

	SOF	TD
SOF	0.2069	
TD	0.0000	0.1098

Table 22A. Covariance matrix for Semna South Christian sample

	SOF	TD
SOF	0.0909	
TD	-0.0273	0.2182

APPENDIX B

Table 1B. Tetrachoric correlations for Mesolithic - C-Group samples

	SOF	TD
SOF	1	
TD	-0.1735	1

Table 2B. C matrix for Mesolithic - C-group

	MESO	CGRP	AGRP	SAYC
MESO	0.2073			
CGRP	0.0450	0.1593		
AGRP	-0.1109	-0.0422	0.1744	
SAYC	-0.1413	-0.1621	-0.0212	0.3246

Table 3B. R matrix for Mesolithic - C-Group

	MESO	CGRP	AGRP	SAYC
MESO	0.0492			
CGRP	0.0107	0.0378		
AGRP	-0.0263	-0.0100	0.0414	
SAYC	-0.0335	-0.0384	-0.0050	0.0770

Table 4B. Covariance matrix for Mesolithic sample

	SOF	TD
SOF	0.3000	
TD	0.1000	0.1667

Table 5B. Covariance matrix for C-Group sample

	SOF	TD
SOF	0.2519	
TD	-0.0009	0.1723

Table 6B. Covariance matrix for A-Group sample

	SOF	TD
SOF	0.2395	
TD	0.0026	0.1342

Table 7B. Covariance matrix for Sayala C-Group sample

	SOF	TD
SOF	0.0769	
TD	0.0064	0.0769

APPENDIX C

Table 1C. Tetrachoric correlations for Mesolithic - Kerma

	SOF	TD
SOF	1	
TD	0.1149	1

Table 2C. C Matrix for Mesolithic - Kerma

	MESO	CGRP	AGRP	PANG	SAYC	KERM
MESO	0.2128					
CGRP	0.0786	0.2331				
AGRP	0.0392	0.0332	0.3335			
PANG	-0.1947	-0.2343	-0.3677	1.1861		
SAYC	-0.1513	-0.0745	0.1200	-0.5416	0.9836	
KERM	0.0153	-0.0361	-0.1582	0.1522	-0.3362	0.3630

Table 3C. R matrix for Mesolithic - Kerma

	MESO	CGRP	AGRP	PANG	SAYC	KERM
MESO	0.0468					
CGRP	0.0173	0.0512				
AGRP	0.0086	0.0073	0.0733			
PANG	-0.0428	-0.0515	-0.0808	0.2606		
SAYC	-0.0332	-0.0164	0.0264	-0.1190	0.2161	
KERM	0.0034	-0.0079	-0.0348	0.0334	-0.0739	0.0798

Table 4C. Covariance matrix for Mesolithic sample

	SOF	TD
SOF	0.3000	
TD	0.1000	0.1667

Table 5C. Covariance matrix for C-Group sample

	SOF	TD
SOF	0.2519	
TD	-0.0009	0.1723

Table 6C. Covariance matrix for A-Group sample

	SOF	TD
SOF	0.2395	
TD	0.0026	0.1342

Table 7C. Covariance matrix for Pan-Grave sample

	SOF	TD
SOF	0.1429	
TD	-0.0714	0.2857

Table 8C. Covariance matrix for Sayala C-Group sample

	SOF	TD
SOF	0.0769	
TD	0.0064	0.0769

Table 9C. Covariance matrix for Kerma sample

	SOF	TD
SOF	0.2271	
TD	0.0269	0.1933

APPENDIX D

Table 1D. Tetrachoric correlations for Meroitic investigations

	ASB	OL	SOF	TD
ASB	1			
OL	0.3299	1		
SOF	-0.0221	0.1461	1	
TD	0.0524	0.0635	0.1508	1

Table 2D. C matrix for Meroitic investigations

	KULI	KULM	CGRP	PANG	SAYC	HABA	KERM	XGRP	MERO	SEMC
KULI	0.5127									
KULM	0.0934	0.4013								
CGRP	-0.1025	-0.1883	0.7733							
PANG	-0.0300	0.0882	-0.4493	1.0378						
SAYC	-0.2175	-0.3190	0.6086	-0.5286	1.5225					
HABA	-0.1832	-0.1370	0.1581	-0.2726	0.1325	0.4970				
KERM	-0.0183	0.0965	-0.1303	0.0071	-0.2098	0.0209	0.3368			
XGRP	0.0546	-0.1158	-0.1583	-0.0817	-0.2219	-0.0440	-0.0496	0.5397		
MERO	-0.0302	0.0357	-0.1132	-0.1287	-0.2525	0.0068	-0.0201	0.0369	0.3932	
SEMC	-0.0791	0.0450	-0.3979	0.3577	-0.5142	-0.1786	-0.0331	0.0400	0.0721	0.6881

Table 3D. R matrix for Meroitic investigations

	KULI	KULM	CGRP	PANG	SAYC	HABA	KERM	XGRP	MERO	SEMC
KULI	0.0591									
KULM	0.0108	0.0463								
CGRP	-0.0118	-0.0217	0.0892							
PANG	-0.0035	0.0102	-0.0518	0.1197						
SAYC	-0.0251	-0.0368	0.0702	-0.0610	0.1756					
HABA	-0.0211	-0.0158	0.0182	-0.0314	0.0153	0.0573				
KERM	-0.0021	0.0111	-0.0150	0.0008	-0.0242	0.0024	0.0388			
XGRP	0.0063	-0.0134	-0.0183	-0.0094	-0.0256	-0.0051	-0.0057	0.0623		
MERO	-0.0035	0.0041	-0.0131	-0.0148	-0.0291	0.0008	-0.0023	0.0043	0.0454	
SEMC	-0.0091	0.0052	-0.0459	0.0413	-0.0593	-0.0206	-0.0038	0.0046	0.0083	0.0794

Table 4D. Covariance matrix for Kulubnarti island sample

	ASB	OL	SOF	TD
ASB	0.0945			
OL	-0.0027	0.0256		
SOF	-0.0378	-0.0094	0.2362	
TD	-0.0378	0.0169	0.0783	0.2362

Table 5D. Covariance matrix for Kulubnarti mainland sample

	ASB	OL	SOF	TD
ASB	0.0879			
OL	0.0046	0.0879		
SOF	0.0084	0.0500	0.2283	
TD	0.0110	0.0249	0.0573	0.2188

Table 6D. Covariance for C-Group sample

	ASB	OL	SOF	TD
ASB	0.1544			
OL	-0.0110	0.0588		
SOF	0.0551	0.0184	0.2206	
TD	-0.0221	0.0551	0.0368	0.1103

Table 7D. Covariance matrix for Pan-Grave sample

	ASB	OL	SOF	TD
ASB	0.1429			
OL	0.1429	0.1429		
SOF	-0.0238	-0.0238	0.1429	
TD	0.0952	0.0952	-0.0714	0.2857

Table 8D. Covariance matrix for Sayala C-Group sample

	ASB	OL	SOF	TD
ASB	0.2564			
OL	-0.0321	0.0769		
SOF	0.0321	0.0064	0.0769	
TD	-0.0321	-0.0064	0.0064	0.0769

Table 9D. Covariance matrix for Hesa/Biga sample

	ASB	OL	SOF	TD
ASB	0.1870			
OL	0.0136	0.1116		
SOF	-0.0209	0.0029	0.2491	
TD	-0.0222	0.0036	0.0122	0.0821

Table 10D. Covariance matrix for Kerma sample

	ASB	OL	SOF	TD
ASB	0.1667			
OL	0.0071	0.1051		
SOF	0.0113	0.0102	0.2247	
TD	0.0112	-0.0162	0.0248	0.1889

Table 11D. Covariance matrix for X-Group sample

	ASB	OL	SOF	TD
ASB	0.1502			
OL	-0.0079	0.0435		
SOF	-0.0316	-0.0079	0.1502	
TD	0.0217	-0.0059	-0.0237	0.1186

Table 12D. Covariance matrix for Meroitic sample

	ASB	OL	SOF	TD
ASB	0.0750			
OL	0.0195	0.0575		
SOF	-0.0035	0.0066	0.2079	
TD	0.0105	0.0048	0.0009	0.1075

Table 13D. Covariance matrix for Semna South Christian sample

	ASB	OL	SOF	TD
ASB	0.0909			
OL	-0.0091	0.0909		
SOF	-0.0091	-0.0091	0.0909	
TD	-0.0273	0.0727	-0.0273	0.2182

APPENDIX E

Table 1E. Tetrachoric correlations for X-Group investigations

	HGCB	TD	SOF	TZS	OL	PNB	ASB	BAS	OMB
HGCB	1								
TD	-0.0247	1							
SOF	-0.0665	0.1541	1						
TZS	-0.0340	0.0926	0.1064	1					
OL	-0.0071	0.0635	0.1554	0.0790	1				
PNB	0.1004	0.2816	-0.0277	0.0716	0.2380	1			
ASB	-0.0143	0.0485	-0.0522	-0.0566	0.3273	0.4568	1		
BAS	0.1129	-0.0644	-0.0598	-0.0139	0.0788	0.1388	0.2250	1	
OMB	-0.0244	-0.0069	0.1122	-0.0706	0.1892	0.1039	0.3295	0.1035	1

Table 2E. C matrix for X-Group investigations

	KULI	KULM	HABA	KERM	XGRP	MERO	SEMC
KULI	0.5508						
KULM	0.0219	0.5945					
HABA	-0.2285	-0.1761	0.6994				
KERM	-0.1392	-0.2030	0.0861	0.5247			
XGRP	0.0777	-0.0529	-0.1612	-0.1786	0.5556		
MERO	-0.1203	-0.1832	0.0334	0.0791	-0.1446	0.4808	
SEMC	-0.1624	-0.0013	-0.2532	-0.1690	-0.0960	-0.1453	0.8272

Table 3E. R matrix for X-Group investigations

	KULI	KULM	HABA	KERM	XGRP	MERO	SEMC
KULI	0.0377						
KULM	0.0015	0.0407					
HABA	-0.0156	-0.0121	0.0479				
KERM	-0.0095	-0.0139	0.0059	0.0359			
XGRP	0.0053	-0.0036	-0.0110	-0.0122	0.0380		
MERO	-0.0082	-0.0125	0.0023	0.0054	-0.0099	0.0329	
SEMC	-0.0111	-0.0001	-0.0173	-0.0116	-0.0066	-0.0099	0.0566

Table 4E. Covariance matrix for Kulubnarti island sample

	HGCB	TD	SOF	TZS	OL	PNB	ASB
HGCB	0.1851						
TD	-0.0460	0.2299					
SOF	-0.0805	0.0575	0.2299				
TZS	0.0448	-0.0345	0.0000	0.0931			
OL	-0.0080	0.0230	-0.0115	-0.0034	0.0333		
PNB	0.0023	0.0230	-0.0460	-0.0138	-0.0046	0.1195	
ASB	0.0103	-0.0345	-0.0345	-0.0103	-0.0034	0.0552	0.0931

Table 5E. Covariance matrix for Kulubnarti mainland sample

	HGCB	TD	SOF	TZS	OL	PNB	ASB
HGCB	0.0976						
TD	-0.0130	0.1962					
SOF	-0.0231	0.0623	0.2322				
TZS	0.0178	0.0142	0.0183	0.1096			
OL	-0.0118	0.0339	0.0550	0.0022	0.0976		
PNB	-0.0050	0.0034	-0.0010	-0.0058	-0.0050	0.0447	
ASB	0.0038	0.0183	0.0082	0.0178	0.0038	0.0106	0.0976

Table 6E. Covariance matrix for Hesa/Biga sample

	HGCB	TD	SOF	TZS	OL	PNB	ASB
HGCB	0.2164						
TD	-0.0035	0.0809					
SOF	0.0017	0.0079	0.2501				
TZS	-0.0075	0.0026	0.0269	0.1299			
OL	-0.0025	0.0041	0.0020	0.0034	0.1185		
PNB	0.0318	0.0150	0.0086	0.0244	0.0180	0.0939	
ASB	0.0052	-0.0213	-0.0216	-0.0126	0.0155	0.0071	0.1839

Table 7E. Covariance matrix for Kerma sample

	HGCB	TD	SOF	TZS	OL	PNB	ASB
HGCB	0.1845						
TD	0.0176	0.1972					
SOF	0.0181	0.0199	0.2222				
TZS	-0.0110	0.0023	0.0020	0.0804			
OL	-0.0081	-0.0164	0.0073	0.0051	0.1050		
PNB	0.0170	0.0122	-0.0045	-0.0060	-0.0014	0.1519	
ASB	0.0121	0.0062	0.0077	-0.0044	0.0092	0.0354	0.1763

Table 8E. Covariance matrix for X-Group sample

	HGCB	TD	SOF	TZS	OL	PNB	ASB
HGCB	0.1286						
TD	-0.0214	0.1286					
SOF	0.0214	-0.0286	0.1619				
TZS	-0.0143	-0.0143	0.0810	0.0905			
OL	-0.0071	-0.0071	-0.0095	-0.0048	0.0476		
PNB	-0.0143	0.0357	-0.0190	-0.0095	-0.0048	0.0905	
ASB	0.0214	0.0214	-0.0381	-0.0190	-0.0095	0.0310	0.1619

Table 9E. Covariance matrix for Meroitic sample

	HGCB	TD	SOF	TZS	OL	PNB	ASB
HGCB	0.1854						
TD	-0.0065	0.1094					
SOF	-0.0222	0.0050	0.2135				
TZS	-0.0021	0.0036	-0.0003	0.0458			
OL	0.0028	0.0060	0.0082	-0.0032	0.0628		
PNB	-0.0079	0.0175	-0.0039	0.0004	0.0131	0.0830	
ASB	-0.0138	0.0121	-0.0054	-0.0046	0.0224	0.0345	0.0870

Table 10E. Covariance matrix for Semna South Christian sample

	HGCB	TD	SOF	TZS	OL	PNB	ASB
HGCB	0.1778						
TD	0.0667	0.1778					
SOF	-0.0222	-0.0222	0.1000				
TZS	-0.0222	-0.0222	-0.0111	0.1000			
OL	-0.0222	0.0889	-0.0111	-0.0111	0.1000		
PNB	-0.0222	-0.0222	0.1000	-0.0111	-0.0111	0.1000	
ASB	-0.0222	-0.0222	-0.0111	-0.0111	-0.0111	-0.0111	0.1000

APPENDIX F

Table 1F. Tetrachoric correlations among Semna South samples

	HGCB	CCP	TD	JFB	SOF	TZS	OL	TD
HGCB	1							
CCP	0.0278	1						
TD	-0.0255	-0.1134	1					
JFB	0.2883	-0.0550	0.1029	1				
SOF	-0.1635	0.0313	0.0307	-0.0582	1			
TZS	0.0150	0.2551	0.2090	-0.1705	0.0972	1		
OL	0.1290	0.0071	0.2396	0.5411	0.1839	0.0352	1	
TD	-0.2171	0.0921	0.2992	0.2038	-0.1026	-0.0872	0.578	1

Table 2F. C matrix among Semna South samples

	XGRP	MERO	SEMC
XGRP	0.4426		
MERO	-0.0442	0.4146	
SEMC	-0.3985	-0.3705	0.7690

Table 3F. R matrix among Semna South samples

	XGRP	MERO	SEMC
XGRP	0.0268		
MERO	-0.0027	0.0251	
SEMC	-0.0241	-0.0224	0.0465

Table 4F. Covariance matrix for X-Group sample

	HGCB	CCP	TD	JFB	SOF	TZS	OL	ASB
HGCB	0.1342							
CCP	-0.0342	0.2605						
TD	0.0211	-0.0105	0.1684					
JFB	0.0289	-0.0342	-0.0316	0.1342				
SOF	0.0211	-0.0105	-0.0421	-0.0316	0.1684			
TZS	-0.0158	-0.0053	-0.0211	-0.0158	0.0842	0.0947		
OL	-0.0079	-0.0289	-0.0105	-0.0079	-0.0105	-0.0053	0.0500	
ASB	0.0211	-0.0105	0.1684	-0.0316	-0.0421	-0.0211	-0.0105	0.1684

Table 5F. Covariance matrix for Meroitic sample

	HGCB	CCP	TD	JFB	SOF	TZS	OL	ASB
HGCB	0.1859							
CCP	0.0074	0.2487						
TD	-0.0149	0.0052	0.0921					
JFB	0.0200	-0.0052	0.0105	0.1267				
SOF	-0.0241	0.0054	-0.0058	-0.0045	0.2135			
TZS	-0.0010	0.0100	-0.0047	-0.0068	0.0013	0.0440		
OL	0.0029	-0.0015	0.0234	0.0253	0.0088	-0.0033	0.0667	
ASB	-0.0149	0.0052	0.0921	0.0105	-0.0058	-0.0047	0.0234	0.0921

Table 6F. Covariance matrix for Semna South Christian sample

	HGCB	CCP	TD	JFB	SOF	TZS	OL	ASB
HGCB	0.1778							
CCP	-0.0444	0.1778						
TD	-0.0222	-0.0222	0.1000					
JFB	0.0667	-0.0444	-0.0222	0.1778				
SOF	-0.0222	0.0889	-0.0111	-0.0222	0.1000			
TZS	-0.0222	-0.0222	-0.0111	-0.0222	-0.0111	0.1000		
OL	-0.0222	-0.0222	-0.0111	-0.0222	-0.0111	-0.0111	0.1000	
ASB	-0.0222	-0.0222	0.1000	-0.0222	-0.0111	-0.0111	-0.0111	0.1000

APPENDIX G

Table 1G. Tetrachoric correlations among Christian samples

	HGCB	CCP	TD	JFB	SOF	TZS	OL	PNB	ASB
HGCB	1								
CCP	0.1833	1							
TD	-0.1128	-0.0742	1						
JFB	0.2089	0.0086	-0.1299	1					
SOF	-0.1737	0.1884	0.2334	-0.1575	1				
TZS	0.1487	0.1091	0.0821	-0.1794	0.2355	1			
OL	0.0376	-0.0450	0.2834	0.2091	0.2047	0.1765	1		
PNB	0.2773	-0.2416	0.2806	0.0449	0.0200	0.2675	0.3164	1	
ASB	0.0925	0.1154	-0.1896	0.3185	-0.0834	0.0465	0.2737	0.2723	1

Table 2G. C matrix for Christian samples

	KULI	KULM	HABA	SEMC
KULI	0.5935			
KULM	-0.0605	0.6337		
HABA	-0.1772	-0.2344	0.6639	
SEMC	-0.3559	-0.3387	-0.2523	0.9469

Table 3G R matrix for Christian samples

	KULI	KULM	HABA	SEMC
KULI	0.0317			
KULM	-0.0032	0.0339		
HABA	-0.0095	-0.0125	0.0355	
SEMC	-0.0190	-0.0181	-0.0135	0.0506

Table 4G. Covariance matrix for Kulubnarti island sample

	HGCB	CCP	TD	JFB	SOF	TZS	OL	PNB	ASB
HGCB	0.1897								
CCP	-0.0222	0.2586							
TD	-0.0505	0.0296	0.2340						
JFB	-0.0172	-0.0012	0.0111	0.0665					
SOF	-0.0862	0.0653	0.0554	0.0111	0.2340				
TZS	0.0456	-0.0197	-0.0369	-0.0074	-0.0012	0.0961			
OL	-0.0086	-0.0185	0.0234	-0.0025	-0.0123	-0.0037	0.0345		
PNB	0.0012	-0.0025	0.0222	0.0259	-0.0493	-0.0148	-0.0049	0.1232	
ASB	0.0099	-0.0554	-0.0369	0.0283	-0.0369	-0.0111	-0.0037	0.0567	0.0961

Table 5G. Covariance matrix for Kulubnarti mainland sample

	HGCB	CCP	TD	JFB	SOF	TZS	OL	PNB	ASB
HGCB	0.1004								
CCP	0.0323	0.2074							
TD	-0.0143	-0.0184	0.2002						
JFB	-0.0036	0.0023	0.0005	0.1464					
SOF	-0.0215	0.0645	0.0699	-0.0108	0.2258				
TZS	0.0179	0.0207	0.0136	-0.0064	0.0215	0.1126			
OL	-0.0108	0.0115	0.0384	0.0154	0.0484	0.0038	0.0876		
PNB	-0.0054	-0.0023	0.0031	-0.0084	0.0000	-0.0061	-0.0046	0.0461	
ASB	0.0036	0.0161	0.0179	-0.0036	0.0108	0.0179	0.0054	0.0108	0.1004

Table 6G. Covariance matrix for Hesa/Biga sample

	HGCB	CCP	TD	JFB	SOF	TZS	OL	PNB	ASB
HGCB	0.2152								
CCP	0.0153	0.2416							
TD	-0.0007	-0.0081	0.0753						
JFB	0.0370	-0.0030	-0.0140	0.1427					
SOF	0.0001	-0.0075	0.0043	-0.0278	0.2492				
TZS	-0.0071	0.0035	0.0037	-0.0184	0.0287	0.1317			
OL	-0.0021	-0.0227	0.0051	0.0008	0.0033	0.0031	0.1201		
PNB	0.0327	-0.0261	0.0159	-0.0018	0.0097	0.0245	0.0181	0.0953	
ASB	0.0060	0.0168	-0.0200	0.0400	-0.0198	-0.0134	0.0152	0.0068	0.1859

Table 7G. Covariance matrix for Semna South Christians

	HGCB	CCP	TD	JFB	SOF	TZS	OL	PNB	ASB
HGCB	0.1778								
CCP	-0.0444	0.1778							
TD	0.0667	-0.0444	0.1778						
JFB	0.0667	-0.0444	0.0667	0.1778					
SOF	-0.0222	0.0889	-0.0222	-0.0222	0.1000				
TZS	-0.0222	-0.0222	-0.0222	-0.0222	-0.0111	0.1000			
OL	-0.0222	-0.0222	0.0889	-0.0222	-0.0111	-0.0111	0.1000		
PNB	-0.0222	0.0889	-0.0222	-0.0222	0.1000	-0.0111	-0.0111	0.1000	
ASB	-0.0222	-0.0222	-0.0222	-0.0222	-0.0111	-0.0111	-0.0111	-0.0111	0.1000

VITA

Kanya Mia Godde was born September 25, 1978 in Sacramento, California. She graduated from Nevada Union High School in 1996 and started attending Sierra College in 1997. She transferred to California State University, Sacramento in 2000 and graduated with her Bachelor of Arts in 2002 and Masters of Arts in 2004. In 2005, she began working on her doctorate degree at the University of Tennessee. She is hopeful about finding employment after completing her PhD.