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Biological Distance in Middle and Late Archaic Populations of the Mid-South United States

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BIOLOGICAL DISTANCE IN MIDDLE AND LATE ARCHAIC POPULATIONS OF THE MID-SOUTH UNITED STATES

by

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M.A., Wichita State University, 2005

A Dissertation
Submitted in Partial Fulfillment of the Requirements for the
Doctor of Philosophy

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DISSERTATION APPROVAL

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Meadow Lea Campbell

A Dissertation Submitted in Partial

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Doctor of Philosophy

in the field of Anthropology

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TITLE: BIOLOGICAL DISTANCE IN MIDDLE AND LATE ARCHAIC POPULATIONS OF THE MID-SOUTH UNITED STATES

MAJOR PROFESSOR: Dr. Robert Corruccini, Co-Chair

Dr. Susan Ford, Co-Chair

This dissertation used osteometrics to assess the level of congruence between biological distance and long-distance material exchange in three Middle and Late Archaic groups living in the mid-South United States. Dental and cranial data support greater biological affinity between groups in southern Illinois (represented by individuals from the Black Earth site) and central Tennessee (individuals from Eva and surrounding sites) while groups in the Green River region of western Kentucky (Shell Mound Archaic) were somewhat more removed or perhaps more isolated. Females were more biologically variable than males for the majority of metrics used. This finding is suggestive of a patrilocal residence pattern, if only loosely followed.

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CHAPTER 1

INTRODUCTION AND THEORETICAL CONSIDERATIONS

This dissertation was borne out of an interest in what life was like for people living in North America circa 4,000 years ago. Compared to later populations in the mid-South, we know much less about these early groups' lived experience beyond that they were hunter/gatherer/collectors who traded and used designated cemeteries to bury their dead. While that is reductionist in scope, the literature on Archaic Period peoples of the North American Southeast is not much better (notable exceptions being Emerson et al., 2009; Sassaman, 2010). Who were these people? What were their lives like? What could we learn about human social structure(s) from the way they negotiated kin relations?

Issues of kinship, reproduction, and mate selection are among some of the principal concerns of human life and anthropological inquiry. Navigation of these issues, guided by culture at the macro level and idiosyncrasies and personal agency at the individual level, directly influence one of the most basal of all human behaviors – bringing new life into the social group by reproduction. Given that framework I test the following hypotheses:

→ Hypothesis 1: Biological distance and archaeological patterns of cultural exchange are congruent.

Briefly, patterns of cultural exchange in the archaeological record support interactions between all groups used in the present analysis, though at varying levels. The Green River groups of the Shell Mound Archaic in western Kentucky appear to have remained insulated, though they could have been trading more with groups to their south in the Middle Tennessee River Valley rather than with groups more proximal to them across the Ohio River in southern Illinois. These patterns will be discussed in detail below.

→ Hypothesis 2: Females will show higher levels of biological variation reflective of patrilocal residence patterns.

The patterned exchange of mates can be an effective strategy to build alliances and provide a buffer in times of stress (Levi-Strauss, 1969; Kelly, 1992; Fix, 1999; Hill, 2009; Kidder and Sassaman, 2009). Prior work in the region suggests that the groups under analysis here practiced patrilocal residence patterns (Lewis and Lewis, 1961; Herrmann, 2002). Specific evidence for male versus female movements in regards to post-marital residence patterns is discussed in detail below.

Given that group composition is constructed by the combined interaction between residence patterns, alliances, feuds, and wars; is shaped by climate patterns, fluctuations, and seasonality; and influenced by trade carrying goods and stories of other people in faraway places – who, then, was in a group? Did women marry and leave their home groups, presumably to live with related males? Or did men systematically go to live with related women in another group? Was this a strictly-held practice or a rather fluid one, negotiated by each individual throughout their lifetime?

Anthropological questions, like humans themselves, are complex. The introductory sections of this work lay the background needed to interpret the patterns of biological relatedness resultant from the analysis of skeletal remains. With an aim to explore what life may have been like for Archaic peoples in the mid-South, we (the author and the reader) will explore the messy stuff of who, what, when, where, and why. Of the "what" we will discuss the material goods that evidence exchange and interaction, as well as skeletons, each manifesting an individual lived experience to the extent that it is recorded in bones. Of the "when and where" we will focus on the Middle and Late Archaic periods (ca 8,900 to 3,200 cal yrBP) as we visit the riverine bottomlands and the dissected uplands of the lower Ohio and lower Mississippi Rivers, the bends of the Green River further southeast in what is now western Kentucky, to the Cypress Creek, a tributary of the Tennessee River. That leaves the "who and the why" – the most fundamental of anthropological questions, in my opinion. Minimally, the "who" are the men and women who came to be buried and found again in the cemeteries used in this analysis. They lived, foraged, ate, birthed, traded, created, warred, celebrated, mourned, and loved during their lives. They were actors operating within their specific cultural contexts; their skeletons are records of habitual behavior, shared ancestry, relative health and trauma(s), biological sex, and age at death. Their material effects reflect their status, role, gender, cultural affiliations, and interaction with other groups. Collectively, these biological and material remains are the tangible evidence of their culture. Some of my questions cannot be answered fully. However, a better understanding of Archaic-period hunter/gatherer/collector lifeways in the mid-South United States will situate these groups in the broader flow of human expansion and adaptation in the region. Their ancestors migrated to and settled the Americas. Their progeny independently developed horticulture and then agriculture; constructed hamlets, villages, and then cities; they built monumental architecture of a new scale and participated in continent-wide trade networks – all of which have roots in Archaic period populations.

Provided both of the hypotheses above are supported it will show a pattern of greater female residential and post-marital mobility along emerging or established trade routes in the Archaic mid-South. If, however, the pattern of preferential female mate exchange along exchange routes does not in fact follow the same pattern as biological distances, then a few explanations may be the cause. It is possible that the data are not fine-grained enough to pick up subtle aspects of population structure within the region of the mid-South during the Archaic. Similarly, it is also possible that these populations did not adhere strictly or allowed considerable flux in the rules regarding male versus female philopatry and with which specific neighboring groups they exchanged mates. Chapter 6, Discussion, will review these possibilities in detail.

Organization of the Dissertation

The remainder of Chapter One will provide the theoretical construct from which I will interpret the pattern seen in skeletal remains. The body of theory takes references from cultural, archaeological, and biological anthropological efforts to understand the lived experience of past populations using skeletal and material remains. Chapter Two will provide the “when” and the “where” in terms of climate and environment 6,000 to 2,000 years ago in the mid-South region of the United States, as well as the “what” in terms of material goods and patterns of exchange seen in the archaeological record. The chapter will introduce the three main geographical areas of interest and review what is known about the people who inhabited the archaeological sites from which the skeletal remains were excavated. Here the focus is on mortuary styles, patterns of post-marital residence, mobility and sedentism, and anything that would have moved goods and/or people across the landscape. Chapter Three reviews how biological relationships are estimated using skeletal remains. The chapter reviews methods using cranial morphology, aspects of the dentition, and post-cranial dimensions pursuant to the examination of group interaction and biological exchange. Chapter Four presents the results of several statistical analyses including univariate and multivariate methods designed to recognize patterns in the more strongly-inherited skeletal morphology presented in the previous chapter. Chapter Five returns to the original question of which groups were composed of unrelated females and related males (or vice versa) and how these societal dimensions may have been effected by the networks of exchange evidenced in the archaeological record.

Anthropological Approaches to Exchange

The section that follows includes details regarding theories of exchange as related to material goods and draws parallels to the exchange of people when appropriate. The middle section reviews theories of kinship, migration, residency patterns, and mobility – all of which have bearing on the movement/exchange of people as well as goods. The last section delves into the efforts of biological anthropologists to study exchange, migration, and other sociocultural structures that influence group composition through biological distance analyses. The discussion below is not meaning to treat or portray people as goods or commodities.

Since our way of being, our ethnicity, our tribe, and our cultural affiliations by any other name, contribute to or even structure the interactions we have with one another on a daily basis and over a lifetime, these interactions reflect and are the root source for many processes of interest to anthropologists such as interactions between groups. We must infer prehistoric interactions based on the archaeological record of artifactual and contextual materials that demonstrate similarities of style and symbolism, construction and manufacture, or source materials. We can also do this by comparing biological variation and population structure.

In this work the concept of exchange is used to refer to the transfer of goods or people in relation to the social interactions they evidence. Anthropologists study exchange, or reciprocity and redistribution of cultural materials, to understand how prehistoric groups maintained relationships of power and social ties (Earle, 2010; Hill, 2009, 2012), meaning that anthropologists have fostered a rich engagement with systems of exchange. The act of exchanging goods is symbolic of bonds being solidified, of relationships being fostered and maintained, of shared ideology, and is a way for group members to differentially wield status and therefore better position their own family in their group (Hill, 2009). Similarly, a lack of exchange – of interaction – is symbolic of different ideology and worldview or of different economic values.

Levi-Strauss (1969) focused on the function of exchanged items to form bonds and alliances. Food, manufactured items, and especially women were the ultimate gift in building relationships between disparate groups (Levi-Strauss, 1969: 52-68). He illustrates the primacy of women in the exchange process by presenting the case of two nomadic bands in Brazil that fear and avoid one another yet must exchange goods and women to meet their subsistence and other needs. Over time, a reciprocal arrangement develops out of which Levi-Strauss (1969: 68) sees:

> …a continuous transition…from war to exchange, and from exchange to intermarriage, [whereby] the exchange of brides is merely the conclusion to an uninterrupted process of reciprocal gifts, which effects the transition from hostility to alliance, from anxiety to confidence, and from fear to friendship.

Differential exchange of males versus females produces differing levels of variation for biological traits as novel alleles appear from neighboring groups (gene flow). High heterozygosity and variation within a particular sex is indicative of sustained dispersion of that sex from their natal group(s) (Lane and Sublett, 1972). Thus, if women are the preferred object of exchange then they will be more biologically variable within the group to which they move. The reverse would be true for males – they would be more similar and with less biological variation than females. Such a scenario describes a patrilocal society where related males live together in the group of their birth along with (largely) unrelated females who moved in from neighboring groups or beyond. Rules about who is or is not a suitable partner get to the crux of how kinship, or the "interpersonal relationships based upon a recognized biological connection arising out of common ancestry or marriage" is defined and maintained within a group (Matras, 1973). Sahlins (2011: 2) conceptualizes kinship as:

> …the mutuality of being: persons who are members of one another, who participate intrinsically in each other's existence" whether by birth or cultural construction, meaning that kin "live each other's lives and die each other's deaths.

Archaeologists, too, have historically had a long engagement with the study of exchange. Archaeologists investigate exchange by analyzing the spatial distribution of common and exotic source materials and manufactured goods (Earle, 1982). Post-processual archaeologists have placed their foci more locally, seeing exchange as part of (and not separate from) the cultural structure out of which meaning is created by actions (Earle, 2010; Hodder, 1992). Contextual analysis of exchanged items contributes to anthropological understanding of individual and group identity, as well as the ways the very presence of exchange is embedded within a given society and within the various spheres of action in any human group (political, economic, ritual, etc.) (Earle, 2010). These spheres are "dynamic, integrated systems of flows, connections, dependencies, and power" (Earle, 2010: 209), even amongst the temporally distant Archaic-period groups.

A formalist approach to exchange analyzes the outcome of individual and small group decisions in reference to subsistence and settlement location (Earle, 1982). These theories can be used to investigate the evolution and organization of exchange systems by utilizing cost-benefit analyses (Earle, 1982; Hodder, 1982). A substantivist approach, one more in line with the present study, has a different focus in that it seeks to understand broader social and political institutions within which exchange occurs (Earle, 1982; Hodder, 1982). These theories can be used to explain social organization and the development of prehistoric cultures because they assume the broad similarity between the patterning of materials exchanged and the cultural contexts in which they were exchanged (Earle, 1982; Hodder, 1982). A substantivist approach can investigate culture change by tracking the "social, political, economic, and ecological variables that interrelate to form a system that changes in response either to exogenous factors or to the internal interaction among the variables" (Earle, 1982: 3) to maintain a balance with the environment (making substantivism a functionalist approach) (Hodder, 1982).

The hypotheses of the present work employ a substantivist approach in that they examine mate exchange and the movement of males relative to females (and vice versa) within Middle (8,900 to 5,800 cal yr BP) and Late (5,800 to 3,200 cal yrBP) Archaic period peoples of the mid-South United States. The hypotheses proceed from the notion that biological exchange (and therefore kinship rules) more or less mirrors the exchange of cultural materials because the two operate within the same, or similar, structural contexts.

The above discussion is predicated on the notion that a group recognized differences between male and female roles (gender) and that those differences were meaningful (Claassen, 2001). One way gender roles are made meaningful in any society is to serve as the organizing principle for rules regarding sexuality (Claassen, 2001). Rules regarding sexuality also stem from prescribed access to mate(s), usually in the form of culturally recognized marriage and post-marital residence.

Post-marital residence patterns are reflected in the relative biological variation of males versus females within a particular site and/or time. Greater variation of one sex over the other indicates that the more variable sex was the one migrating into the site, whereas less variation means the individuals were likely sampled from the established local gene pool for that sex (Lane and Sublett, 1972). Similarly, the exchange of mates (and therefore alleles) leads to increased phenotypic similarity between the groups participating in the exchange; groups outside of the sphere of exchange look less phenotypically similar to other groups over time (Stojanowski and Schillaci, 2006).

The formalist and substantivist schools of thought are not mutually exclusive though, as each seeks to understand exchange as relationships between individuals, between social groups, and between individuals and social groups and their broader cultural framework and environmental circumstances. Of particular interest to the present study, Hodder (1982) sees all social relations as forms of social exchange. For instance, the “flow of transactions between interdependent individuals produces apparent structures such as the ‘family’” (Hodder, 1982: 204). Through a Marxist and historical particularlist lens Bender acknowledges ecological and/or biological advantages to exchange but contends that exchange is largely about social relations and social reproduction (1985). Here the exchange of goods or people comes down to the labor involved in production. The family is maintained daily by members’ allocation of time and effort pursuant to its continued functioning (Hodder, 1982). In this way, it becomes obvious that it matters who is in a family or even a member of the larger social group. "...[O]ne might reasonably suggest that what distinguishes hominid [sic] development is the importance of the social strategies of exchange built into the adaptive repertoire" (Bender, 1985: 55). Though Claassen (2001) reminds us that there are more ways to organize labor in a society than by gender (she lists class, age, and craft specialty), it remains that the exchange of mates – of kin, family, or group members – between clans within a social group, as well as those in neighboring or even distant groups, matters greatly.

Humans embody culture through the ways we use our bodies in the pursuit of culturally constructed behaviors, and through the unique biological profile carried in our genomes (Sofaer, 2006). Just as specific patterns in DNA segments reflect shared genetic ancestry and previous affiliation between people or groups, similar patterns of morphology in the skeleton reflect long-term adaptations, a degree of ancestral relationships, and habitual and/or patterned behaviors that occur in one’s lifetime. Both biological patterns (genetic and environmental) are culturally constructed, though. Cultural values regarding who is or is not a suitable partner for the purposes of reproduction structure how kinship is reckoned in that group and therefore too, the genetic exchanges out of which the next generation is born. Shared ancestry may reflect shared histories, shared interactions, and common cultural mores. Culturally appropriate ideas regarding specific roles individuals might play based on their gender, age, clan, or status also leave their mark on their actors’ skeletons as bones remodel in response to mechanical strains and metabolic processes through one’s lifetime (Sofaer, 2006). Ancient culture then, can indeed be studied by the use of bodies – skeletons, teeth, and genomes – in an effort to understand the contexts and social structure in which people operated in the past (Goodman and Leatherman, 1998; Sofaer, 2006). The section below details ways in which mobility and settlement systems can impact biological (allelic) variation among human populations.

The Articulation of Exchange Patterns with Other Spheres of Hunter-Gatherer Lifeways

Issues of hunter-gatherer lifeways have a long interest within anthropology. Traditional thinking envisioned primitive, small, nomadic groups hunting big game in marginal environments (Lee, 1968; Netting, 1986). A seminal piece on hunter-gatherers is Lee's (1968) work with the !Kung San, who depend entirely on hunting and gathering for subsistence. They do not have a need for cultivation because their needs are easily met by gathering and hunting. Their diet consists mostly of nuts and vegetables collected by women, supplemented by game hunted by men. With the exception of their dry season, food is secured relatively consistently. The !Kung San enjoy an ease of life without agriculture. Men, and even women, have ample time for resting, visiting other camps, dancing, and entertaining. Their children enjoy good health in comparison to children in neighboring agricultural groups (Lee, 1968).

In many ways, the Middle and Late Archaic peoples of the mid-South resemble the !Kung San of Lee's ethnographies. The southeastern United States was and remains a biologically rich host to a variety of subsistence resources such as oak, hickory, and walnut trees; deer and small game; water and terrestrial fowl; freshwater mussels; many species of fish; and plants like goosefoot, knotweed, maygrass, sunflower, and marsh-elder (Schroeder, 2004). Through a combination of gathered nuts and later seeds, along with hunted deer, fish, and other small game, the peoples of the Archaic mid-South were able to provide suitably for their group. Even during the warm and dry Hypsithermal (~8,500 to 5,000 BP), when prairies spread east of the Mississippi River, the accompanying increase in hickory nuts and white-tailed deer provided ample fat, protein, hides, and bone/antler resources for Middle Archaic groups in the Eastern Woodlands (Wolverton, 2005; Hollenbach and Carmody, 2010).

Social change that accompanies fluctuations in settlement are far-reaching and extend into shifting gender and age roles, time spent together and with children, kin, and other groups, changes in birth spacing and population densities, increasingly non-egalitarian social structure, more leisure time (at least until agriculture begins in earnest), the development of persistent places on the landscape for ritual and burial use, increased attention to mortuary style and differentiation, and non-subsistence related exchange of non-functional items (Kelly, 1992, 1995; Hollenbach and Carmody, 2010; Thompson, 2010). Clearly, mobility and sedentism are more than just mapping onto available subsistence resources. Human groups may need to move for non-food resources such as firewood, ceremonial items, raw material for tools, to avoid insects, for political reasons, to find a mate, to seek allies, or to see a shaman (Kelly, 1992). Over time, changes in settlement patterns become enculturated in peer-group interactions (Kelly, 1992).

Other processes can function to move people and their genomes across a landscape. Migration studies are quite old in the field of anthropology, though they have taken various iterations and interpretations. Cabana (2011) reviews anthropological studies of migration and identifies several key themes. Historically, anthropologists have been overly concerned about the role of migration in cultural change, particularly abrupt change. This may be due to the nature of archaeological data (especially older archaeological data with less temporal resolution than we can achieve today). In this context, seemingly abrupt changes evidenced in the archaeological data were equated with migration. However, archaeologists now operate under the notion that material cultural change may have appeared abrupt, but may not have actually been so. Novel elements of material culture do not necessarily mean a new culture and new people were responsible via migration. Processual archaeologists challenged the pervasive use of migration to explain culture change, but they did not study migration themselves, as they were more interested in universals and general trends that could explain cultural change and evolution due to internal mechanisms (Cabana, 2011). From a neo-evolutionary, Processual, systems-based approach, migrations are historical events external to a culture and are therefore not useful or predictive towards explaining culture change and evolution (Cabana, 2011). Post-processualists criticized their predecessors' use of universal explanations and the neo-evolutionary approach (Cabana, 2011). Instead, migrations can be studied as situational events not necessarily indicative or part of a universal mechanism of cultural change. Today, migrations are viewed as population mixing rather than wholesale population replacement (Cabana, 2011). We recognize that culture change and culture continuity are part of the same process and that migrations are more than historical events. As Fix reminds us, "Genes, like potsherds, do not travel by themselves: migrating/colonizing organisms are required. The environmental and/or cultural (including kinship) mechanisms promoting and structuring migration need to be taken into account to evaluate these stories" (here, Fix uses "stories" in reference to explanations of the global distribution of human genomes that are not informed by the cultural history or circumstances of the groups involved) (2012: 88).

The discussion of migration is offered as additional context for thinking about the movement of hunter-gatherer-collectors during the Archaic period in the mid-South. While there may be evidence for migrations out of the area during the late Pleistocene and early Holocene (Sassaman, 2010), there is no archaeological evidence for wholesale migration during the Middle or Late Archaic. What there is evidence for, though, is long-distance trade and exchange routes

(Jefferies, 1997, 2004; Kidder and Sassaman, 2009). The biological component to this evidence is missing and the present analysis attempts to address that.

Embedded in the prior discussion of settlement system theory is the issue of social complexity which is an emerging, dissolving, and dynamic phenomenon (Thompson, 2010). Reduced mobility typically occurs in tandem with a non-egalitarian structure, as seen in some foraging groups who have political structure, unequal wealth distribution, and social or gender inequalities (Kelly, 1992). The opportunity for unequal relationships is always present, but the scale and duration, as well as concentration and frequency of interactions, must also be considered (Thompson, 2010). Kelly (1992) thinks that sedentism replaces the constraints of looking for resources with new constraints of increasing social complexity, placing new emphasis on increasing production rates, restricting sharing networks, controlling labor, investing more time in alliance-building, arranged marriages, and territory defense.

Even a generation ago many archaeologists denied, due to a lack of evidence, that Archaic people were even somewhat sedentary. This facet of social complexity was thought to appear in the subsequent Woodland period. Social “complexity” was already present by the Middle Archaic, though not with an institutionalized hierarchy (Kidder and Sassaman, 2009; Thompson, 2010). Early Archaic hunter-gatherers lived in mobile, dispersed familial groups. High residential mobility and low population density persisted until the late Middle Archaic/Late Archaic when groups that had been hunter-gatherer-cultivators for thousands of years became more sedentary (Charles and Buikstra, 1983). The Hypsithermal climate change had some impact on human settlement and subsistence patterns. High availability of deer and hickory nuts allowed for more efficient foraging over smaller areas. The overall effect was reduced residential mobility accompanied by increased population size and density (Stafford, 1994;

Hollenbach and Carmody, 2010), particularly after 7,000 BP which was the maximum expression of the Hypsithermal (Nolan and Fishel, 2009). Domesticated crop complexes including squash, sunflowers, chenopodium, and marshelder at sites like Riverton, Hayes, Phillips Spring, and Napoleon Hollow have been radiocarbon dated to at least 3,800 BP (Smith and Yarnell, 2009). Three of those sites lie squarely within the geographic boundaries of interest in the present study (Phillips Spring is in southwest Missouri, outside of the area of interest). Cooler and wetter conditions following the Hypsithermal brought an expansion of deciduous forests back into upland areas, and presumably Late Archaic peoples could have also returned to these areas. However, cultural adaptations that developed over the course of the Hypsithermal remained ingrained as these increasingly sedentary people remained in the lowlands and near major rivers where they had moved during the Hypsithermal (O'Brien, 2001 in Wolverton, 2005) and established ties to the land in the form of corporate cemeteries and villages (Charles and Buikstra, 1983).

The shift to greater sedentism accompanied by steady population growth across the region brought about cultural change in the Middle and Late Archaic. Enhanced exchange networks carried goods of high prestige along major river valleys (Moore, 2010a; Shields, 2010). These goods are found in mortuary contexts that provide evidence of non-egalitarian social status among group members. Gender roles shifted as logistical mobility increased for men who spent more time away from home on hunting, fishing, ritual, or trade excursions while women's decreased residential mobility meant their foraging and processing activities remained close to home. "Coupled with increased evidence of sedentism, long-distance trade appears to have supplanted group mobility as a mechanism for the movement of ideas and, possibly, as a medium for exchanging mates and cementing alliances" (Kidder and Sassaman, 2009: 675). By the Late

Archaic trade networks in the mid-South collapsed, leading to increasingly localized patterns of interaction (Anderson, 2008; Gibson, 2010).

Social anthropologists and archaeologists are not the only anthropologists to theorize about issues related to exchange – especially when that exchange involves bodies and genes rather than, or instead of, manufactured goods or ritual objects. Biological anthropologists have historically been interested in biological kin – those individuals with whom one shares alleles as the result of having a common ancestor (Fix, 2012). Conscious or not, human behavior is motivated to nurture these relationships as a means to increase one's inclusive fitness (Hamilton, 1964). Similarly, humans have elaborate cultural systems to avoid inbreeding and potential negative fitness outcomes (Fix, 2012). These systems can be far-reaching in both distance and time, creating the framework by which human mobility and mate exchange occurs (Fix, 2012). As discussed above, females are or were the nearly universal gold standard for exchange (Levi-Strauss, 1969) because they represent the labor (Bender, 1985) and progeny that will result from a marriage exchange.

Biological Distance Studies

Measures of biological distance between and among human groups are useful to anthropologists for many reasons. Biological distance studies investigate the patterns of microevolution and inheritance (Stojanowski and Schillaci, 2006). These studies answer fundamental anthropological questions regarding the evolutionary history of human groups including post-marital residence patterns and the movement of men versus women within and between groups, the large-scale movement of entire populations, the biological continuity of a given human group, and as a framework within which paleodemography and paleopathology analyses can be interpreted (Buikstra et al., 1990; Konigsberg, 2006; Stojanowski and Schillaci, 2006; Pietrusewsky, 2008). Simply, biological distance is a measure of relatedness within a sample or between samples.

The primary evolutionary mechanisms that drive the likeness or separation between groups are gene flow and genetic drift (Relethford and Lees, 1982; Fix, 1999; Stojanowski and Schillaci, 2006). Given the small population sizes and likely short temporal window commonly encountered in archaeological samples, microevolutionary processes like genetic drift and gene flow become even more relevant (Stojanowski and Schillaci, 2006).

Quantifying biological distance involves several statistical tests using either qualitative (non-metric, ‘discrete’) traits or quantitative (linear, continuous) measures which are analyzed statistically with MMD (mean measure of divergence) and Mahalanobis D analyses respectively (Mahalanobis analyses will be discussed in detail below). Bioarchaeologists use phenotypic data from the skeleton – morphometrics and qualitative traits – to compare means and frequencies of traits between two groups (Stojanowski and Schillaci, 2006). Analyses using such data have the advantage of being non-destructive while also allowing comparisons between living and ancient (skeletal) populations (Buikstra et al., 1990; Stojanowski and Schillaci, 2006). Gene flow/migration and therefore mate exchange increases the phenotypic similarity between the participating groups, allowing for measures of biological distance to be calculated based on these traits (Stojanowski and Schillaci, 2006).

Ideally, data used in biological distance studies should be as little influenced by ontogenetic and environmental processes as possible (in cases where DNA sequencing is not feasible or utilized). An assumption of biological distance studies based on such data is that any environmental effects are distributed randomly and are minimal within the populations under study (Stojanowski and Schillaci, 2006). Similarly, measures with the greatest influence from genetics as opposed to environment should be used (i.e. those that are less plastic, or with a narrower range of inherent variation). Stature, for instance, would not make for the best (or most accurate) estimate of biological distance if used on its own because it is highly influenced by relative levels of nutrition and/or stress during childhood (Stinson, 1990). When combined with measures of body breadth and intralimb indices, variation in stature can be useful to identify patterns in the data (Auerbach, 2010).

The study of biological distance has naturally undergone quite a revolution in the last century, mirroring paradigm shifts that accompanied changing conceptions of race, populations, and “varieties” of man. By the 1970s and certainly into the 1980s, anthropologists were shifting their foci from racial groups, “types,” or “varieties,” to the “population” and the structure of variation therein. Biological distance studies are not interested in “types” per se, or in necessarily classifying skeleton X into group X (Stojanowski and Schillaci, 2006). They are instead interested in the biological structure within sites and between sites within a region (Buikstra et al., 1990).

The term population structure refers to the frequency of genes or genotypes in a population or subpopulation (Relethford and Lees, 1982) or similarly, the sizes of local demes and the amount and pattern of migration among them (Fix, 1999). Studies of population structure have historically taken a regional focus (Fix, 2012). In their review of biodistance studies from mid-1950 to 1985, Buikstra et al (1990) finds that intrasite studies of human genetic variation took second place to research into paleodemography and paleopathology. The authors see biodistance as important for interpreting changes in demography and pathology. Stress and disease processes, as well, vary between groups and populations (Wood et al, 1992), so biodistance analyses can provide a framework for evaluating levels within sites. Additionally, Buikstra et al

(1990) argue that biodistance can be used to help interpret archaeological patterns of material remains (like Konigsberg, 1990, for the central and lower Illinois River valleys where there was little evidence for biological exchange amongst sites that were separated by considerable space and did not share mortuary patterns from the Middle Woodland to Mississippian periods) and post-marital residence patterns (Corruccini, 1998; Lane and Sublett, 1972; Stojanowski and Schillaci, 2006).

Wright (1943) developed the isolation by distance model whereby individuals and groups that live(d) closer to one another tend to be more genetically similar. While seemingly straight-forward, this model distributes individuals across infinite subpopulations evenly (with random exchange, and no spatial structure – only temporal) – something that never happens in real human groups. Stepping stone models incorporate spatial structure and assume that all populations are arranged linearly with migration happening more frequently with closer nodes/groups than with others (Bodmer and Cavalli-Sforza, 1968; Konigsberg, 1990). Some of the more sophisticated statistical procedures for ascertaining biological distance would have to wait for advanced multivariate statistical procedures and computers that became widely available in the mid-1970s.

Defining population structure takes either a model-free or model-bound approach, or perhaps a combination of the two. Model-free approaches measure the pattern of population differentiation within a group overall, regardless of the forces that created that differentiation (Pietrusewsky, 2008; Relethford and Lees, 1982) with gene flow, genetic drift, or localized selection acting as the primary forces that drive population structure and change (Fix, 1999).

Model-bound approaches try to estimate genetic parameters (like admixture and isolation by distance) using theoretical models of population structure (Relethford and Lees, 1982). One method for doing this is the migration matrix method which targets genetic drift and isolation by distance specifically (Harpending and Ward, 1982; Konigsberg, 1990; Fix, 1999). The migration matrix method assumes “a matrix M, representing the probability that an individual in subpopulation *j* came from subpopulation *i*, is used in conjunction with a diagonal matrix of deviations resulting from drift to predict a variance-covariance matrix (R) of standardized gene frequencies between groups” (Konigsberg, 1990:55). In other words, observed rates of migration between subpopulations can be used to predict what the pattern of genetic variation at equilibrium would look like (Fix, 1999). The matrix migration model method is a model-bound approach to understanding population structure specifically good for genetic drift and isolation by distance (Konigsberg, 1990). The method does not carry some of the rather linear and restrictive parameters that earlier methods like isolation by distance (Wright, 1943) or the stepping-stone model (Kimura and Weiss, 1964) required. These earlier models were aimed at a more general application across genera and species (Fix, 1999) whereas the migration matrix method was more malleable to and incorporated observational data on actual human populations. To develop the migration matrix though, one needs detailed information regarding past migrations and kin relationships (Fix, 1999). These data are simply not readily available for Archaic groups of antiquity.

Many researchers today use a migration matrix model (Bodmer and Cavalli-Sforza, 1968; Konigsberg, 1988, 1990) incorporating matrices for biological distance, temporal distance, and geographic distance. Konigsberg (1990) used the migration matrix method to look at isolation by geographic and temporal distance. This work is important because it was among the first (perhaps *the* first) to analytically tackle the issue of biological distance within a site over time – diachronic, or temporal distance using a more realistic statistical approach like migration matrix method. The method is good for use within a region among a finite set of subpopulations (like the type of regional analyses undertaken here). His data set included nonmetric dental traits among central and lower Illinois River valley populations from the Middle and Late Woodland periods, as well as Emergent Mississippian and Mississippian periods – all populations that came after the Archaic period samples used in the present work. Konigsberg ran several matrices of partial correlations of biodistance on temporal distance (controlling for spatial distance) and biodistance on spatial distance (controlling temporal distance). His results confirmed the expectation that in a region that has subdivisions of populations linked by migration, space and biodistance will be positively correlated (isolation by distance) while biodistance and temporal distance will be negatively correlated within the region when controlling for space (1990). The results of his study support archaeological data for the central and lower Illinois River valleys with their variable mortuary practices during this time (Charles and Buikstra, 1983), as well as considerable spatial distance between the sites in his sample. Konigsberg's conclusion is that there was likely little biological exchange happening among the people in his Woodland and Mississippian samples (1990).

Since the exchange of goods, services, ideas, and genes is something that happens person to person within the context of broader social and cultural mores, it is of utmost importance to understanding how the Archaic peoples of the mid-South understood each other and themselves. What was the nature of interactions between groups at the Black Earth site and those living along tributaries of the Green River in western Kentucky, for instance? Did their goods and/or a few brave persons from amongst them make it to that region or even further into central Tennessee? In what ways may the structure of mate exchange have shaped lived experience and the history of the region – who was considered kin and who was not? The pattern of how this exchange was systematized, if at all, among the hunters, gatherers, and collectors of the Archaic period mid-South is what the present work tries to illuminate.

CHAPTER 2

ARCHAEOLOGICAL BACKGROUND

Physiography and Environment

Archaeologists define the southeastern United States as the area encompassing roughly all the landmass east and south of the Mississippi and Ohio rivers respectively, allowing some westward expansion across what is now Missouri, Arkansas, and Louisiana (an area south of ~38º N, 95º W) (Anderson and Sassaman, 2012). The region encompasses several distinct physiographic regions including the hills of the eastern Ozark Mountains, Central Lowlands prairie land, portions of the southern Appalachian Mountains and Piedmont, the Interior Low Plateau of what is now Kentucky and Tennessee, and the broad swath of the South known as the Coastal Plain (Gremillion, 2004; Anderson and Sassaman, 2012). In the heart of the interior Southeast, oak-hickory forests dominated the landscape where southern regions held evergreen and mixed deciduous forests of oak, hickory, and pine (Gremillion, 2004). Many portions of the Southeast contain large rivers such as the Mississippi, Ohio, and Tennessee – all of which drain tributaries from waterways between bluffs and mountains.

Archaeology in and of the Southeast

The archaeological record for the Southeast is extensive. The area benefited greatly from an expanded workforce during the WPA (Works Progress Administration) and TVA (Tennessee

Valley Authority) projects of the 1930s and 1940s. A good portion of that work went into excavations that resulted in rich archaeological samples and many subsequent researchers have made the Southeast their home. Work in the region has long taken a culture-historical approach (Sassaman, 2010; Anderson and Sassaman, 2012), pinning down ceramic and lithic sequences and defining their parent archaeological culture(s). Archaeological field method protocols were developed at the Mississippian site of Kincaid Mounds, where strict horizontal control methods came to be known as the "Chicago style" after the University of Chicago field school that trained many of the region's prominent archaeologists (Muller, 2002). A bit of functionalism also came out of the Southeast among some University of Chicago graduates (an example being Bennett, 1943, though the work nor functionalism played a large role in archeological theories of the Southeast) (Muller, 2002). It was in the Southeast that the challenge to the predominant culture-historical approach – processualism or New Archaeology – was developed at large, deeply stratified sites like Koster (located along the lower Illinois River Valley, with occupations from Early Archaic through Woodland periods) (Struever and Holton, 1979). The archaeology of the Southeast now encompasses several theoretical approaches that incorporate interests of gender identities, adaptation to past climate change, local creation of history and tradition, and the creation of space through modifications to the landscape (Muller, 2002). The approach has been described as "ecumenical and tolerant, even Catholic…" (Anderson and Sassaman, 2012: 31).

A brief overview of the archaeological record will situate Archaic period groups contextually and provide the archaeological framework of patterned cultural and material exchange out of which the hypotheses regarding mate exchange were developed.

Human occupation of the southeastern United States is evident in the archaeological record around 11,500 to 10,900 BP. Geologically speaking the Paleoindian time period begins at the end of the last glacial maximum, coincident with the initial colonization of the New World (Anderson, 2001). Like much of the rest of North America, the archaeological record in the Southeast begins with Clovis fluted lanceolate projectiles (Anderson, 2001). The points were left by small groups of hunter-gatherers who favored resource-rich areas along the region’s major rivers – the Ohio, Mississippi, Illinois, Cumberland, and Tennessee (Anderson, 2001). Clovis points are traditionally tied to a fairly mobile lifestyle hunting megafauna and other big game for subsistence. Once people reached the bountiful river areas of the Southeast their lifeways changed. They preferred the riverine environments and used them as staging areas from which to further explore and settle the region (Anderson, 1995). The once-ubiquitous Clovis points disappear from the archaeological record of the area by 10,800 BP. Lithic style in the subsequent Middle Paleoindian (10,900 to 10,500 BP) is somewhat variable across southeastern portions of North America. In the South the fluted points become smaller, or broad unfluted points (Anderson, 1995). The subsequent Late Paleoindian period (10,500 to 10,000 BP) lithic materials consist of Dalton, Hardaway, and later side-notched Taylor, Big Sandy, or Bolen styles (Anderson, 1995).

The Archaic period in the Southeast spanned nearly 9,000 years of human history in North America (Emerson et al., 2009) from 11,500 calBP to 3,200 calBP (Anderson and Sassaman, 2012). Early Archaic human adaptations in the Southeast included widely scattered groups of hunter-gatherers in uplands and riverine bottomlands (Wolverton, 2005). Archaeological evidence of abandonment across many portions of the Southeast from 9,500-8,500 calBP is coincident with the transition from late Early Archaic to early Middle Archaic (Sassaman, 2010). Those that remained in the region continued a generalized hunter-gatherer subsistence and settlement system throughout most of the Middle Archaic period. By 6,000 BP, the late Middle

Archaic period, human focus turned to resource-rich areas near major rivers and wetlands (Wolverton, 2005), where the effects of the warm and dry Hypsithermal climate episode were moderated. Sedentism and population growth increased and long-distance trade networks picked up in earnest (Charles and Buikstra, 1983). Adaptations in the Late Archaic saw much variation between sites and regions as tribal identity, ethnicity, and social hierarchy are evidenced by trade and differential mortuary patterns (Charles and Buikstra, 1983; Jefferies, 2004; Moore, 2010).

The beginning of the Woodland period is variable across the Southeast. Many archaeologists agree that the transition from Late Archaic to Early Woodland happened between 3,200 and 2,400 calendar yrBP (Kidder, 2006). The following period included many changes in lifeways, perhaps accompanied by population replacements (Sassaman, 2010). Early Woodland groups were more restricted in their subsistence and settlement ranges, participated less in long-distance trade networks, decreased their architectural, burial, and artifact diversity, and exhibited less complex societies in general than their Archaic predecessors (Kidder, 2006). One archaeological interpretation for this difference points to climate change which increased the frequency and magnitude of flooding events (Fiedel, 2001; Kidder, 2006). Other interpretations invoke gradual *in situ* change or diffusion of ceramic technology from points along the Atlantic coast. In some areas of the Southeast, namely the American Bottom region in west-central Illinois, archaeological assemblages change so much from the Late Archaic to Early Woodland periods that some have argued population replacement must have been at work (Emerson and McElrath, 2001; Kidder, 2006).

The influence of what came to be known as the Hopewell tradition was far reaching across portions of Ohio, Illinois, and Indiana during the Middle Woodland. The period and people are known for interregional exchange networks that carried raw materials into the area; obsidian from Yellowstone, copper and silver from the Great Lakes, shell from the Atlantic and Gulf coasts, galena stone from the Mississippi River Valley, and animal parts, steatite, and mica from Appalachia (Bolnick and Smith, 2007). The Hopewell burial pattern was complex and consisted of grave goods made from these imported materials as well as more locally-available resources. Site plans include burial mounds surrounded by large earthworks. Considerable cultural variation existed across the Hopewell landscape (Carr and Case, 2006; Bolnick and Smith, 2007), but functionally these groups cooperated enough to buffer themselves in times of resource stress, to build alliances, and to mark corporate identity or territory.

Beginning around 800 AD Mississippian maize farmers began building fortified villages with wall-trench houses, produced shell-tempered pottery, and had stratified societies (Yerkes, 1988). Mississippian populations in the Southeast are now known for their these villages and platform mound centers such as Kincaid or Cahokia.

Exchange in the Archaic Period

Exchange is an integral part of every human culture. Ancient exchange patterns are frequently measured by material culture. Exchange and interactions leave a mark in the biology of individuals as well, if cultural exchange is accompanied by exchange of mates or at least mating. As reviewed above, systematic patterns of mate exchange result in a pattern of gene movement or migration, reflected in differential degrees of genetic variation between men and women at individual sites. Growing archaeological evidence suggests greater cultural complexity among Archaic peoples of the mid-South than was previously recognized (Emerson et al., 2009), including periods of long-distance material and cultural exchange. The movement of goods in such a way is predicated on human action. This study hypothesizes that Middle and Late Archaic groups in the mid-South exhibit patterns of mate exchange that served to reinforce their existing cultural and material exchange of ideas, goods, behavior, and other aspects of social life.

Following Ritchie's (1932) description of the archetypical Archaic site of Lamoka Lake, researchers working in the eastern United States viewed the Archaic period as a boring middle-ground between the grand feat of Paleoindian colonization(s) and the Woodland period when agriculture, ceramics, and sedentism were believed to emerge (Sassaman, 2010; though as Sassaman points out, see Prufer, 2001: 195 for a persistent and truly archaic view of the Archaic Southeast). Early to mid-Twentieth Century archaeologists, reflecting the mores of their time, were quick to plug the newly-minted Archaic period into established cultural evolutionary sequences whereby hunter-gatherers were either unable, or unwilling, to adopt the supposedly advanced hallmarks of complex society – pottery, agriculture, and sedentism (Sassaman, 2010). Neo-evolutionary views of Archaic peoples persisted until the 1960s and 1970s when processualism, a paradigm that embraced scientific methodologies, empirically-based data, and deductive logic to understand human cultural variation and change, became the main school of archaeological thought (the New Archaeologists) (Sassaman, 2010). Through empirically-minded fieldwork a new picture of hunter-gatherers emerged in which hunter-gatherers can live long lives of relative leisure accompanied by adequate and reliable food (Netting, 1986). As comprehensive datasets emerged in the 1960s, the picture of the Archaic period as a long North American "Dark Ages" began to dissolve. It was replaced, and is still being replaced in the minds of some, with notions of local and regional distinctiveness based on cultural or ethnic distinctions embodied in place-making through the construction of burial mounds and settlements. Rather than hopeless wanderers barely subsisting without pottery and agriculture, Archaic peoples are now understood to be more adept and socially complex than previously thought.

Several examples of exchange within the mid-South United States are pertinent to the present discussion. Archaic exchange networks detectable in the archaeological record appeared in the Middle Archaic period when seasonal population aggregations allowed for exchange of materials less abundant than those in the immediate surroundings (Brown, 2004). The most common exchange items found in archaeological assemblages include marine shell and artifacts moving north from the Gulf Coast while copper artifacts flowed south from the Great Lakes (Brown, 2004). Indian Knoll, a large site that was part of the Green River Shell Mound Archaic tradition in western Kentucky, received both shell and copper goods (Brown, 2004).

Jefferies (1997, 2004) makes an argument for patterned regional interaction and exchange through material culture as an adaptation to reduced mobility (see Kidder and Sassaman, 2009 for support of this hypothesis). Middle and particularly Late Archaic bone pin artifacts from a broad swath of the Southeast demonstrate preferential interaction partners and patterned habits of exchange. Early bone pins dating to the late Middle Archaic from the Green River region of western Kentucky are stylistically simple with little effort made to decorate the pins with engravings or other details (Jefferies, 2004). Assemblages of Late Archaic bone pins from this region are still likely to include rather simple designs but may also hold an occasional crutch-top head style common to much of the Southeast, or painted rather than incised decorations on the pin shafts (Jefferies, 2004). Based on technological and stylistic similarities the Middle and Late Archaic people of the Green River region were participating in regional exchange with peoples south of them but not across the Ohio River, though it was geographically more proximate (Jefferies, 2004; Moore, 2010b). Societies along the Mississippi River and into southern Illinois, however, share much similarity in bone pin styles indicating regular exchange of information, goods, and perhaps people throughout that region (Jefferies, 2004).

Moore’s (2010b) examination of fishhooks from the Green River region supports Jefferies’ (1997, 2004) assertions that interactions were patterned. Fishhooks of the typical Green River style are found in high numbers at the Archaic sites of Eva and Anderson in Tennessee (both included in the present analysis), into Indiana (McCain site), and even into Oklahoma (Moore, 2010b). Green River fishhooks were found in fewer numbers at other Archaic sites in Illinois (Black Earth site), Indiana (Crib Mound and Firehouse sites), other parts of Kentucky (Rosenberger site), and at Russell Cave in Alabama (Moore, 2010b). The presence of Green River fishhooks throughout the region suggests that people of the Middle and Late Archaic periods experienced regional diversification in material culture.

In addition to bone pins and fishhooks, Late Archaic lithic material from southern Indiana bears similarity to Middle Archaic points from southern and western Illinois, though the pieces are quite different from lithics recovered from along the Green River in western Kentucky (Jefferies and Butler, 1982).

The Benton Interaction Sphere in the middle Tennessee Valley demonstrates regional exchange of material goods as a mechanism to reduce intergroup conflicts (Johnson and Brookes, 1989; Kidder and Sassaman, 2009). The interaction network was in operation from 3,600 to 3,000 BC (Johnson and Brookes, 1989) or 5,600 to 5,000 BP (Jefferies, 1996). Collections of large Middle Archaic Benton, Cache, and Turkey-tail points cluster in the middle Tennessee and Tombigbee River drainages, but are also found in an expanded area of the central Southeast region (Kidder and Sassaman, 2009). Source analysis of the Benton points showed that the raw material, blue-gray Fort Payne chert, came from areas south of the drainage

(Johnson and Brookes, 1989). Interpretations of the exchange patterns are similar to those discussed above for the Green River region of Kentucky. Increasing population sizes in the late Middle and Late Archaic, in conjunction with increased sedentism, meant that material goods were used to mediate intergroup conflicts, define identity, facilitate the exchange of mates, and build alliances (Johnson and Brookes, 1989; Jefferies, 1996).

Sassaman (2010) refers to groups living in the middle Tennessee River Valley in the Middle and Late Archaic as “middlemen” between the Benton sphere to the south and the core of the Shell Mound Archaic communities along the Green River to their north.

In summary, considerable temporal and geographic variation in settlement systems, social complexity, subsistence, mortuary styles, and even skeletal morphology existed in the Archaic period of the Southeast (Jefferies, 1996; Kidder and Sassaman, 2009; Milner et al., 2009). Archaeologists working within a regional framework are in fact recognizing more cultural and biological diversity in even the most remote time depths of human occupation of the continent.

These examples of Archaic period material culture exchange within the geographic bounds of the present study (Figure 2) serve to highlight just how much interaction Archaic groups had with one another, particularly during the Middle Archaic. The examples also show that the exchange was patterned – Green River groups in western Kentucky traded items mostly south, avoiding groups north and west of them across the Mississippi and Ohio Rivers – while the groups in southern Illinois and Indiana exchanged materials with one another. At least three spheres of exchange (or absence of exchange) were operating in southern Illinois, western Kentucky, and central Tennessee. It is still unclear whether similar distinctions were made in regards to the biological composition of these Middle and Late Archaic groups. Preferential exchange of goods with one group, but not another, should reflect the social and political climate of the Archaic groups participating in the exchange. This study will speak to whether the same pattern of exchange is seen in markers of biological affinity or relatedness.

Cultural manifestations such as mortuary style also show variation in regional and temporal patterns, particularly in the Middle to Late Archaic. Reflecting a less sedentary lifestyle, Early Archaic peoples were buried where needed (except at more permanent habitations like Koster's Horizon 11) (Streuver and Holton, 1979). Late Middle Archaic customs, reflective of residential sedentism, included repeated-use burial sites located outside of the living spaces or burial mounds on top of nearby bluffs (Charles and Buikstra, 1983). While mortuary customs varied in the Late Archaic, by this time individuals were typically buried in planned cemeteries with local and exotic grave goods (Milner et al., 2009). Beyond the choice of location, some variation in body position is seen in the Middle and Late Archaic sites of Black Earth in southern Illinois and the Shell Mound Archaic sites in western Kentucky. Unlike their Shell Mound Archaic neighbors, individuals at the Black Earth site were likely to be found in the extended rather than flexed position (46% of the sample at Black Earth versus 2.6% at Green River sites) (Milner et al., 2009). This is yet another example of the separation between groups in southern Illinois, Indiana, and Ohio with those just across the river in western Kentucky and northern Tennessee who were trading with each other or with groups south of the Mississippi and Ohio Rivers.

The above discussion of bone pins, fishhooks, lithics, and mortuary practices demonstrate patterned, preferential exchange among Archaic peoples in the western Southeast. Given these archaeological patterns – that the Mississippi and Ohio Rivers were major barriers to cultural and material exchange – the present analysis will assess the degree to which markers of biological exchange (mating) match the patterns produced by the exchange of cultural and material goods.

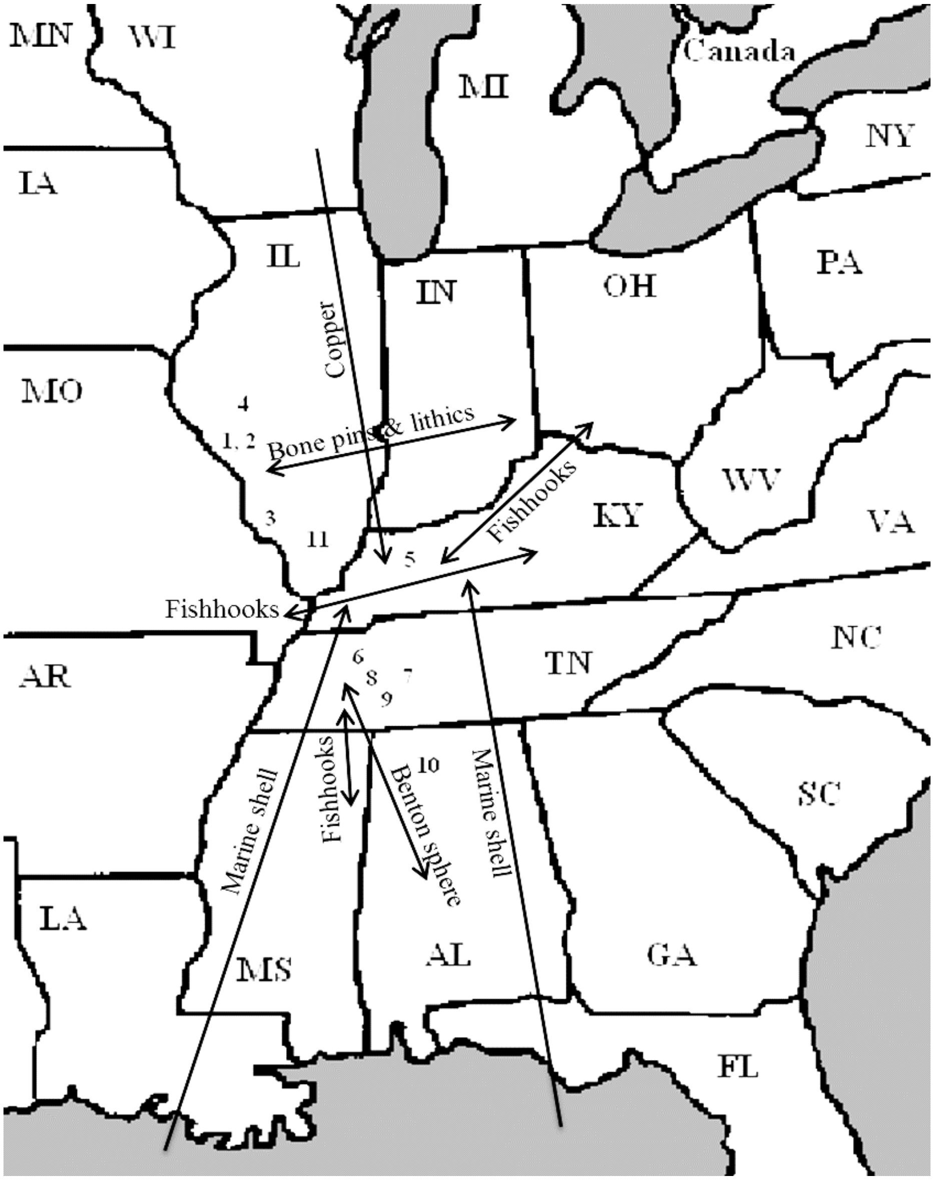

Figure 1. Prominent sites in the mid-South overlain by simplified pattern of material culture exchange.
1: Koster; 2: Elizabeth Mounds; 3: Modoc Rock Shelter; 4: Tree Row; 5: all Green River sites;
6: Big Sandy, Eva, Kay's Landing; 7: Anderson; 8: Cherry, Ledbetter Landing;
9: Oak View Landing; 10: Guntersville Basin; 11: Black Earth

Pre-Archaic Biological Variation in the New World

While most scholars agree that modern *Homo sapiens* colonized the New World from parts of Asia, little agreement exists beyond these details due to incommensurable data sets which demonstrate linguistic, cultural/material, and biological homogeneity as well as heterogeneity within Native American samples. Questions remain regarding the size and number of founding populations, the exact timing of migration(s), where founding groups originated (especially earlier versus later migrations), and whether biological continuity exists through time. Additional problems inherent in these studies include issues common to anthropological endeavors such as small sample size (particularly for the earliest material from North America), massive population movements, epidemic disease outbreaks, genetic bottlenecks within the recent Historical period (Merriwether, 2006), and legal issues in North America that potentially limit analyses of human remains (NAGPRA, for a review see Buikstra, 2006).

For decades anthropologists have envisioned the peopling of the New World as multiple waves of small groups of nomadic big-game hunters moving swiftly across the Bering Land Bridge from Asia to North America through an ice-free corridor between 14,000 and 18,000 years ago. They hunted Pleistocene megafauna such as mammoth, bears, sabre cats, giant beavers, and many other now-extinct animals using large, sophisticated projectile points of the Clovis tradition. They moved south and east quickly, reaching southern Chile by 12,500 years ago (Meltzer, 2013). Initially, many purported pre-Clovis sites suffered complications with dating, as well as whether lithics recovered at these sites were anthropogenic or taphonomic in origin. Claims of pre-Clovis occupations from California to Pennsylvania were met with skepticism. Thus, the land-bridge/big-game Clovis-first model persisted. Recently, evidence for pre-Clovis occupations in the Americas suggests that later Archaic-period populations, having undergone evolutionary processes such as genetic drift, likely harbored considerable biological and genetic variation within regions of North and South America.

The special circumstance surrounding the peopling of the New World offers a unique setting in which to think about human adaptation and microevolution. Small, mobile groups carried with them considerable genetic diversity as they migrated down the coast and/or through the interior towards the Southeast. Each successive generation negotiated their place on the landscape – whether by forming alliances with neighbors or fighting with enemies, participating in long-distance trade networks or remaining relatively isolated, engaging in ritual ceremonies both near and far, exchanging mates between groups, diversifying their language, changing their subsistence and residential lifeways, and in some cases building earthworks that still remain.

The search for ancestral Native Americans as well as the specific details regarding the peopling of the New World have long-interested the anthropological community. The topic has attracted considerable and ongoing anthropological efforts from human morphologists (Jantz and Owsley, 2001; Auerbach, 2012), archaeologists (Meltzer, 2013), linguists (Greenberg et al., 1986), and especially geneticists (Malhi et al., 2002; Kemp et al., 2007; Fagundes et al., 2008a; Fagundes et al., 2008b; Kitchen et al., 2008; Mulligan et al., 2008; Kemp and Schurr, 2010) in an effort to test models of human occupation on the continent, but also to study human adaptations, both cultural and biological, that occurred along the way.

Models that seek to explain phenotypic heterogeneity in the New World generally are limited to two explanations: multiple waves of migration (and replacement) or *in situ* change due to genetic drift and local adaptations (Powell, 2005). The three-wave migration model for the peopling of the New World relied heavily on linguistic and dental morphological groupings (Aleut-Eskimo, Na-Dene, and Amerindian), and to a lesser extent employed genetic evidence

(Greenberg et al., 1986). More dental variation was observed in the north rather than in the south and Mean Measure of Divergence analysis based on 28 dental traits showed that all New World native samples were found to resemble each other more than Old World samples. However, the samples were from late prehistoric or historic samples, most from the last 3,000 years, meaning they may not adequately reflect the earliest entrants into the continent (Powell, 1995). The Greenberg et al. (1986) "three wave" paper was, and remains, controversial. Yet, the deliciousness of a straight-forward, three-wave model backed by three different lines of evidence was snatched up and widely reprinted by popular media. Jantz and Owsley (2001) also employed models of dispersion including waves, citing more cranial diversity in Paleoindian samples as evidence for two waves of migration along a coastal route. The earliest entrants into the New World exhibited distinct cranial morphology with long, narrow cranial vaults, greater facial forwardness, and lower facial height in comparison to later individuals. When compared to samples outside the New World, the early individuals look more similar to Circumpacific populations (Jantz and Owsley, 2001). The situation in South America is comparable in that early crania from Sumidouro Cave, Brazil (8,500 yBP) look more like Africans and Australo-Melanesians with long, narrow crania, low projecting faces, and low, wide orbits and noses (Neves et al., 2007). The level of heterogeneity in South America implies two waves of migration with replacement (Neves et al., 2007). Lastly, *in situ* genetic drift is frequently used to explain heterogeneity of New World samples. Genetic drift, as a contributor to increased heterogeneity between samples, has a disproportionate effect on small groups. The first entrants into the New World likely migrated in small groups (Powell, 1995; Merriwether, 2006). Whether they spent long periods of time in Beringia waiting for an ice-free corridor to expand (Tamm et al., 2007), or they followed a route along the coast (Jantz and Owsley 2001; Jantz, 2006), the small size of founding populations would yield a pattern of homogeneity in markers closely determined by genetics. However, as population sizes grew and subsequent generations moved throughout the New World, biological variables that exhibit less genetic influence and higher rates of plasticity would cause phenotypic heterogeneity as an adaptation to many different environments in the Americas. These tenets are a question of scale and level of analysis. No matter the cause, the earliest entrants in the New World are morphologically distinct from later colonizers (González-José et al., 2001; Jantz and Owsley, 2001; Neves et al., 2007).

The situation surrounding the peopling of the New World and the subsequent dispersal across continents is immensely complex. Archaeologists working within a regional framework are recognizing more cultural and biological diversity in even the most remote time depths of human occupation of the continent (e.g. the Topper and Cactus Hill sites on the Eastern seaboard, the Channel Islands off California). Given the level of morphological diversity seemingly present in the early entrants to the New World, it is common at this point to turn to genetic data for solid answers. However, genetic analyses are still only one avenue towards understanding New World migrations. Genetic markers specific to Native Americans have not been found outside western continents. Unlike the phenotypic data, mitochondrial (Merriwether, 2006) and Y-chromosome (Karafet et al., 2006) data have been used as evidence of relative biological homogeneity within Native Americans as explained by a single migration wave with rapid expansion after the last glacial maximum (Karafet et al., 2006; Merriwether, 2006). However, the Y-chromosome (and the mtDNA molecule) is a small segment that acts as a single locus (Merriwether, 2006); it therefore may be more affected by genetic drift and mutation rather than selection (Karafet et al., 2006). Diversity does exist within the continent however, and as previously stated these differences have been attributed largely to genetic drift which occurred after colonization.

Genetic studies of Native American genomes have garnered much attention and contention over the past 30 years. Though homogenous when compared with the levels of diversity found on other continents, Native American genomes reveal considerable diversity within their larger population. Extensive genomic sampling across the Americas demonstrates a single origin of Native Americans from populations in northeast Asia (Smith et al., 2005; Tamm et al., 2007; Wang et al., 2007; Fagundes et al., 2008b). Unlike morphological or phenotypic data, both mitochondrial and Y-chromosome DNA variation show evidence of relative biological homogeneity within the Americas as explained by a single source population or migration wave with rapid expansion after the Last Glacial Maximum ~ 18 kyBP (Merriwether, 2006; Tamm et al., 2007; Fagundes et al., 2008b; Kemp and Schurr, 2010). With a comprehensive sample of autosomal microsatellite markers Wang et al. (2007) found low genetic diversity within populations and a high degree of differentiation compared to what is seen on other continents.

A growing consensus of geneticists think migrants to the New World stayed in Beringia for quite some time (the ‘Beringian Incubation Model’ or ‘Out of Beringia’ model) (Tamm et al., 2007; Achilli et al., 2008; Fagundes et al., 2008b; Kemp and Schurr, 2010). Five-thousand years before the Last Glacial Maximum an ancestral population moved into Beringia (Fagundes et al., 2008b). Over the subsequent 5,000 years small groups were affected by genetic drift and underwent a reduction in population size, further contributing to a loss of genetic diversity while in Beringia (Fagundes et al., 2008b). As the glacial stage came to a close around 18,000 ya the population expanded and began migrating quickly south (Fagundes et al., 2008b). This model has received criticism from archaeologists due to a lack of material evidence for the purported

5,000-plus years of habitation on the Beringian Land Bridge (Meltzer, 2013). It is likely that these sites have been lost to taphonomic processes related to the harsh tundra and coastal environment (nearly all would be under water), hampering reconciliation between genetic and material sets of data.

Genetic diversity of autosomal microsatellite markers decreases in a clinal fashion, indicating a north to south migration (Wang et al., 2007) whether along the coast or through the interior. In fact, the distribution and frequency pattern of mtDNA led Torroni et al. (1993) to conclude that tribalization of groups moving south began early. No matter their route, the first entrants into the New World likely migrated in small groups (Powell, 1995). Therefore, genetic drift and population bottlenecks (Fagundes et al., 2008b) contributed to the pattern of genomic variation we see today.

Though a single genetic origin is favored by most geneticists today, interpretations vary regarding the specific route(s) colonizers took southward. Ice-free zones along the Pacific coast west of the Cordilleran ice sheet may have been in place by 14 kya (Wang et al., 2007), allowing for a coastal migration. The ice-free corridor of the interior land mass opened around 14 kya and would not have been suitable habitat for human populations prior to then (Fagundes et al., 2008). Wang et al. (2007) favor a coastal route based on autosomal markers and language. Perego et al. (2009) favor two routes of colonization following time spent in Beringia – one that carried haplogroup D4h3 down the Pacific coast, and another that carried X2a through an ice-free corridor. Kemp et al. (2007) found a variant of mtDNA haplogroup D and Y-chromosome haplogroup Q-M3* in a 10,300 yrBP male from On Your Knees Cave on Prince of Wales Island, Alaska. This same mtDNA variation is shared with the Cayapa of modern Ecuador (Rickards et al., 1994; Perego et al., 2009; Kemp and Schurr, 2010) and this distribution has been used to support a swift, coastal migration route south.

Many studies over the past two decades have identified four and then five mtDNA haplogroups present in indigenous peoples of the New World: A, B, C, D, and X (Schurr et al., 1990; Torroni et al., 1993; Achilli et al., 2008; Fagundes et al., 2008b; Kemp and Schurr, 2010). The structure of mtDNA haplogroups indicates they coalesced 18,000 to 21,000 yrBP, coincident with receding glaciers at the end of the Last Glacial Maximum and the colonization of the Americas (Achilli et al., 2008). More than 95% of Native American mtDNA haplogroups fall into haplogroups A-D (Jobling et al., 2004). Many groups share some frequency of at least three of the five main mtDNA haplogroups (A-D, X) (Kemp and Schurr, 2010), though there are some interesting exceptions. Na-Dene speakers are nearly fixed for haplogroup A and 27% of them have a specific type of A with a base substitution of A to G at locus 16331 (Torroni et al., 1993; Kemp and Schurr, 2010). Parr and colleagues (1996) analyzed haplotype diversity in the Fremont culture (250-1300 AD) of the Great Basin (northern Utah in this case). None of the individuals carried haplogroup A, the most common haplogroup among indigenous Americans (Parr et al., 1996). The majority of the Fremont sample had haplotype B with low frequencies of C and D (Parr et al., 1996). The authors attribute the irregular distribution of haplotypes in their Fremont sample to genetic drift. Haplogroup D3 is found exclusively in Eskimo populations, whereas D2a is found among a broader swath of indigenous peoples including Aleuts, Eskimos, and Na-Dene speakers (Achilli et al., 2008; Perego et al., 2009). X2a haplogroup is found in high frequency (25%) amongst Ojibwas of northern Ontario but is also found in other North American groups such as the Sioux and Yakima, though at low frequencies (Malhi et al., 2002; Perego et al., 2009).

In a survey of 21 Native American samples and 54 world-wide samples, Schroeder et al. (2009) finds that a 9-repeat allele located at microsatellite D9S1120 on the Y chromosome is shared by all sampled native genomes – a private marker, so to speak. The findings support a shared genetic Asian origin for Native Americans and that founding populations could have been isolated from other Asian groups prior to colonizing the New World.

Relative levels of Y-chromosome and mtDNA variation for males and females respectively are indicative of the rate and pattern of gene flow, genetic drift, and the impact of sex-specific differences in population size on genetic variation (Bolnick et al., 2006). Male and female movements across much of the North American landscape differ. Many comparative studies have found that females are more variable in their mtDNA than males, indicative of more movement of females relative to males (Bolnick et al., 2006). The pattern is not the same across the Americas, however. In some North and Central American populations the pattern is reversed where in some South American populations there are no differences between male and female patterns of genetic variation (Bolnick et al., 2006). The patterns reflect the population and cultural histories of individual groups.

Using autosomal genetic markers, Schroeder et al (2009) found a correlation between geographic and genetic distances in their sample of Native American genomes, but that models of geographically-structured population fissions were a better fit for the data than was an explanation for population structure based solely on isolation by distance.

While native populations are more homogenous when compared to levels of diversity on other continents, evolutionary forces made these small groups of mobile hunter-gatherers rather heterogeneous between groups (Wang et al., 2007). Following the end of the Last Glacial Maximum when these groups quickly moved south either via a coastal or inland route (or some of both) they carried their group-specific genomic variation with them as they populated the rest of the Continent. The preceding review serves to situate groups in the Southeast within the broader context of Native American genomes. We will now turn to genomic diversity within the Southeast specifically.

Many DNA samples from the Middle Woodland Hopewell people are available and reveal some interesting interactions and migrations in the Southeast during this time. Bolnick and Smith (2007) analyzed mtDNA haplogroups from Middle Woodland individuals buried at Pete Klunk mound group, located on the Illinois River near Kampsville, IL, and Mound 25 from Ross County, OH. The frequency of haplogroups was not significantly different between males and females, between burial mounds, or different mortuary styles defined in the literature. Males showed greater haplogroup, haplotype, and nucleotide diversity in their mtDNA supporting matrilocal postmarital residence patterns. Matrilineal descent did not influence the placement of individuals during Hopewell times, though. Status in these groups was not inherited maternally and likely was not ascribed (Bolnick and Smith, 2007). Morphologically speaking, females from these sites are more variable than males, supporting contentions that females migrated into the area from outside the group (perhaps a patrilocal residence pattern) (Bolnick and Smith, 2007). However, males inherit the mtDNA of only their mother. Presumably, if mate exchange networks were stable then patterns of variation in mtDNA would even out between males and females (Bolnick and Smith, 2007). These Hopewell peoples likely practiced matrilocal residence and experienced environmental stress that disproportionately affected females (Bolnick and Smith, 2007). Alternatively, mate exchange networks and patterns of residence may not have been stable or consistent due to demographic instability in the region during this time (see Charles, 1992; Bolnick and Smith, 2007). Surprisingly little gene flow is required to counteract drift (more than one migrant per generation is needed to prevent differences that could result from drift) (Bolnick and Smith, 2007). Two computer programs that estimate gene flow (MIGRATE and IM) estimated between three and 141 migrants per generation among Middle Woodland Hopewell groups living in the Illinois and Ohio River Valleys (Bolnick and Smith, 2007). It seems from the mtDNA data that gene flow amongst the Middle Woodland Hopewell was westward from Ohio to Illinois (Bolnick and Smith, 2007).

Mississippian and modern groups in the Southeast have also been sampled to assess their genomic variation. The Mississippians were maize agriculturalists now known by their construction of massive earthen mound centers and smaller villages throughout much of the Southeast after ~900 AD. The largest center is Cahokia, located near the Mississippi River in what is now East St. Louis, IL. Samples from Mound 72 at Cahokia revealed three mtDNA haplogroups: B (62.5%), A (25%), and C (12%) (Napier, 2000; Pritchett, 2012). The Schild site (IL) revealed more haplogroups present amongst Mississippians living there: 38.3% A, 23.4% C, 12.8% B, 8.5% D, 17% X (Raff, 2008; Pritchett, 2012). Marshall's (2011) analysis of mtDNA from the Mississippian site of Angel Mounds found 52% haplogroup A2, 20% C1, 12% D1, 8% C4c, and 4% B2. While haplogroup C1 is found in many Native American samples, the C4c form is very rare (Marshall, 2011; Pritchett, 2012). These studies show a range of genomes in Mississippian groups, including X and a rare variant C4c.

Bolnick and Smith (2003) found that mtDNA variation in the Southeast was significantly impacted following European contact. Using markers from across the genome, Wang et al. (2007) also found evidence for a recent bottleneck in Choctaw peoples of the Southeast. Other studies have found that European contact did not significantly impact native genomic variation among late pre-historic Oneota groups (Stone and Stoneking, 1998). Modern-day Cherokee mtDNA variation differs from other populations in the Southeast (Bolnick and Smith, 2003; Bolnick et al., 2006) however, their Y-chromosomes share broad similarities with Muskogean speakers. Both sets of aDNA show differences between the Cherokee and northeastern populations. Bolnick et al. (2006) postulate that the Cherokee originated or lived in the Southeast for long enough to share similarities with those neighbors via gene flow; but later Iroquoians migrated to the northeast, retaining their matrilocal residence system and restricting gene flow with neighboring patrilocal groups in the northeast.

Bolnick et al. (2006) divided their sample of modern Native American genomes into north and south culture groups based on language, lineage, and residence patterns. Analyzing the effect of culture on haplogroup variation, they found that groups from the same culture area share similar patterns of Y-chromosome variation and that this difference accounted for a significant portion of the total genetic variance they found in the eastern Woodlands as a whole (Bolnick et al., 2006). Southeastern groups, as opposed to those from the northeastern portion of the Eastern Woodlands, exhibit similar frequencies of Y-chromosome haplogroups, exhibit nearly the same haplotypes, and cluster together in a multi-dimensional scaling analysis of genetic relationships among populations (Bolnick et al., 2006). The same pattern is not shown in samples of groups from the northeast (Bolnick et al., 2006).

In review, Southeast Native American groups harbor all four major mtDNA haplogroups in decreasing frequency from A to D (Bolnick and Smith, 2003; Smith et al., 2005). Small effective population sizes means that genetic drift likely played a role in structuring genetic diversity once these groups were on the American continent (Wang et al., 2007). Though largely limited for now to later Holocene samples, the pattern of genomic diversity within the region demonstrates gene flow often enough that later Mississippian samples still harbor all haplogroups identified in the founding samples. The pattern for the Southeast also differs from the Northeast in that males from the Southeast participated in considerable gene flow between groups (Bolnick et al., 2006).

The genomic research reviewed above was performed largely on populations that came after the ones used in the present study. It also reviews mtDNA and Y-chromosomal data which are not the same as studying the morphology of long bones, teeth, or crania. What the genetic structure of later groups reveals is considerable variation within a relatively homogenous group.

The composition of human groups embodies issues paramount to human concern – ancestral relationships, reproduction, mate selection, residence patterns, and bio-cultural interactions. The picture emerging from recent anthropological data on Archaic-period peoples of the mid-South suggests considerable genetic and cultural differentiation may already have been in place by the Early Archaic period (Sassaman, 2010). Subsequent population replacement(s) and/or migrations, combined with Middle and Late Archaic-period networks of interaction and exchange based on alliances and kinship, produced a mosaic of cultural expressions across the Southeast by the close of the Archaic period.

CHAPTER 3

MATERIALS

Archaic Populations in the Mid-South Sampled Here

The present study comprises data from individuals excavated from Archaic period sites in the mid-South United States. Key archaeological sites in the Green River region of western Kentucky, the Carrier Mills Archaeological District in southern Illinois, and the middle Tennessee Valley are included to provide an expansive, though bounded geographic region (Figure 2 and Table 1).

Green River Region of Western Kentucky

Situated in western Kentucky, the Green River is a small tributary of the Ohio River and home to a cluster of many Archaic period archaeological sites (Figure 3). Collectively, the sites are known for thick shell midden deposits and numerous human burials that span 6,500 to 4,500 cal yrBP, the late Middle Archaic to Late Archaic periods (Crothers and Bernbeck, 2004). The Green River group includes many sites: Barrett (15McL4), Butterfield (15MCL7), Carlston Annis (15BT5), Chiggerville (15OH1), Parrish (15HK45), Read (15BT10), Ward (15McL11), and perhaps the most famous of Archaic period sites, Indian Knoll (15OH2).

Table 1. Archaeological sites included in this study

Geographic area	Site	Period
Green River, KY	Indian Knoll (15OH2)	Middle to Late Archaic (8,900 to 3,200 cal yrBP)
Middle TN Valley	Big Sandy (25HY18) Cherry (84BN74) Eva (6BN12) Ledbetter Landing (9BN25) Oak View Landing (1DR1)	Late Early Archaic to Late Archaic (9,500 to 3,200 cal yrBP)
Southern Illinois	Black Earth (Sa-87)	Middle to Late Archaic (8,900 to 3,200 cal yrBP)

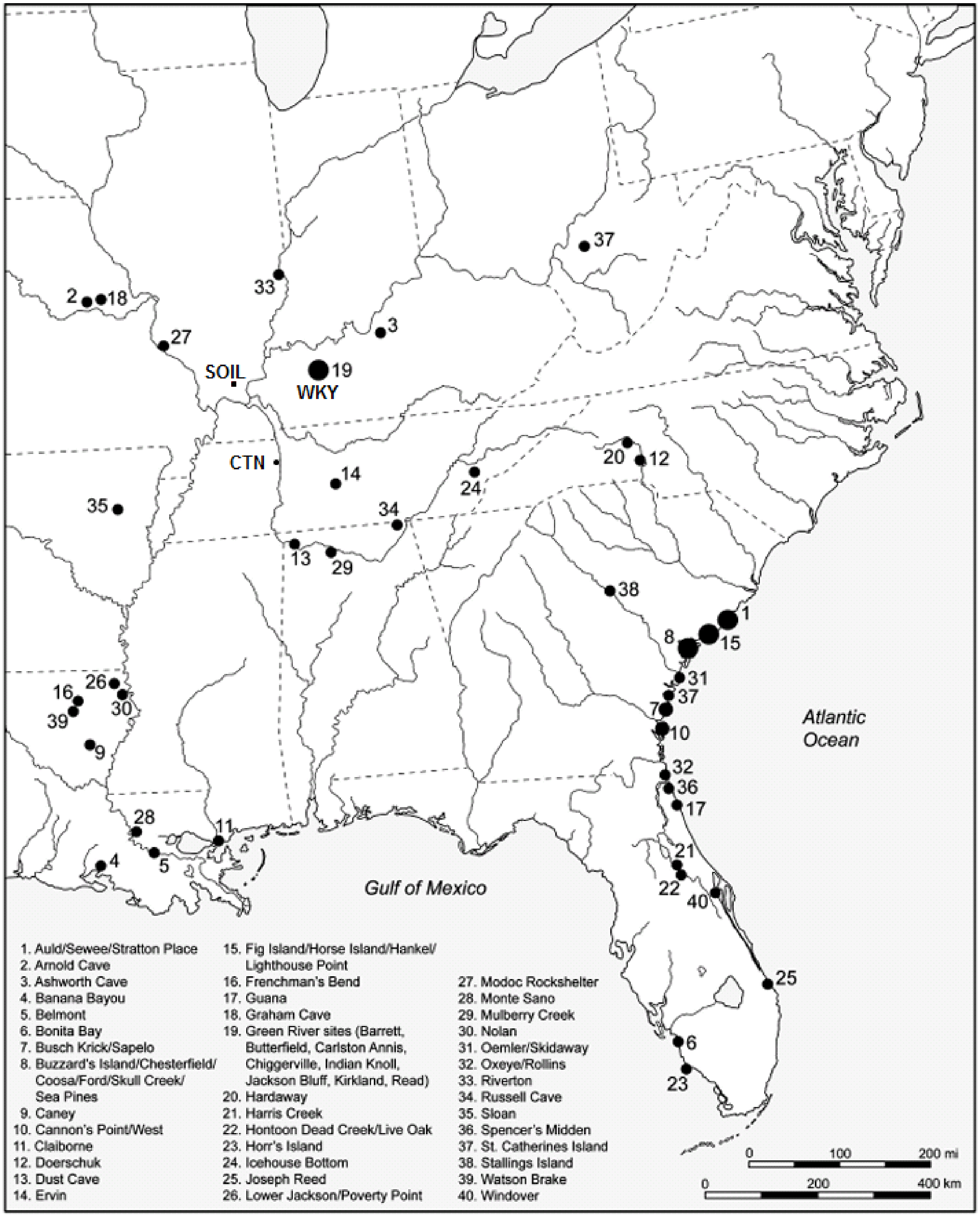

Figure 2. Locations of Archaic period sites. Modified from Anderson and Sassaman, 2012 (p. 68 Figure 3-1). Sites used in the present analysis are denoted with SOIL for the Black Earth site in the Carrier Mills Archaeological District in southern Illinois, CTN for sites long the Middle Tennessee River Valley (Eva, Cherry, Ledbetter Landing, Big Sandy, and Cherry), and WKY for Indian Knoll along the Green River in western Kentucky.

The history of archaeology at the Green River sites deserves review. The shell mounds were known to interested laymen and professional archaeologists going back to Clarence B. Moore who surveyed the area from 1913 through 1917, traversing the interior waterways in the Gopher of Philadelphia (or, the Gopher), his steamboat (Polhemus, 2002). Moore recorded and later published his meticulous field notes in which he described the geography, mounds, and burials of many sites now inundated by damming along the Tennessee River during the middle of the last century (Polhemus, 2002).

Moore's investigations along the Green River in the Gopher lasted from November 8, 1915 to February 27, 1916. His time at Indian Knoll lasted just under a month, during which time he identified 298 burials and many disturbed remains (Polhemus, 2002). Moore's work along the Green River drew the attention of later archaeologists such as William S. Webb who directed Works Progress Administration labor in the excavation of mounds and shell middens in this area from the late 1930s into the 1940s. C.B. Moore's legacy lies both in his meticulous and copious notes, journals, and published reports, and in creating awareness of ancient Indian sites for preservation and protection.

William S. Webb picked up in the Green River where Moore's investigations left off. The resulting WPA projects in the region are well known. Webb visited Indian Knoll in 1937 and recorded 880 burials in addition to what Moore identified 20 years earlier (Polhemus, 2002). Additionally, where Moore saw fishing nets and netting needle artifacts, Webb realized that the grave goods unearthed at Indian Knoll were atlatl weights (Polhemus, 2002).

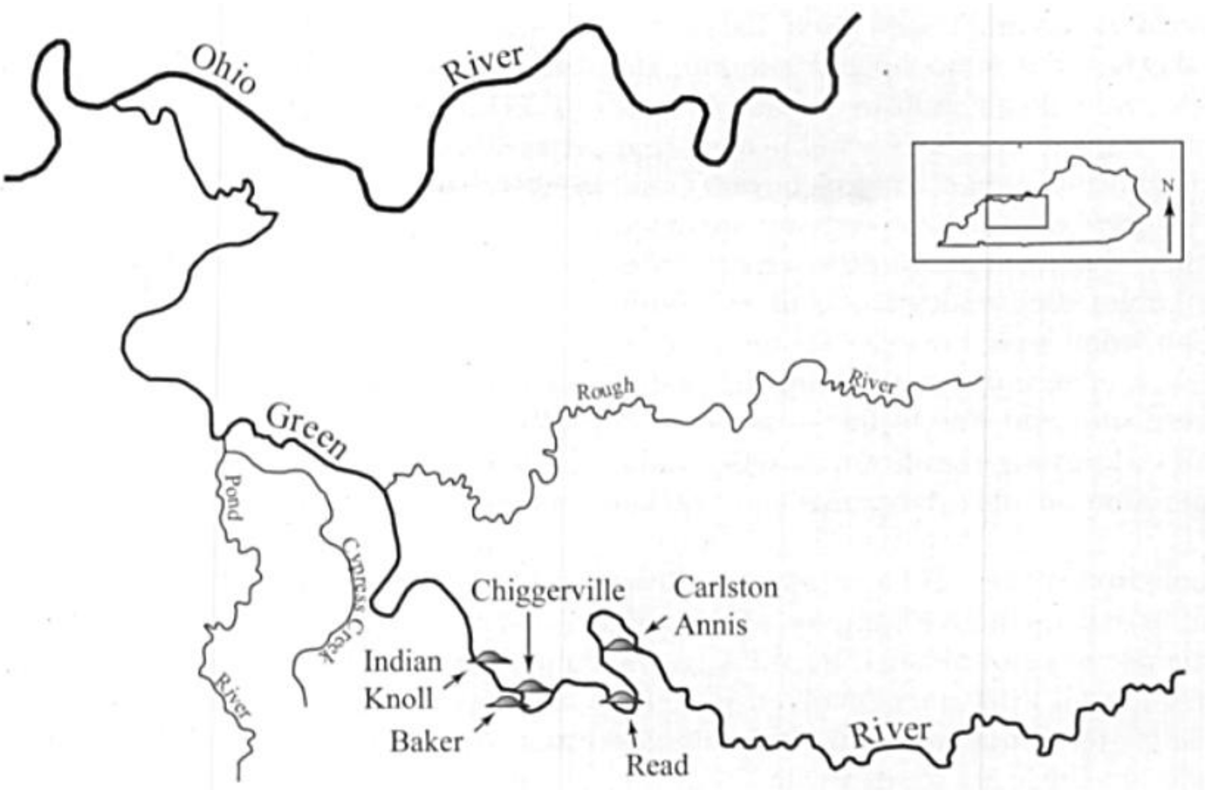

Figure 3. Green River region of western Kentucky. From: Moore (2010, Figure 1).

The Green River sites have been used to demonstrate increased sedentism in the lower Ohio River Valley with the assumption that the thick, dark shell middens are indicative of sustained occupation in those areas (Crothers and Bernbeck, 2004; Milner et al., 2009). Mortuary treatment at Green River sites consisted of placing human remains in the shell middens without planning or structure (Crothers and Bernbeck, 2004; Milner et al., 2009). Most skeletons were found flexed, in shallow pits, and were usually placed in single internments with shell and middens overlaying them (Milner et al., 2009). Unlike their neighbors in southern Illinois, some Green River burials included strings of marine shell-disk beads in high quantity and most were unlikely to be covered in red ocher (Milner et al., 2009). The mounds of shell were not constructed for the express purpose of holding burials but were instead an opportune place to dispose of both the human remains and the remains of ceremonial feasting (Crothers and Bernbeck, 2004).

Comparisons of skeletal morphology within the Green River area are numerous and represent some of the most intensive and pioneering in all of bioarchaeology. The Indian Knoll site (4508 ± 365 to 6100 ± 315 BP) is a Late Archaic shell-midden (Rothschild, 1979). Given the alkaline soil due to high quantities of shell in the burial middens, many of the remains recovered from Indian Knoll are of good preservation (including the youngest members of the sample). Clyde Snow (1948) provided analysis of more than 1,200 individuals recovered from the large site. Snow’s analysis shows the residents interred at Indian Knoll are of slender, medium body size and build with adult stature around 65” for males and 61” for females. They had long arms when compared to modern Europeans, with specifically longer forearms and lower legs. Though variants were found, the vast similarity of skull morphology within the Indian Knoll sample led Snow (1948) to describe them as inbred or isolated. Their basic head morphology is a roof-shaped, high cranial vault with slight to medium slope to the forehead, medium expression at the glabellar region, large faces with prominent zygomatic bones, square/everted angular mandibles with moderate chins, medium proportions of nasal aperature breadth and height, sharp nasal sills, and an high apex to the occipital bone (Snow, 1948). Their teeth are larger and less complex than Woodland period samples from the Ohio Valley (Sciulli, 1979) and Mesolithic and Australoid groups (Perzigian, 1976).

More recent work on the Green River skeletal material shows geography played a large role in keeping the Green River peoples rather cohesive as a group (Sciulli, 1979; Herrmann, 2002). Females were found to have greater variation in cranial non-metric traits, indicative of patrilineal or patrilocal post-marital residence patterns (Herrmann, 2002).

Archaic peoples living along the Green River and its tributaries participated in networks of exchange that moved goods and people across the landscape of the mid-South and Southeast. Copper artifacts and fragments of artifacts were recovered from Indian Knoll, Barrett, and Carlston Annis burial contexts (Marquardt and Watson, 1983; Brown, 2004). Marine shell from the Carolinas and Florida also turned up in Green River shell midden burials (Marquardt and Watson, 1983; Brown, 2004).

Of note to the present study, Winters postulated that the Green River region was a little too far removed from the mainstream of exchange routes along the Mississippi River (in Marquardt and Watson, 1983: 334). Marquardt and Watson (1983) agree that significant engagement by the Green River peoples in overland or river trade routes remains to be demonstrated, despite the presence of non-local grave goods. This study will investigate the degree to which humans, too, may have moved between the Green River groups and neighbors to their north in southern Illinois and south in central Tennessee.

Carrier Mills Archaeological District in Southern Illinois

Intensive excavations in 1978 and 1979 at the Carrier Mills Archaeological District (Figures 4-5) in central southern Illinois revealed over 500 human skeletal remains in a multicomponent site along the north side of the South Fork of the Saline River (Jefferies and Butler, 1982; Jefferies and Lynch, 1983). The work is detailed in a large monograph, The Carrier Mills Archaeological Project: Human adaptation in the Saline Valley, Illinois by Richard Jefferies and Brian Butler (1982). The following details come from that monograph unless noted.

The District is located on low uplands (380-400 m above sea level) overlooking large lowland areas and the Saline River. The District is bisected by a small stream which separates it into east and west sections. Sitting in the western half of the Carrier Mills site, Sa-87 consists of three areas (A, B, and C). This portion of the site is known as the “Black Earth site” due to 52% of the total 52,000 m^2 area (27,000 m^2) being marked black by middens. The westernmost portion of Sa-87, covering 17,000 m^2, is known as Area A and yielded the oldest and deepest deposits. The earliest radiocarbon date from Carrier Mills site 11Sa87 is 3,955 BC (Middle Archaic) (Miller, 1981), meaning that the site was occupied by humans beginning in the Middle Archaic and lasting 5,500 years to the historic African American settlement known as Lakeview. Area A dates to the late Middle Archaic and was composed of a concentration of midden debris as well as human remains (Jefferies and Butler, 1982; Jefferies and Lynch, 1983).

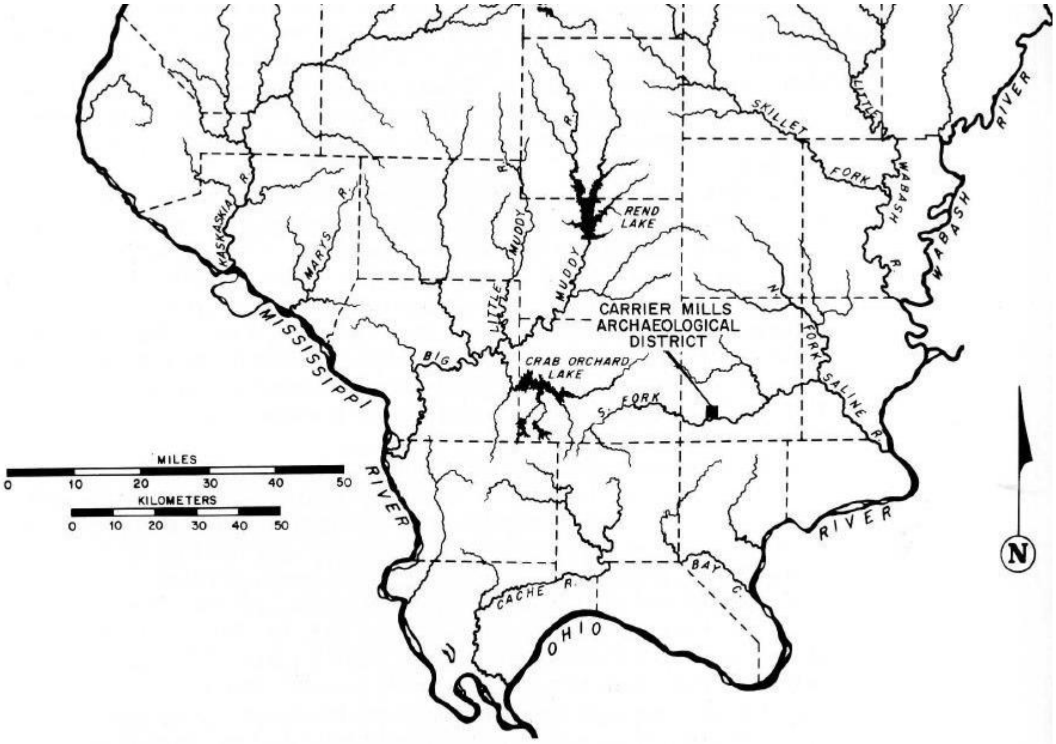

Figure 4. Carrier Mills Archaeological District location. Jefferies and Lynch (1983, Figure 14.1).

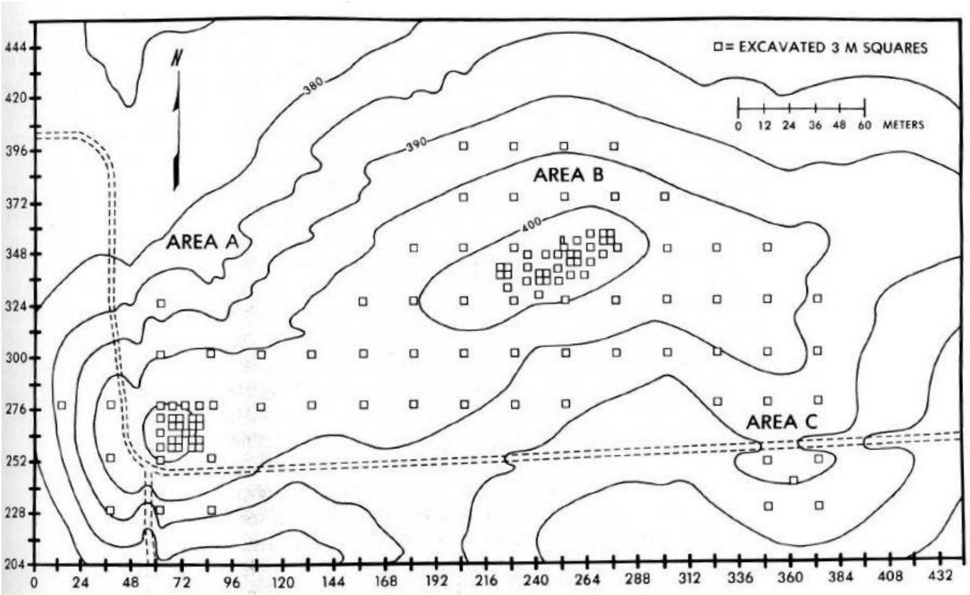

Figure 5. Three areas within the Carrier Mills Archaeological District. Jefferies and Lynch (1983, Figure 14.2).

Other Middle Archaic to Late Woodland components of the Carrier Mills site are found in Area B of Sa-87 which covers 26,000 m^2 and also includes middens. Skeletal materials dating to the Middle Archaic from Area B are poorly preserved (whereas skeletons from Area A are relatively well preserved). Given the state of bone preservation, Area B is better known for its Late Woodland component which survived somewhat better than the earlier skeletal materials. Area C is the smallest unit within Sa-87. Occupation in this portion was less intense than in Areas A or B, representing Middle Archaic through Late Woodland components. The midden in this area was heavily disturbed prior to archaeological investigation.

Sa-88, covering 30,000 m^2 along the ridge line just south of Sa-87, contained two middens and multiple sets of human remains from the Middle Archaic to Late Woodland time periods. The preservation and stratigraphic context of these remains is less than that seen in Area A of Sa-87, and is a closer match to Area B of Sa-87. The other area is Sa-86, in the eastern half of the project district, contains Middle Archaic through Mississippian materials.

Lithics from southern Indiana dated to the Late Archaic bear similarity to Middle Archaic points from southern and western Illinois. However, exchange networks did not pick up in earnest until the Middle Woodland, and not all that marked in the lower Ohio Valley (Jefferies and Butler, 1982). Middle Archaic lithic complexes at Carrier Mills are very similar to what was recovered from nearby sites along the lower Illinois River Valley (Helton phase) and American Bottom (Jefferies and Butler, 1982). Jefferies and Butler (1982) call for more research on the Carrier Mills skeletal collection to better understand the "physical, demographic, and health characteristics of the local population" (Jefferies and Butler, 1982: xii) and add that "the Saline River drainage basin in southeastern Illinois is an area very poorly understood in terms of its prehistory" (Jefferies and Butler, 1982: 9).

Middle Tennessee River Valley

Sites near Cypress Creek, a tributary of the Tennessee River as it runs north-south through western Tennessee, provide a geographical outlier to some of the more proximate sites like Carrier Mills and Green River, KY. Many excavated sites yielded human remains, including: Anderson (40WM9), Big Sandy (25HY18), Cherry (84BN74), Eva (6BN12), Kay's Landing (15HY13), Ledbetter Landing (9BN25), and Oak View Landing (1DR1). Of these, the Eva site is the best-known (Figure 6). Human occupation at the Eva site began during the early Middle Archaic period (Eva phase), around 7,500 BC with a core of Middle Archaic habitation from 6,000 to 4,000 BC. Two other phases are also present: Three Mile (late Middle Archaic, circa 4,000 to 2,000 BC) and Big Sandy (Late Archaic, circa 2,000 to 1,000 BC). These were sedentary hunter-gatherers who favored deer meat and utilized the nearby river to supplement their diet with available plant, fish, and animal remains.

Excavations at Eva revealed 180 flexed human burials (Lewis and Lewis, 1961). Many remains were of poor preservation and fragmentary. Early craniometric analyses show patterns of similarities and dissimilarities between the early Eva individuals and those from the Indian Knoll site in the Green River region of Kentucky (at the time of Lewis and Lewis's 1961 monograph, Indian Knoll individuals were used as the archetype for Archaic human morphology). Very broadly speaking, both populations exhibit an overall pattern of mesocephalic crania with high cranial vaults, bifrontal flattening, protruding occipitals, square or oblong orbits, relatively short and broad faces, and medium-sized mandibles with typical sex-marked characteristics in morphology. Differences between the early Eva material and that excavated at Indian Knoll include an absence of auditory exostoses in the Eva series, medium-sized zygomatic bones at Eva (in contrast to the comparatively larger morphology seen at Indian

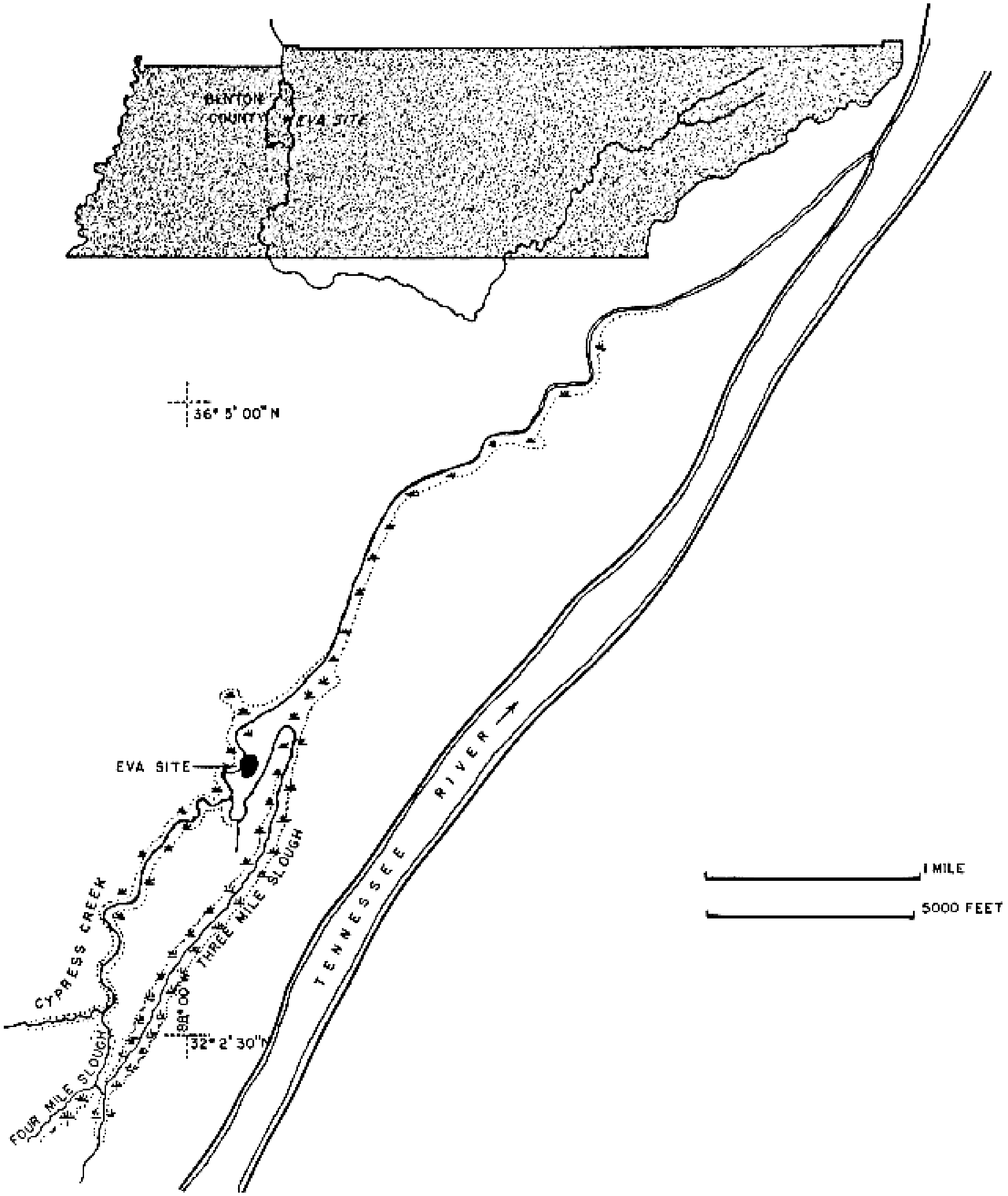

Figure 6. Eva site. From Lewis and Lewis (1961, Figure 1).

Knoll and later sites in Tennessee), narrow nasal bones in many Eva males whereas Indian Knoll people are considered to have moderately wide nasal bones, less facial prognathism in the Eva material than seen at Indian Knoll, maxillary palate shape is elliptical or U-shaped in the Eva series where at Indian Knoll it is parabolic or hyperbolic, and an overall lessening in the occurrence and expression of shovel shaped incisors at Eva contrasts with Indian Knoll and the vast majority of other Native American groups (Lewis and Lewis, 1961).

As related to the present question of biological continuity in the Southeast Archaic period, Lewis and Lewis (1961) see the Eva individuals as representative of a long, continual habitation that likely began prior to 8,000 years ago. The peculiar pattern seen at Eva in terms of maxillary shape and relative lack of shoveled incisors could be due to abnormally large and long canines noted in the Eva sample. Displacement of other teeth in the maxilla was fairly common at Eva, with a marked occurrence among Eva males. The abnormal morphology is present across strata and given the strong genetic inheritance of dental traits is supportive of a hypothesis of long-term habitation by genetically related populations at Eva. Additionally, males exhibit the trait twice as often as females and is therefore indicative of male philopatry and patrilocal organization of Archaic groups in general (Lewis and Lewis, 1961).

With a better understanding of what is known about Archaic peoples living in the mid-South, let us now turn to the skeletal material.

CHAPTER 4

METHODS

Undertaking a study as such this one required the collection of a large body of dental, cranial, and skeletal metric data in addition to information regarding patterns of exchange seen in the remains of material culture. The present study is not an archaeological one in that the skeletal remains used here were excavated decades ago. No further excavation was necessary. The patterns of cultural exchange evidenced in the archaeological record were mined from relevant archaeological literature (cited and discussed above). Additionally, geographic distances between all sites were recorded. The archaeological and geographic data sets were used to represent a framework of interactions. For example, it is clear from the archaeological record that the Ohio and Mississippi Rivers were somewhat of a geographical boundary between groups living in southern Illinois and Indiana and those living across the rivers to the south in western Kentucky and northern Tennessee. The statistical tests described below will test if the same pattern holds true for human genetic swaps, or biological exchange.

The remaining portions of this chapter include a discussion of the three subsets of morphometrics used here and information on how missing data were treated in each subset.

Principal Components Analysis and Mahalanobis D to Estimate Biological Distance

Here, univariate and multivariate analyses will test levels of biological homogeneity within and between the samples using morphometric methods that target biologically stable (canalized) skeletal traits as proxies for destructive, molecular genetic analyses. Hypothesis 1 compares estimates of biological distance with patterns of cultural exchange evidenced in the archaeological record. Hypothesis 2 compares male versus female biological variation reflective of relative levels of male versus female post-marital residence and mobility. Several statistical methods were employed to evaluate these hypotheses. Patterns of variation in the sample were first identified using principal components analysis (PCA). With that basis, measures of biological distance were estimated using Mahalanobis Distance (D). Both procedures and their applications to the present sample are discussed below.

James et al (2013) describe the type of statistical analyses used in applications such as this one as “unsupervised” (as opposed to “supervised” statistical procedures where predictions can be made and cross-validated – such as in the migration matrix methods discussed above). Unsupervised statistical procedures are data exploration tools (James et al, 2013). Validating the results of such procedures is not as straight-forward as in more traditional, supervised, methods. The true answer is, in fact, unknown – “the problem is unsupervised” (James et al, 2013: 374). As the authors point out though, data exploration and pattern recognition aid us in understanding all manner of problems from targeted advertising based on habits of internet usage to genomic similarities between individuals with cancer (James et al, 2013). It is useful to look for patterns in the data.

Biological data often include correlated variables – in fact, this characteristic is used to make accurate predictions (estimating stature based on femur length, for example). Principal components analysis (PCA) summarizes the set of correlated variables and identifies which ones contribute to the observed variation and to what degree (James et al, 2013). Visualizing the variation, either between observations/individuals or among the variables, is also possible with

PCA (James et al, 2013). The way PCA works is described beautifully by "each of the *n* observations lives in *p*-dimensional space, but not all of these dimensions are equally interesting. PCA seeks a small number of dimensions that are as interesting as possible, where the concept of *interesting* is measured by the amount that the observations vary along each dimension" (James et al, 2013: 375, emphasis in original). PCA thus looks for shared variation between the variables.

Given the high likelihood that many of the variables included in this study are correlated, Mahalanobis generalized distance matrices (D) were calculated to assess the isolation by distance between region-wide sub-samples (e.g. Konigsberg, 1990). The square root of Mahalanobis generalized distance (D) (1936) is a linear estimate of morphometric distance using the covariance of individual measurements to adjust the sample means (unlike the Penrose, 1954 "size and shape" distance statistic) to estimate biological relationships between subpopulations (Scott and Turner, 1997). This specific method allows for the differing contributions of absolutely "smaller" versus "larger" measures and allows for correlated variables (Scott and Turner, 1997). A small D value between two groups means those groups share a recent common ancestry and a closer biological relationship than with groups with whom their D value was high (Scott and Turner, 1997). Scott and Turner (1997) give several points to keep in mind when utilizing distance statistics. Divergence between groups (higher D scores) are primarily driven by genetic drift and founder effect. Similarly, gene flow can mask phylogenetic patterns. More variables used in the analysis will yield more reliable results (Livingstone, 1991), but these will be used to estimate distance with equal weight (Scott and Turner, 1997).

Quantitative Methods

Independent variables include biological sex, age, and geographic location of each sample. Only skeletally mature adults were included in the analysis. To qualify for observation an individual skeleton needed to exhibit fusion of long bone epiphyseal plates and morphological changes in the pubic symphyses and auricular surfaces consistent with adult morphology (Todd, 1921 phases 2-10, or Suchey-Brooks, 1990 phases 2-5 as seen in Buikstra and Ubelaker, 1994). If available, estimates of adult age were cross-checked with analyses made by previous researchers of the respective skeletal collections. Sex estimation was estimated from pelvic (Buikstra and Ubelaker, 1994; Phenice, 1969) and cranial morphology (Buikstra and Ubelaker, 1994) and referenced to original reports made by prior analysts. Each sample was coded with an identifier unique to geographic origin and sex. Age and sex tables are given in the next chapter: Results.

All variables were chosen because they are relatively slower to respond to the effects of gene flow than genetic drift, making them more useful for studying long-term patterns of migration (Hanna, 1962 in Relethford and Lees, 1982). Metrics utilized in the present study are reflective of continuous, polygenic variation (as opposed to discrete, monogenic variation). Dependent variables include dental, cranial, and post-cranial linear dimensions. Metrics of the cranium, dentition, and post-cranial skeleton were recorded by individual on skeletal remains with sufficient preservation to allow for the maximum number of dimensions per individual to be recorded.

Missing data points are a common concern for skeletal biologists using data sets from ancient remains. Measures of biological distance, such as Mahalanobis, require complete data sets (i.e. no missing values). This issue was addressed in several ways. First, the data were subdivided into cranial, dental, and post-cranial data sets. Parsing of the data this way allows for larger data sets and avoids having to exclude individuals who only had a measureable skull, for instance. Second, individuals who were missing more than half of the variables within each subset were excluded from observation and measurement. The third method for dealing further with missing data is different for each subset of data and those specific methods will be outlined individually below. Additional clarification can be found in Appendices I and II.

The Cranial Subset

Researchers investigating broad-scale population movements have long turned to cranial variation as a means to assess residence patterns (Tomczak and Powell, 2003) and population affinities (biological distance) (Howells, 1973; Guglielmino-Matessi et al., 1979; Falk and Corruccini, 1982; Relethford, 1994). Cranial measurements sort populations slightly better than dental metrics (Falk and Corruccini, 1982). Some regions of the skull are better than others for this purpose. For instance, the cranial vault is more plastic than the basicranium in response to temperature and humidity (Guglielmino-Matessi et al., 1979). The splanchnocranium (face) has been shown to remodel faster than the basal cranium and temporal bones (Harvati and Weaver, 2006) and to be more responsive to environmental and masticatory pressures (Powell and Neves, 1999). Craniometrics used here include standard measures that would be measured in the vast majority of comparative studies (cranial breadth and length, for example) but otherwise the measures targeted the basicranium (Table 2).

Table 2. Craniometric variables used in the present study

Measure	Description
XCL	Maximum cranial length (g-op) (1) A chord from glabella to opisthocranion
XCB	Maximum cranial breadth (eu-eu) (2) The maximum width of the skull perpendicular to the midsagittal plane, excepting inferior temporal lines and immediate surrounding area
BAB	Biasterionic breadth The breadth across the cranium between right and left asterion landmarks – the junction of the lambdoidal and parieto-mastoid sutures
FB	Frontal breadth The width of the frontal bone taken at the intersection of the coronal suture and the superior temporal line.
BAUR	Biauricular breadth (au-au) (9) The least exterior breadth across the roots of the zygomatic processes at auriculare
OC	Occipital chord (l-o) (21) The distance from lambda to opisthion in the midsagittal plane
NB	Nasal breadth (al-al) (14) The transverse breadth across the nasal aperture
MXAB	Maxillo-alveolar breadth (ecm-ecm) (7) The width of the maxilla taken on the alveolar bone above M1
FMB	Foramen magnum length The distance between basion and opisthion
CBL	Cranial base length (ba-n) (5) A chord from nasion to basion
BZB	Bizygomatic breadth (zy-zy) (3) The breadth across the face between the most lateral points on the left and right zygomatic arches
FML	Foramen magnum breadth The distance between the lateral margins of the foramen magnum at the points of greatest curvature
BPL	Basion-prosthion length (ba-pr) (6) The distance from basion to prosthion

Notations in parentheses refer to craniometric landmarks referenced in the table text. Numbers in parentheses refer to the numbers used by Buikstra and Ubelaker, 1994 and Moore-Jansen et al., 1994.

All measures in the cranial subset were either taken in the midline or transversely between matched landmarks on the skull. Side-substitution was not appropriate or possible here. Imputation was used to fill in the missing cranial data. The imputation process is described in detail in Appendix I. The average of five imputations were used in the final analysis (Table 10, Chapter 5: Results). Finally, to mitigate the effects of size, all cranial measures were standardized by the area of the foramen magnum (approximated by multiplying the foramen magnum width by the foramen magnum breadth).

The Dental Subset

Nearly all skeletal biology that incorporates biological distance does so using either the cranium (discussed above) or the dentition (Corruccini, 1972; Sofaer et al., 1972; Berry, 1976; Falk and Corruccini, 1982; Haydenblit, 1996; Hillson, 1996; Scott and Turner, 1997; Coppa et al., 1998; Corruccini and Shimada, 2002; Hanihara, 2008; Turner 1987, 1990). Teeth in particular are useful because enamel is the hardest substance in the body, is laid down in a highly regular and genetically regulated pattern, and other than attrition due to diet or cultural modification, are relatively unaffected by environment (Scott and Turner, 1997). Teeth are durable and often survive where other skeletal tissues may not, they can be directly compared between the living and the dead (Buikstra et al., 1990), they are under tight genetic control, and they vary consistently across human populations (Hillson, 1996). Heritability of dental morphology is moderate to high, and sufficient for separating groups (Sofaer et al., 1972). Dental size reflects dietary factors, while dental shape is useful for phylogenetic and intraspecies comparisons (Bernal et al., 2009), Townsend and Brown (1978) found ~64% of the variation in tooth size was due to genetic influence. Both size and shape contain genetic and environmental components and both track reasonably well with genetic and craniometric data (Hanihara and Ishida, 2005).

Metric data collected from the dentition include buccal-lingual dimensions of maxillary and mandibular premolars (P3 and P4) and molars (M1 and M2), as well as the mesio-distal measure across both maxillary and mandibular canines. Buccal-lingual dimensions are much less resistant to interproximal attrition than the mesio-distal dimension. The buccal-lingual breadth of a tooth is measured at its widest diameter from the buccal (cheek) side to the lingual (tongue) side.

Side-substitutions were made in cases where one side was observed but the anti-mere was not. That still left missing data points for some individuals (perhaps both maxillary P3's were missing, for example, leaving no option for side substitution). The side-substituted data were then passed through the imputation process five times and the average of those passes was used (Table 14, Chapter 5: Results).

If an individual had all teeth of interest in the present analysis, twenty dental measures were collected (four posterior teeth from each quadrant plus maxillary and mandibular canines on both sides), meaning that for further analyses there were too many variables relative to cases for some of the samples. The dental data was then split into maxillary, mandibular, and alternating anti-mere subsets. All the maxillary teeth were analyzed together, as were the mandibular teeth, and a third subset of data consisted of a mix of maxillary, mandibular, canines and posterior teeth – specifically this subset included maxillary and mandibular mesio-distal measures of the left canines, and the buccal-lingual dimensions of the left maxillary P3 and M1, and left mandibular P4 and M2 – “alternating anti-meres” (Table 3). Each subset of dental data was treated, and is presented, separately in the Results and Discussion chapters.

Table 3. Odontometric variables used in the present study	
Abbreviation	Dental metric
XCMD	Maxillary canine mesio-distal breadth
XP3BL	Maxillary 3rd pre-molar buccal-lingual breadth
XP4BL	Maxillary 4th pre-molar buccal-lingual breadth
XM1BL	Maxillary 1st molar buccal-lingual breadth
XM2BL	Maxillary 2nd molar buccal-lingual breadth
NCMD	Mandibular canine mesio-distal breadth
NP3BL	Mandibular 3rd pre-molar buccal-lingual breadth
NP4BL	Mandibular 4th pre-molar buccal-lingual breadth
NM1BL	Mandibular 1st molar buccal-lingual breadth
NM2BL	Mandibular 2nd molar buccal-lingual breadth
Both left and right teeth were measured for all variables when present	

Lastly, the dental data (consisting now of the side-subbed then imputed measures) were standardized with C-scores to remove size. The data were transposed in Excel (flipped so that cases were columns and variables were rows) and the mean and standard deviation of each column (really an individual since the data were transposed) were calculated. The mean was subtracted from each value in a column. Those values were divided by the standard deviation, resulting in z-scores. The data were then transposed back into the appropriate format (cases as rows, variables as columns) and the z-score process was repeated – resulting in C-Scores.

The Post-Cranial Subset

Human limb development commences during the fourth week of fetal development. Controlled by homeobox-containing (HOX) genes, limb buds develop from mesenchyme and ectoderm and continue to grow under HOX regulation. Being part of a system, though, growth and maturation of the skeleton is influenced also by epigenetic factors such as uterine environment, metabolic stress during any pre- or post-natal period, activity levels, and nutritional supplies (Mielke et al., 2006; Stinson, 1990).

While the use of dental and cranial variables for the purpose of biological distance studies is well-supported and has a long history in bioanthropology, the post-cranial skeleton has been used to a far less degree; however, recent studies indicate that these bones too, may be useful for biological distance analyses (Auerbach, 2010). Studies of body proportions are informative regarding processes of gene flow and phylogenetic signatures (Stinson, 1990; Weinstein, 2005), climatological influence (Ruff, 1994, 2002; Holliday, 1995, 1999; Holliday and Ruff, 2001), and activity patterns or biomechanical adaptations (Trinkaus, 1981; Porter, 1999). Patterns of human long-bone metric variation for the purpose of estimating biological affinity, however, have largely been ignored (Stojanowski and Schillaci, 2006; see notable recent exceptions in Case, 2003; Auerbach, 2010). Specifically, intra-limb proportions/indices, established early in ontogeny (Holliday, 1995; Holliday and Ruff, 2001) hold promise for the purpose of separating groups.

Osteometric data of the post-cranial skeleton consists of maximum long bone lengths (Table 4). These measures were used to calculate brachial, crural, and total inter-membral indices of post-cranial morphology. Brachial indices were computed by dividing the maximum length of the radius by the maximum length of the humerus and multiplying the result by 100 (Holliday, 1995; Porter, 1999). Crural indices were similarly computed by dividing the maximum length of the tibia (note method of measurement in Table 4) by the bi-condylar length of the femur and multiplying the result by 100 (Holliday, 1995; Porter, 1999). Total limb lengths are computed by adding the maximum lengths of the humerus and radius in the arm, and the femur and tibia in the leg. For the purposes of this work only, the maximum length of the femur rather than the bi-condylar length of the femur was used for calculating the crural index and also in calculating the total limb length for intermembral indices. These results are not directly comparable to other works who use these indices calculated from the bi-condylar length of the femur.

While they are typically spoken of together, brachial and crural indices (the relative length of the bones within the arm and leg, respectively) tell us something different than total limb length (Auerbach, 2010). Indices are set early in ontogeny (Holliday, 1995; Holliday and Ruff, 2001) and are therefore more reflective of phylogenetic changes rather than developmental plasticity or climatological influence (Holliday, 1999). Based on Allen’s rule (1877) for thermoregulation it might seem that both types of data would be reflective of climate as shorter limbs should be found in cold climates and longer limbs in warm climates. However,

Table 4. Post-cranial metrics used in the present study (measured and calculated)

HXL	Humerus maximum length (40) The maximum length of the humerus as measured with this proximal end against the fixed upright of an osteometric board and a moveable end placed gently against the distal end of the bone. The bone is rotated to achieve the maximum length of the bone.
RXL	Radius maximum length The maximum length of the radius as measured with the proximal end placed against the fixed upright of an osteometric board while a moveable upright is placed gently against the distal end (the tip of the styloid process). The bone is rotated to find the maximum length.
FXL	Femur maximum length (60) The maximum length of the femur from the most superior point on the head to the most inferior projection of the distal condyles.
FBCL	Femur bicondylar length (61) The condyles are placed flat against the fixed end of an osteometric board while the moveable end is adjusted to the tip of the femur head. The bone will be at an angle to the plane of the osteometric board.
TXL	Tibia maximum length (69) I measured this bone as the length of the diaphysis, excepting the lateral malleolus and the intercondylar eminence. This is slightly different from traditional measures of tibial maximum length in that it excludes the malleolus.
BRACHIAL INDEX	The ratio of the length of the radius to the length of the humerus (Radius max length / Humerus max length) x 100
CRURAL INDEX	The ratio of the length of the tibia to the length of the femur (Tibia max length / Femur bicondylar length*) x 100 *the maximum length of the femur was used here instead
INTERMEMB INDEX	The ratio of the total length of the upper limb to the total length of the lower limb ((Radius max length + Humerus max length) / (Tibia max length + Femur length)) x 100

Allen’s rule only applies to total limb length and not to intra-limb proportions of long bones. Even though studies have shown high correlations of brachial and crural indices with mean annual temperature (r=0.86 and r=0.81 respectively) (Trinkaus, 1981; Holliday, 1995) we should not automatically assume that brachial and crural indices are affected by climate (Stinson, 1990). Mean annual temperature is not likely the best measure of climate which includes other variables such as precipitation and humidity. It is more likely that temperature extremes drive selective processes acting on limb morphology (Jantz, 2006).

It is therefore not surprising that changes in limb proportions are not highly correlated with overall change in limb lengths (Holliday, 1999; Auerbach and Sylvester, 2011). Reasons for this may include biomechanical adaptation to differing patterns of mobility or different thermoregulatory response of distal versus proximal segments due to their higher surface area relative to mass (Holliday, 1999). Recent work on the evolution of human limb proportions shows that the distal elements within each limb are affected by environmental stress to a greater degree than more functionally critical body elements such as the head, hands, and feet (Pomeroy et al., 2012). In a sample of over 400 Peruvian children aged six to 14 years, Pomeroy et al. (2012) found that children raised in highland, more environmentally stressful environments, had significantly shorter distal limb segments (the tibia and ulna) while effects on other areas of the body such as the head, hands, and feet, were minimized. The authors suggest that limb proportions follow a “thrifty phenotype” model of developmental plasticity that conserves more critical resources at the expense of other less critical components of the body system.

When considered together, these data show that it is necessary to speak of proportions within each limb separately from total limb length, as absolutely long limbs may still hold low indices within them and vice versa (Trinkaus, 1981; Holliday, 1999; Auerbach, 2010; Auerbach and Sylvester, 2011). Unlike within-limb proportions, total limb length (and therefore adult stature) is heavily influenced by sexual dimorphism and nutrition (Holliday, 1999). Additional considerations for the retention of high indices within shorter limbs may be given to biomechanical advantages (Porter, 1999) and a high level of genetic influence (Holliday, 1999).

Given the above review, post-cranial data were collected with a more exploratory approach in mind. Where possible, long bone lengths were measured for the humerus, radius, femur, and tibia, from which inter-membral indices and intra-limb proportions were calculated.

The post-cranial subset of data is composed of measures from both the right and left sides. Side-substitution in this case, though, would mask any asymmetry. Missing data in the post-cranial subset (lengths of longs bones) was estimated by using sex-specific regression formulae developed from individuals in which all bones of interest were observed (discussed below) (Tables 17-18, Chapter 5: Results). For a detailed comparison of regression versus imputation for calculating long bone lengths in missing cases, see Appendix A.

CHAPTER 5

RESULTS

Summary Statistics Results

Summary descriptive statistics were run on each sub-set of data (cranial, dental, post-cranial) using R, a programming language and software environment for statistical analyses (Venables and Smith, 2014).

All data were collected by the author to eliminate inter-observer error. To estimate intra-observer error a subsample from the Carrier Mills Black Earth site in southern Illinois was measured twice approximately one year apart. Non-directional t-tests found no significant intra-observer error for any of the subsets of data and the measurements are highly correlated (Tables 5-7).

Cranial Results

The table below (Table 8) presents summary statistics for all cranial measures. In this table, individuals with missing data have been removed. No imputations or standardizations were performed on these data. Variables are listed in order from lowest to highest sample size (least to most “missingness”).

Table 5. Intra-observer error (t-test for cranial variables)		
	Observation 1	Observation 2
Mean	96.477	95.889
Variance	2247.20	2206.00
Difference between means	0.58764	
t	0.074721	
p (same mean)	0.94054	
Correlation (Pearson’s r)	0.94313	

Table 6. Intra-observer error (t-test for dental variables)		
	Observation 1	Observation 2
Mean	9.7846	9.7864
Variance	3.0271	2.9583
Difference between means	0.0018889	
t	-0.0073246	
p (same mean)	0.99416	
Correlation (Pearson’s r)	0.98657	

Table 7. Intra-observer error (t-test for post-cranial maximum long bone lengths)		
	Observation 1	Observation 2
Mean	337.78	338.53
Variance	5283.90	5317.80
Difference between means	0.75	
t	-0.046068	
p (same mean)	0.96337	
Correlation (Pearson’s r)	0.99989	

Table 8. Summary statistics for cranial measures

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
XCL	All sites								
	Males	134	176.78	6.10	0.53	162.00	190.00	176.68	3.45
	Females	135	171.76	5.46	0.47	151.00	187.00	171.68	3.18
	Central TN								
	Males	56	177.20	6.46	0.86	162.00	189.00	177.08	3.64
	Females	65	173.03	5.96	0.74	151.00	187.00	172.93	3.44
	Southern IL								
	Males	20	176.65	5.68	1.27	165.00	184.00	176.56	3.21
	Females	5	170.00	6.08	2.72	177.00	177.00	169.91	3.58
	Western KY								
	Males	58	176.43	5.97	0.78	165.00	190.00	176.33	3.39
	Females	65	170.63	4.64	0.58	160.00	180.00	170.57	2.72
FB	All sites								
	Males	128	106.94	5.66	0.50	91.00	121.00	106.79	5.29
	Females	141	105.24	5.27	0.44	92.00	120.00	105.11	5.01
	Central TN								
	Males	64	108.89	5.42	0.68	99.00	121.00	108.76	4.97
	Females	73	106.55	5.39	0.63	97.00	120.00	106.41	5.06
	Southern IL								
	Males	0	0	0	0	0	0	0	0
	Females	1	107	0	0	107.00	107.00	107.00	1.83
	Western KY								
	Males	61	104.77	5.16	0.66	91.00	116.00	104.64	4.92
	Females	67	103.78	4.81	0.59	92.00	114.00	103.67	4.63
XCB	All sites								
	Males	129	136.98	4.94	0.43	126.00	156.00	136.89	3.60
	Females	139	132.53	4.62	0.39	123.00	146.00	132.45	3.48
	Central TN								
	Males	56	137.39	4.58	0.61	129.00	148.00	137.32	3.33
	Females	67	134.18	4.93	0.60	124.00	146.00	134.09	3.67
	Southern IL								
	Males	18	138.47	7.05	1.66	127.00	156.00	138.31	5.09
	Females	5	131.60	2.41	1.08	129.00	135.00	131.58	1.83
	Western KY								
	Males	55	136.07	4.67	0.59	126.00	145.00	136.00	3.21
	Females	67	130.94	3.81	0.47	123.00	140.00	130.89	2.91
BAB	All sites								
	Males	116	121.64	7.94	0.74	105.00	140.00	121.38	6.53
	Females	121	117.80	7.44	0.68	104.00	136.00	117.56	6.32
	Central TN								
	Males	47	125.62	4.98	0.73	115.00	134.00	125.52	3.97
	Females	52	123.40	5.54	0.77	106.00	136.00	123.28	4.49
	Southern IL								
	Males	14	128.00	9.36	2.50	106.00	140.00	127.66	7.32
	Females	3	122.33	2.89	1.67	119.00	124.00	122.31	2.36
	Western KY								
	Males	55	116.62	6.49	0.87	105.00	133.00	116.44	5.56
	Females	66	113.18	5.49	0.68	104.00	126.00	113.05	4.85

Table 8. Summary statistics for cranial measures (continued)

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
BAUR	All sites								
	Males	112	125.43	4.89	0.46	113.00	139.00	125.34	3.90
	Females	117	119.42	5.00	0.46	109.00	132.00	119.32	4.19
	Central TN								
	Males	43	126.07	4.80	0.73	114.00	135.00	125.98	3.81
	Females	51	121.69	4.66	0.65	110.00	132.00	121.60	3.83
	Southern IL								
	Males	15	127.77	6.28	1.62	115.00	139.00	127.62	4.91
	Females	3	119.00	5.57	3.21	114.00	125.00	118.91	4.68
	Western KY								
	Males	54	124.28	4.26	0.58	113.00	136.00	124.21	3.43
	Females	63	117.61	4.55	0.57	109.00	131.00	117.53	3.87
OC	All sites								
	Males	101	99.43	5.37	0.53	89.00	118.00	99.29	5.40
	Females	100	96.93	4.58	0.46	86.00	112.00	96.83	4.73
	Central TN								
	Males	30	98.70	4.14	0.76	92.00	108.00	98.62	4.19
	Females	41	96.95	5.12	0.80	89.00	112.00	96.82	5.28
	Southern IL								
	Males	14	101.20	6.15	1.64	91.75	116.00	101.03	6.07
	Females	2	94.20	1.13	0.80	93.40	95.00	94.20	1.20
	Western KY								
	Males	57	99.38	5.73	0.76	89.00	118.00	99.22	5.77
	Females	57	97.02	4.25	0.56	86.00	105.00	96.93	4.38
NB	All sites								
	Males	95	23.84	1.71	0.18	19.93	27.86	23.78	7.16
	Females	93	23.15	2.07	0.21	18.25	32.12	23.06	8.92
	Central TN								
	Males	29	24.18	1.50	0.28	20.50	26.77	24.13	6.22
	Females	34	23.64	2.28	0.39	19.55	32.12	23.54	9.63
	Southern IL								
	Males	17	24.40	1.69	0.41	21.65	27.36	24.34	6.94
	Females	7	24.44	1.31	0.50	22.28	26.36	24.41	5.37
	Western KY								
	Males	49	23.45	0.25	0.25	19.93	27.86	23.39	7.51
	Females	52	22.65	0.26	0.26	18.25	27.20	22.57	8.25
MXAB	All sites								
	Males	91	64.24	3.15	0.33	57.76	72.07	64.16	4.90
	Females	84	61.51	2.70	0.29	56.17	67.66	61.45	4.39
	Central TN								
	Males	30	64.37	2.96	0.54	57.76	70.48	64.30	4.60
	Females	29	61.84	2.61	0.48	58.18	67.21	61.79	4.22
	Southern IL								
	Males	18	65.86	3.30	0.78	60.09	70.89	65.78	5.01
	Females	6	63.12	3.07	1.25	59.18	67.13	63.05	4.86
	Western KY								
	Males	43	63.47	3.01	0.46	58.21	72.07	63.40	4.74
	Females	49	61.12	2.66	0.38	56.17	67.66	61.06	4.36

Table 8. Summary statistics for cranial measures (continued)

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
FMB	All sites								
	Males	85	29.65	2.08	0.23	24.01	36.77	29.58	7.02
	Females	79	28.11	1.74	0.20	23.98	33.29	28.05	6.18
	Central TN								
	Males	27	29.48	2.38	0.46	26.57	36.77	29.39	8.07
	Females	23	28.08	1.28	0.27	26.02	30.84	28.05	4.56
	Southern IL								
	Males	10	30.34	1.84	0.58	27.40	33.30	37.01	9.04
	Females	1	23.98	0	0	23.98	23.98	32.09	0
	Western KY								
	Males	48	29.61	1.96	0.28	24.01	34.64	29.54	6.62
	Females	55	28.19	1.83	0.25	24.30	33.29	28.13	6.51
CBL	All sites								
	Males	83	102.45	3.96	0.43	93.00	113.00	102.37	3.86
	Females	79	97.57	4.46	0.50	89.00	119.00	97.47	4.57
	Central TN								
	Males	26	103.58	4.54	0.89	96.00	113.00	103.48	4.38
	Females	23	99.65	6.06	1.26	90.00	119.00	99.49	6.09
	Southern IL								
	Males	10	103.3	4.42	1.40	95.00	109.00	103.21	4.28
	Females	0	0	0	0	0	0	0	0
	Western KY								
	Males	47	101.64	3.37	0.49	93.00	109.00	101.58	3.32
	Females	56	96.71	3.31	0.52	89.00	104.00	96.66	3.42
BZB	All sites								
	Males	82	137.12	4.61	0.51	126.00	150.00	137.04	3.36
	Females	79	127.99	5.98	0.67	118.00	148.00	127.85	4.67
	Central TN								
	Males	30	138.53	4.72	0.86	126.00	150.00	138.46	3.41
	Females	32	130.59	6.39	1.13	121.00	148.00	130.45	4.90
	Southern IL								
	Males	11	136.95	6.11	1.84	128.00	146.00	136.83	4.46
	Females	1	121.00	0	0	121.00	121.00	121.00	0
	Western KY								
	Males	41	136.12	3.89	0.61	127.00	146.00	136.07	2.86
	Females	46	126.33	5.00	0.74	118.00	143.00	126.23	3.96
FML	All sites								
	Males	81	35.76	2.92	0.32	29.63	44.31	35.64	8.18
	Females	71	33.80	2.42	0.29	28.24	40.40	33.71	7.17
	Central TN								
	Males	25	35.99	2.49	0.50	31.27	41.46	35.91	6.91
	Females	20	34.68	2.22	0.50	30.64	39.50	34.61	6.41
	Southern IL								
	Males	10	37.45	3.36	1.06	33.41	44.31	37.01	9.04
	Females	1	32.09	0	0	32.09	32.09	32.09	0
	Western KY								
	Males	46	35.33	3.00	0.44	29.63	41.60	35.21	8.50
	Females	50	33.48	2.45	0.35	28.24	40.40	33.39	7.32

Table 8. Summary statistics for cranial measures (continued)

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
BPL	All sites								
	Males	71	98.30	4.63	0.55	88.00	109.00	98.19	4.71
	Females	60	93.88	3.74	0.48	84.00	105.00	93.81	3.98
	Central TN								
	Males	22	99.86	4.41	0.94	93.00	107.00	99.77	4.42
	Females	16	94.13	4.57	1.14	86.00	105.00	94.02	4.86
	Southern IL								
	Males	10	97.90	5.61	1.77	92.00	107.00	97.76	5.73
	Females	0	0	0	0	0	0	0	0
	Western KY								
	Males	39	97.51	4.38	0.70	88.00	109.00	97.42	4.49
	Females	44	93.80	3.44	0.52	84.00	102.00	93.73	3.67

The cranial data for both males and females were put through the imputation process to bolster sample sizes and estimate missing data. Table 9 provides information as to the number of imputations per each subsample and variable.

Table 10 provides summary statistics for cranial measures after averaging five imputations. Variables are still listed in order from lowest to highest sample size (least to most “missingness”).

For descriptive purposes the coefficient of variation (CV) was isolated from the above data (averaged imputed data set) (Table 11). Coefficients of variation are a normalized measure of dispersion calculated as the ratio of the standard deviation to the mean. They provide a measure of relative variation.

The CV results for males and females from all sites show a slight trend for males to be more variable overall for Maximum Cranial Length (XCL), Frontal Breadth (FB), Maximum Cranial Breadth (XCB), Bi-asterionic breadth (BAB), Occipital Chord (OC), the Maximum Breadth across the Maxilla (at M1) (MXAB), the Foramen Magnum Breadth (FMB), the Foramen Magnum Length (FML), and the distance from Basion to Prosthion (BPL) (9 of 13 variables). Pooled females from all sites have greater Coefficients of Variation for only Bi-auricular Breadth (BAUR), Nasal Breadth (NB), Cranial Base Length (CBL), Bi-zygomatic Breadth (BZB), and Frontal Height (FH) (4 of 13 variables).

Within the central TN sample itself, males have higher CV values only for Maximum Cranial Length (XCL), Maximum Breadth across the Maxilla (at M1) (MXAB), and the Breadth of the Foramen Magnum (FMB) (3 of 13 variables). Across the rest of the cranial variables in this study, central TN females are consistently more variable (higher CV values) than males (10 of 13 variables).

Table 9. Cranial data number of observed and percent of sample imputed

	All sites		Central TN		Southern IL		Western KY	
	Males	Females	Males	Females	Males	Females	Males	Females
XCL (Total)	163	163	73	81	27	11	63	71
Observed	134	135	56	65	20	5	58	65
NA	29	28	17	16	7	6	5	6
% Imputed	18%	17%	23%	20%	26%	55%	8%	8%
FB (Total)	163	163	73	81	27	11	63	71
Observed	128	141	64	73	3	1	61	67
NA	35	22	9	8	24	10	2	4
% Imputed	21%	13%	12%	10%	89%	91%	3%	6%
XCB (Total)	162	163	73	81	27	11	63	71
Observed	129	139	56	67	18	5	55	67
NA	34	24	17	14	9	6	8	4
% Imputed	21%	15%	23%	17%	33%	55%	13%	6%
BAB (Total)	163	163	73	81	27	11	63	71
Observed	116	121	47	52	14	3	55	66
NA	47	42	26	29	13	8	8	5
% Imputed	29%	26%	36%	36%	48%	73%	13%	7%
BAUR (Total)	163	163	73	81	27	11	63	71
Observed	112	117	43	51	15	3	54	63
NA	51	46	30	30	12	8	9	8
% Imputed	31%	28%	41%	37%	44%	73%	14%	11%
OC (Total)	163	163	73	81	27	11	63	71
Observed	101	100	30	41	14	2	57	57
NA	62	63	43	40	13	9	6	14
% Imputed	38%	39%	59%	49%	48%	82%	10%	20%
NB (Total)	163	163	73	81	27	11	63	71
Observed	95	93	29	34	17	7	49	52
NA	68	70	44	47	10	4	14	19
% Imputed	42%	43%	60%	58%	37%	36%	22%	27%
MXAB (Total)	163	163	73	81	27	11	63	71
Observed	91	84	30	29	18	6	43	49
NA	72	79	43	52	9	5	20	22
% Imputed	44%	48%	59%	64%	33%	45%	32%	31%
FMB (Total)	163	163	73	81	27	11	63	71
Observed	85	79	27	23	10	1	48	55
NA	78	84	46	58	17	10	15	16
% Imputed	48%	52%	63%	72%	63%	91%	24%	23%
CBL (Total)	163	163	73	81	27	11	63	71
Observed	83	79	26	23	10	0	47	56
NA	80	84	47	58	17	11	16	15
% Imputed	49%	52%	64%	72%	63%	100%	25%	21%
BZB (Total)	163	163	73	81	27	11	63	71
Observed	82	79	30	32	11	1	41	46
NA	81	84	43	49	16	10	22	25
% Imputed	50%	52%	59%	60%	59%	91%	35%	35%
FML (Total)	163	163	73	81	27	11	63	71
Observed	81	71	25	20	10	1	46	50
NA	82	92	48	61	17	10	17	21
% Imputed	50%	56%	66%	75%	63%	91%	27%	30%
BPL (Total)	163	163	73	81	27	11	63	71
Observed	71	60	22	16	10	0	39	44
NA	92	103	51	65	17	11	24	27
% Imputed	56%	63%	70%	80%	63%	100%	38%	38%

Table 10. Summary statistics for cranial measures (average of five imputations)

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
XCL	All sites								
	Males	163	176.56	5.77	0.45	162.00	190.00	176.46	3.27
	Females	163	172.16	5.25	0.41	151.00	187.00	172.08	3.05
	Central TN								
	Males	73	176.56	6.03	0.71	162.00	189.00	176.46	3.42
	Females	81	173.29	5.61	0.62	151.00	187.00	173.19	3.24
	Southern IL								
	Males	27	176.99	5.09	0.98	165.00	184.00	176.91	2.87
	Females	11	172.88	5.24	1.58	161.00	179.70	172.80	3.03
	Western KY								
	Males	63	176.37	5.81	0.73	165.00	190.00	176.28	3.30
	Females	71	170.77	4.51	0.54	160.00	180.00	170.72	2.64
FB	All sites								
	Males	163	107.29	5.45	0.43	91.00	121.25	107.16	5.08
	Females	163	105.47	5.09	0.40	92.00	120.00	105.35	4.83
	Central TN								
	Males	73	108.88	5.20	0.61	99.00	121.00	108.75	4.78
	Females	81	106.73	5.30	0.59	97.00	120.00	106.61	4.96
	Southern IL								
	Males	27	108.75	4.93	0.95	97.83	121.25	108.64	4.54
	Females	11	106.85	2.72	0.82	100.67	110.22	106.82	2.54
	Western KY								
	Males	63	104.84	5.10	0.64	91.00	116.00	104.71	4.86
	Females	71	103.81	4.69	0.56	92.00	114.00	103.71	4.52
XCB	All sites								
	Males	163	136.75	4.66	0.36	126.00	156.00	136.68	3.41
	Females	163	132.70	4.49	0.35	123.00	146.00	132.62	3.39
	Central TN								
	Males	73	137.04	4.28	0.50	129.00	148.00	136.98	3.12
	Females	81	134.23	4.67	0.52	124.00	146.00	134.15	3.48
	Southern IL								
	Males	27	138.15	6.08	1.17	127.00	156.00	138.02	4.40
	Females	11	133.06	3.34	1.01	129.00	139.20	133.02	2.51
	Western KY								
	Males	63	135.83	4.27	0.54	126.00	145.00	135.76	3.14
	Females	71	130.89	3.77	0.45	123.00	140.00	130.84	2.88
BAB	All sites								
	Males	163	121.62	7.19	0.56	105.00	140.00	121.41	5.91
	Females	163	117.95	6.74	0.53	104.00	136.00	117.76	5.71
	Central TN								
	Males	73	123.94	5.05	0.59	114.32	134.00	123.84	4.08
	Females	81	121.83	5.49	0.61	106.00	136.00	121.71	4.50
	Southern IL								
	Males	27	125.22	8.42	1.62	106.00	140.00	124.95	6.73
	Females	11	119.22	4.46	1.34	111.65	124.63	119.14	3.74
	Western KY								
	Males	63	117.38	6.73	0.85	105.00	136.09	117.19	5.73
	Females	71	113.32	5.32	0.63	104.00	126.00	113.19	4.70

Table 10. Summary statistics for cranial measures (average of five imputations) (continued)

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
BAUR	All sites								
	Males	163	125.07	4.51	0.35	113.00	139.00	124.99	3.60
	Females	163	120.15	4.87	0.38	109.00	132.17	120.05	4.06
	Central TN								
	Males	73	125.44	4.28	0.50	114.00	135.00	125.37	3.41
	Females	81	122.17	4.37	0.49	110.00	132.17	122.09	3.58
	Southern IL								
	Males	27	126.63	5.25	1.01	115.00	139.00	126.53	4.15
	Females	11	121.05	4.46	1.34	114.00	128.88	120.98	3.68
	Western KY								
	Males	63	123.96	4.21	0.53	113.00	136.00	123.89	3.40
	Females	71	117.71	4.41	0.52	109.00	131.00	117.63	3.74
OC	All sites								
	Males	163	99.03	4.43	0.35	89.00	118.00	98.94	4.47
	Females	163	97.27	3.94	0.31	86.00	112.00	97.19	4.05
	Central TN								
	Males	73	98.67	3.11	0.36	92.00	108.00	98.62	3.16
	Females	81	97.52	4.13	0.46	89.00	112.00	97.44	4.23
	Southern IL								
	Males	27	99.65	4.77	0.92	91.75	116.00	99.54	4.79
	Females	11	97.51	2.74	0.83	93.40	101.98	97.47	2.81
	Western KY								
	Males	63	99.19	5.49	0.69	89.00	118.00	99.05	5.54
	Females	71	96.95	3.89	0.46	86.00	105.00	96.87	4.01
NB	All sites								
	Males	163	23.75	1.45	0.11	19.93	27.86	23.71	6.10
	Females	163	23.15	1.70	0.13	18.25	32.12	23.09	7.34
	Central TN								
	Males	73	23.81	1.28	0.15	20.50	26.77	23.77	5.40
	Females	81	23.45	1.65	0.18	19.55	32.12	23.40	7.03
	Southern IL								
	Males	27	23.97	1.53	0.29	21.65	27.36	23.93	6.39
	Females	11	23.73	1.65	0.50	20.34	26.36	23.68	6.94
	Western KY								
	Males	63	23.60	1.59	0.20	19.93	27.86	23.55	6.76
	Females	71	22.72	1.68	0.20	18.25	27.20	22.65	7.41
MXAB	All sites								
	Males	163	64.10	2.65	0.21	57.76	72.07	64.05	4.14
	Females	163	61.94	2.41	0.19	56.17	67.66	61.89	3.89
	Central TN								
	Males	73	64.18	2.35	0.27	57.76	70.48	64.14	3.66
	Females	81	62.36	2.24	0.25	57.20	67.21	62.32	3.59
	Southern IL								
	Males	27	65.28	3.11	0.60	60.09	70.89	65.21	4.76
	Females	11	62.65	2.34	0.71	59.18	67.13	62.61	3.73
	Western KY								
	Males	63	63.50	2.64	0.33	58.21	72.07	63.45	4.16
	Females	71	61.35	2.51	0.30	56.17	67.66	61.30	4.10

Table 10. Summary statistics for cranial measures (average of five imputations) (continued)

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
FMB	All sites								
	Males	163	29.56	1.68	0.13	24.01	36.77	29.51	5.67
	Females	163	28.50	1.54	0.12	23.98	33.29	28.46	5.41
	Central TN								
	Males	73	29.51	1.69	0.20	26.57	36.77	29.46	5.72
	Females	81	28.72	1.34	0.15	26.02	33.27	28.69	4.66
	Southern IL								
	Males	27	29.64	1.46	0.28	27.39	33.30	29.60	4.94
	Females	11	28.70	2.03	0.61	23.98	31.47	28.63	7.06
	Western KY								
	Males	63	29.58	1.77	0.22	24.01	34.64	29.53	5.97
	Females	71	28.22	1.65	0.20	24.30	33.29	28.17	5.84
CBL	All sites								
	Males	163	102.30	3.77	0.29	93.00	113.00	102.23	3.68
	Females	163	99.00	4.48	0.35	87.20	119.00	98.90	4.52
	Central TN								
	Males	73	102.86	3.71	0.43	95.28	113.00	102.79	3.61
	Females	81	100.59	4.70	0.52	87.20	119.00	100.49	4.67
	Southern IL								
	Males	27	102.75	4.10	0.79	95.00	109.24	102.67	3.99
	Females	11	98.89	5.51	1.66	90.93	109.62	98.76	5.57
	Western KY								
	Males	63	101.47	3.58	0.45	93.00	111.67	101.41	3.53
	Females	71	97.19	3.25	0.39	89.00	104.00	97.13	3.34
BZB	All sites								
	Males	163	136.19	4.95	0.39	125.27	151.13	136.10	3.64
	Females	163	129.17	5.72	0.45	115.89	148.00	129.04	4.43
	Central TN								
	Males	73	136.10	5.10	0.60	125.57	150.00	136.00	3.75
	Females	81	131.15	5.66	0.63	115.89	148.00	131.03	4.31
	Southern IL								
	Males	27	137.39	5.65	1.09	128.00	151.13	137.28	4.11
	Females	11	129.95	5.55	1.67	121.00	140.35	129.84	4.27
	Western KY								
	Males	63	135.78	4.44	0.56	125.27	146.00	135.71	3.27
	Females	71	126.79	4.94	0.59	118.00	143.00	126.69	3.90
FML	All sites								
	Males	163	35.91	2.34	0.18	29.63	44.31	35.84	6.52
	Females	163	34.55	2.15	0.17	28.24	40.40	34.48	6.22
	Central TN								
	Males	73	36.20	1.88	0.22	31.27	41.46	36.16	5.20
	Females	81	35.18	1.89	0.21	30.33	39.50	35.13	5.38
	Southern IL								
	Males	27	36.21	2.43	0.47	32.33	44.31	36.14	6.71
	Females	11	34.95	1.45	0.44	32.09	36.85	34.92	4.14
	Western KY								
	Males	63	35.45	2.72	0.34	29.63	41.60	35.35	7.67
	Females	71	33.77	2.28	0.27	28.24	40.40	33.69	6.75

Table 10. Summary statistics for cranial measures (average of five imputations) (continued)

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
BPL	All sites								
	Males	163	97.74	3.74	0.29	88.00	109.00	97.67	3.83
	Females	163	94.64	3.49	0.27	84.00	105.16	94.58	3.69
	Central TN								
	Males	73	98.30	3.50	0.41	90.96	107.00	98.25	3.56
	Females	81	95.28	3.69	0.41	86.00	105.16	95.21	3.87
	Southern IL								
	Males	27	97.70	3.93	0.76	92.00	107.00	97.62	4.03
	Females	11	95.04	2.98	0.90	90.15	98.63	95.00	3.14
	Western KY								
	Males	63	97.11	3.89	0.49	88.00	109.00	97.04	4.01
	Females	71	93.85	3.21	0.38	84.00	102.00	93.80	3.42

Table 11. Coefficient of Variation for imputed cranial data set								
	All sites		Central TN		Southern IL		Western KY	
	Males	Females	Males	Females	Males	Females	Males	Females
XCL	**3.27**	3.05	**3.42**	3.24	2.87	**3.03**	**3.3**	2.64
FB	**5.08**	4.83	4.78	**4.96**	**4.54**	2.54	**4.86**	4.52
XCB	**3.41**	3.39	3.12	**3.48**	**4.4**	2.51	**3.14**	2.88
BAB	**5.91**	5.71	4.08	**4.5**	**6.73**	3.74	**5.73**	4.7
BAUR	3.6	**4.06**	3.41	**3.58**	**4.15**	3.68	3.4	**3.74**
OC	**4.47**	4.05	3.16	**4.23**	**4.79**	2.81	**5.54**	4.01
NB	6.1	**7.34**	5.4	**7.03**	6.39	**6.94**	6.76	**7.41**
MXAB	**4.14**	3.89	**3.66**	3.59	**4.76**	3.73	**4.16**	4.1
FMB	**5.67**	5.41	**5.72**	4.66	4.94	**7.06**	**5.97**	5.84
CBL	3.68	**4.52**	3.61	**4.67**	3.99	**5.57**	**3.53**	3.34
BZB	3.64	**4.43**	3.75	**4.31**	4.11	**4.27**	3.27	**3.9**
FML	**6.52**	6.22	5.2	**5.38**	**6.71**	4.14	**7.67**	6.75
BPL	**3.83**	3.69	3.56	**3.87**	**4.03**	3.14	**4.01**	3.42
Number of variables for which each sex is greater								
	9	4	3	**10**	**8**	5	**10**	3
Variables in order of least to most imputations made in that variable. Bolded values represent the higher value between males and females.								

For the sample from the Black Earth site in southern Illinois, males are more variable for Frontal Breadth (FB), Maximum Cranial Breadth (XCB), Bi-aseterionic Breadth (BAB), Bi-auricular Breadth (BAUR), the Occipital Chord (OC), the Maximum Breadth across the Maxilla (at M1) (MXAB), the Length of the Foramen Magnum (FML), and the distance from Basion to Prosthion (BPL) (8 of 13 variables total). Females have higher CV values only for Maximum Cranial Length (XCL), Nasal Breadth (NB), Foramen Magnum Breadth (FMB), Cranial Base Length (CBL), and Bi-zygomatic Breadth (BZB) (5 of 13 variables).

In the sample from Indian Knoll males are more variable than females for measures of Maximum Cranial Length (XCL), Frontal Breadth (FB), Maximum Cranial Breadth (XCB), Bi-Aseterionic Breadth (BAB), Occipital Chord (OC), Maximum Breadth across the Maxilla (at M1) (MXAB), the Foramen Magnum Breadth (FMB), Cranial Base Length (CBL), Foramen Magnum Length (FML), Frontal Height (FH), and the distance from Basion to Prosthion (BPL) (10 of 13 variables). Only for Bi-Auricular Breadth (BAUR), Nasal Breadth (NB), and Bi-zygomatic Breadth (BZB) are females more variable than males (3 of 13 variables).

Simply counting the number of variables in which a particular sex has higher CV values gives a crude view of the relative variation in these measures between males and females within each sub-region (central Tennessee, southern Illinois, and western Kentucky). Across all sites (pooled samples), males have higher CV values for 9 of 13 cranial variables. When the samples are parsed into geographic origins, central Tennessee and western Kentucky have exactly the opposite pattern of male versus female CV values. Central Tennessee males are more variable across these specific thirteen cranial variables in only three cases. The reverse is true for males from western Kentucky. These males showed higher CV values for ten of the thirteen variables. The Black Earth sample from southern Illinois show a more balanced pattern in terms of variation at these thirteen cranial variables. Males have higher CV values for only eight of the thirteen observations leaving five in which females had higher CV values.

Dental Results

Only buccal-lingual measures of the dentition were used (except for the canines, which necessitate a mesio-distal measurement). Table 12 provides the summary statistics for side-substituted dental metrics. No imputations were performed on the data below.

Since the aim was to use the dental data for purposes of biological relationships and not asymmetry in the dentition, only teeth from the left side were used (after substituting observed rights for missing lefts). Table 13 presents the state of the dental data set after imputations.

Table 14 gives summary statistics for left dental data only (after side substitutions as discussed in methods and above). Imputations were performed on the data in Table 22 and the average of five imputations was used (see Methods).

Following the same simple comparison of CV values between males and females performed above for cranial and post-cranial variables, Table 15 above summarizes just CV for dental variables.

Females are more variable (higher CV values) than males in nine of the ten (9 of 10) maxillary and mandibular dental dimensions in the sample pooled sites. Following this pattern, females from western Kentucky were more variable (higher CV values) for all ten observed variables. The pattern seen in central Tennessee and southern Illinois shows a more even distribution of variation across the ten dental variables observed here, though their patterns are reversed. Males have higher CV values for six of the ten variables (6 of 10) in the central Tennessee sample whereas it was the females from southern Illinois who had higher CV values in six of the ten (6 of 10) observations.

Table 12. Summary statistics for dental measures

		n		Mean		Stand. Dev.		Stand. Error		Min		Max		Geo. Mean		Coeff. Var.	
		L	R	L	R	L	R	L	R	L	R	L	R	L	R	L	R
XCMD	All sites																
	Males	89	92	8.13	8.17	0.42	0.42	0.04	0.04	6.51	7.13	9.18	9.56	8.12	8.15	5.11	5.16
	Females	82	96	7.93	7.98	0.51	0.48	0.06	0.05	6.43	6.5	8.83	9.03	7.92	7.96	6.43	5.96
	Central TN																
	Males	36	35	8.10	8.17	0.43	0.41	0.07	0.07	6.51	7.13	8.74	8.89	8.09	8.16	5.34	5.05
	Females	28	34	8.02	8.01	0.54	0.46	0.10	0.08	6.43	6.70	8.83	9.03	8.00	7.99	6.75	5.80
	Southern IL																
	Males	14	17	8.11	8.13	0.32	0.46	0.09	0.11	7.48	7.19	8.61	8.88	8.10	8.11	4.00	5.64
	Females	12	13	7.74	8.24	0.54	0.38	0.16	0.10	6.72	7.71	8.49	8.77	7.72	8.23	7.00	4.59
	Western KY																
	Males	39	40	8.18	8.17	0.43	0.42	0.07	0.07	7.31	7.25	9.18	9.56	8.16	8.16	5.32	5.17
	Females	41	49	7.94	7.89	0.47	0.49	0.07	0.07	6.88	6.50	8.74	8.75	7.92	7.87	5.98	6.15
XP3BL	All sites																
	Males	92	95	9.75	9.87	0.61	0.56	0.06	0.06	7.91	7.89	11.38	11.39	9.74	9.86	6.21	5.62
	Females	85	91	9.62	9.66	0.63	0.56	0.07	0.06	7.72	8.18	10.89	10.91	9.60	9.65	6.53	5.77
	Central TN																
	Males	38	40	9.70	9.97	0.68	0.54	0.11	0.09	7.98	8.95	11.38	11.39	9.67	9.95	7.03	5.47
	Females	30	35	9.69	9.71	0.73	0.60	0.13	0.10	7.72	8.18	10.89	10.64	9.67	9.69	7.49	6.21
	Southern IL																
	Males	14	16	9.93	9.85	0.61	0.57	0.16	0.14	8.75	8.63	10.67	10.65	9.91	9.83	6.16	5.83
	Females	15	11	9.67	9.69	0.57	0.61	0.15	0.18	8.75	9.04	10.66	10.91	9.65	9.68	5.92	6.30
	Western KY																
	Males	40	39	9.75	9.79	0.53	0.56	0.08	0.09	7.91	7.89	11.00	10.90	9.73	9.77	5.39	5.70
	Females	40	45	9.55	9.61	0.57	0.51	0.09	0.08	8.46	8.75	10.79	10.80	9.53	9.60	6.01	5.35
XP4BL	All sites																
	Males	94	86	9.65	9.62	0.60	0.58	0.06	0.06	8.09	8.14	11.28	10.98	9.63	9.60	6.20	6.00
	Females	94	87	9.26	9.34	0.60	0.58	0.06	0.06	6.80	7.80	10.29	10.54	9.24	9.32	6.50	6.20
	Central TN																
	Males	35	35	9.80	9.80	0.68	0.57	0.12	0.10	8.09	8.64	11.28	10.98	9.77	9.78	6.95	5.83
	Females	33	32	9.30	9.32	0.59	0.66	0.10	0.12	7.59	7.80	10.26	10.54	9.29	9.30	6.36	7.12
	Southern IL																
	Males	18	15	9.60	9.53	0.65	0.65	0.15	0.17	8.30	8.14	10.42	10.35	9.58	9.51	6.73	6.86
	Females	14	10	9.35	9.50	0.66	0.55	0.18	0.17	8.13	8.61	10.29	10.30	9.32	9.48	7.07	5.78
	Western KY																
	Males	41	36	9.54	9.49	0.48	0.52	0.07	0.09	8.20	8.15	10.70	10.57	9.54	9.48	5.03	5.50
	Females	47	45	9.20	9.32	0.60	0.53	0.09	0.08	6.80	8.23	10.26	10.53	9.18	9.30	6.50	5.65

Table 12. Summary statistics for dental measures (continued)

		n		Mean		Stand. Dev.		Stand. Error		Min		Max		Geo. Mean		Coeff. Var.	
		L	R	L	R	L	R	L	R	L	R	L	R	L	R	L	R
XM1BL	All sites																
	Males	95	88	12.04	11.92	0.59	0.57	0.06	0.06	10.78	10.29	14.02	13.36	12.03	11.91	4.87	4.77
	Females	101	95	11.81	11.75	0.53	0.55	0.05	0.06	10.47	9.92	13.20	13.05	11.80	11.73	4.51	4.69
	Central TN																
	Males	35	34	12.00	11.97	0.73	0.67	0.12	0.11	10.78	10.29	14.02	13.34	11.98	11.95	6.12	5.56
	Females	35	38	11.85	11.84	0.60	0.58	0.10	0.09	10.73	10.77	13.16	13.05	11.84	11.82	5.06	4.92
	Southern IL																
	Males	17	15	11.96	11.85	0.54	0.61	0.13	0.16	10.86	10.55	12.73	12.67	11.95	11.83	4.54	5.18
	Females	18	13	11.90	11.88	0.32	0.48	0.08	0.13	11.36	10.99	12.67	12.70	11.90	11.87	2.71	4.02
	Western KY																
	Males	43	39	12.10	11.91	0.46	0.46	0.07	0.07	11.23	10.81	13.23	13.36	12.09	11.91	3.81	3.87
	Females	48	44	11.75	11.63	0.55	0.53	0.08	0.08	10.47	9.92	13.20	12.81	11.74	11.62	4.65	4.56
XM2BL	All sites																
	Males	100	103	12.01	11.92	0.69	0.68	0.07	0.07	10.07	10.03	14.12	14.03	11.99	11.90	5.77	5.68
	Females	111	103	11.65	11.38	0.64	0.62	0.06	0.06	9.50	9.45	13.16	13.04	11.64	11.36	5.46	5.46
	Central TN																
	Males	37	41	11.99	12.01	0.82	0.76	0.14	0.12	10.07	10.30	14.12	14.03	11.96	11.99	6.86	6.36
	Females	35	36	11.60	11.39	0.78	0.75	0.13	0.12	9.50	9.45	13.13	13.04	11.58	11.36	6.76	6.55
	Southern IL																
	Males	18	17	12.06	12.01	0.75	0.71	0.18	0.17	10.18	10.03	13.10	12.78	12.04	11.99	6.23	5.91
	Females	18	17	11.82	11.48	0.63	0.49	0.15	0.12	10.60	10.55	13.16	12.33	11.81	11.47	5.37	4.30
	Western KY																
	Males	45	45	12.02	11.80	0.56	0.57	0.08	0.08	10.81	10.48	13.25	13.02	12.00	11.79	4.64	4.83
	Females	58	50	11.63	11.33	0.53	0.57	0.07	0.08	10.55	9.75	12.79	12.55	11.62	11.32	4.58	4.99
NCMD	All sites																
	Males	98	95	7.22	7.19	0.47	0.46	0.05	0.05	6.15	5.80	8.54	8.53	7.20	7.18	6.51	6.38
	Females	86	97	6.96	6.92	0.43	0.49	0.05	0.05	5.87	5.60	8.34	8.33	6.95	6.91	6.16	7.02
	Central TN																
	Males	32	29	7.28	7.15	0.58	0.56	0.10	0.10	6.15	6.17	8.54	8.53	7.26	7.13	7.98	7.86
	Females	21	26	7.02	6.85	0.37	0.51	0.08	0.10	6.34	5.60	7.72	8.07	7.01	6.83	5.21	7.39
	Southern IL																
	Males	20	19	7.20	7.28	0.40	0.47	0.09	0.11	6.32	6.24	7.83	8.00	7.18	7.27	5.59	6.46
	Females	15	16	7.14	7.10	0.60	0.60	0.15	0.15	6.23	6.04	8.34	8.33	7.12	7.07	8.40	8.51
	Western KY																
	Males	46	47	7.19	7.18	0.41	0.38	0.06	0.06	6.24	5.80	8.29	7.81	7.18	7.17	5.75	5.32
	Females	50	55	6.88	6.91	0.38	0.43	0.05	0.06	5.87	5.61	7.66	7.90	6.87	6.90	5.52	6.27

Table 12. Summary statistics for dental measures (continued)

		n		Mean		Stand. Dev.		Stand. Error		Min		Max		Geo. Mean		Coeff. Var.	
		L	R	L	R	L	R	L	R	L	R	L	R	L	R	L	R
NP3BL	All sites																
	Males	115	105	8.28	8.29	0.44	0.44	0.04	0.04	7.05	7.18	9.38	9.19	8.27	8.28	5.34	5.29
	Females	107	109	7.95	8.01	0.54	0.49	0.05	0.05	6.79	6.66	9.15	9.22	7.93	7.99	6.74	6.12
	Central TN																
	Males	40	37	8.38	8.31	0.50	0.48	0.08	0.08	7.06	7.30	9.38	9.19	8.36	8.30	5.97	5.78
	Females	33	36	7.95	8.13	0.57	0.54	0.10	0.09	6.83	6.87	8.83	9.22	7.93	8.11	7.16	6.63
	Southern IL																
	Males	23	23	8.23	8.17	0.46	0.47	0.10	0.10	7.05	7.18	8.96	9.18	8.22	8.16	5.54	5.79
	Females	18	21	7.95	8.05	0.47	0.42	0.11	0.09	6.99	7.27	8.73	8.84	7.94	8.04	5.97	5.20
	Western KY																
	Males	52	45	8.24	8.33	0.38	0.38	0.05	0.06	7.42	7.55	9.05	9.06	8.23	8.32	4.66	4.56
	Females	56	52	7.94	7.91	0.54	0.47	0.07	0.07	6.79	6.66	9.15	8.82	7.93	7.90	6.83	5.93
NP4BL	All sites																
	Males	116	111	8.46	8.53	0.55	0.47	0.05	0.04	6.75	7.41	10.47	9.87	8.44	8.52	6.56	5.46
	Females	118	127	8.18	8.26	0.50	0.57	0.05	0.05	5.98	6.94	9.33	11.90	8.17	8.24	6.11	6.87
	Central TN																
	Males	40	41	8.59	8.62	0.62	.049	0.10	0.08	6.75	7.49	9.89	9.87	8.57	8.61	7.18	5.63
	Females	41	47	8.19	8.25	0.39	0.42	0.06	0.06	7.34	7.00	8.88	9.05	8.18	8.24	4.81	5.09
	Southern IL																
	Males	22	22	8.51	8.62	0.50	0.49	0.11	0.11	7.14	7.41	9.51	9.41	8.50	8.61	5.84	5.72
	Females	20	22	8.24	8.31	0.57	0.47	0.13	0.10	7.37	7.52	9.33	9.46	8.22	8.30	6.90	5.62
	Western KY																
	Males	54	48	8.34	8.41	0.51	0.42	0.07	0.06	7.28	7.54	10.47	9.60	8.32	8.40	6.13	4.94
	Females	56	58	8.20	8.25	0.47	0.70	0.06	0.09	7.31	6.94	9.29	11.90	8.19	8.22	5.69	8.46
NM1BL	All sites																
	Males	101	111	11.26	11.33	0.50	0.52	0.05	0.05	10.21	10.09	12.95	12.59	11.25	11.32	4.46	4.60
	Females	109	112	11.07	11.08	0.52	0.55	0.05	0.05	9.79	9.66	12.73	12.51	11.05	11.07	4.66	4.92
	Central TN																
	Males	38	40	11.31	11.42	0.60	0.54	0.10	0.09	10.21	10.42	12.95	12.59	11.29	11.40	5.33	4.76
	Females	44	40	11.09	11.11	0.53	0.60	0.08	0.09	9.79	9.88	12.39	12.45	11.08	11.10	4.78	5.39
	Southern IL																
	Males	19	23	11.29	11.36	0.53	0.60	0.12	0.13	10.30	10.29	12.16	12.48	11.28	11.34	4.73	5.29
	Females	19	18	11.06	11.11	0.44	0.45	0.10	0.11	10.13	10.31	12.07	12.25	11.05	11.10	3.94	4.05
	Western KY																
	Males	44	48	11.21	11.26	0.39	0.46	0.06	0.07	10.36	10.09	11.95	12.15	11.20	11.25	3.44	4.08
	Females	46	54	11.05	11.05	0.54	0.54	0.08	0.07	10.00	9.66	12.73	12.51	11.04	11.04	4.90	4.89

Table 12. Summary statistics for dental measures (continued)

		n		Mean		Stand. Dev.		Stand. Error		Min		Max		Geo. Mean		Coeff. Var.	
		L	R	L	R	L	R	L	R	L	R	L	R	L	R	L	R
NM2BL	All sites																
	Males	96	105	10.91	11.00	0.55	0.61	0.06	0.06	9.58	9.47	12.40	12.53	10.90	10.99	5.04	5.54
	Females	116	120	10.72	10.80	0.62	0.55	0.06	0.05	9.13	9.00	12.31	11.94	10.71	10.79	5.76	5.09
	Central TN																
	Males	36	38	10.92	11.07	0.58	0.66	0.10	0.11	9.61	9.47	12.40	12.20	10.90	11.05	5.34	5.98
	Females	39	44	10.72	10.80	0.65	0.60	0.10	0.09	9.13	9.00	12.31	11.94	10.70	10.79	6.07	5.51
	Southern IL																
	Males	16	20	11.07	11.10	0.65	0.67	0.16	0.15	9.85	9.77	12.05	12.06	11.05	11.08	5.86	6.02
	Females	20	21	10.91	11.07	0.71	0.50	0.16	0.11	9.65	10.29	12.01	11.90	10.89	11.06	6.51	4.52
	Western KY																
	Males	44	47	10.85	10.91	0.48	0.54	0.07	0.08	9.79	9.79	11.80	12.53	10.84	10.90	4.44	4.92
	Females	57	55	10.66	10.70	0.55	0.50	0.07	0.07	9.16	9.47	11.91	11.85	10.65	10.69	5.20	4.70

Table 13. Dental data number of observed and percent of sample imputed (left side only, after side substitutions)

	All sites		Central TN		Southern IL		Western KY	
	Males	Females	Males	Females	Males	Females	Males	Females
XCMD (Total)	149	150	61	60	28	23	60	67
Observed	89	82	36	28	14	12	39	42
NA	60	68	25	32	14	11	21	25
% Imputed	40%	45%	41%	53%	50%	48%	35%	37%
XP3BL (Total)	149	150	61	60	28	23	60	67
Observed	92	85	38	30	14	15	40	40
NA	57	65	23	30	14	8	20	27
% Imputed	38%	43%	38%	50%	50%	35%	33%	40%
XP4BL (Total)	149	150	61	60	28	23	60	67
Observed	94	94	35	33	18	14	41	47
NA	55	56	26	27	10	9	19	20
% Imputed	37%	37%	43%	45%	36%	39%	32%	30%
XM1BL (Total)	149	150	61	60	28	23	60	67
Observed	95	101	35	35	17	18	43	48
NA	54	49	26	25	11	5	17	19
% Imputed	36%	33%	43%	42%	39%	22%	28%	28%
XM2BL (Total)	149	150	61	60	28	23	60	67
Observed	100	111	37	35	18	18	45	58
NA	49	39	24	25	10	5	15	9
% Imputed	33%	26%	39%	42%	36%	22%	25%	13%
NCMD (Total)	149	150	61	60	28	23	60	67
Observed	98	86	32	21	20	15	46	50
NA	51	64	29	39	8	8	14	17
% Imputed	34%	43%	48%	65%	29%	35%	23%	25%
NP3BL (Total)	149	150	61	60	28	23	60	67
Observed	115	107	40	33	23	18	52	56
NA	34	43	21	27	5	5	8	11
% Imputed	23%	29%	34%	45%	18%	22%	13%	16%
NP4BL (Total)	149	150	61	60	28	23	60	67
Observed	116	118	40	41	22	20	54	57
NA	33	32	21	19	6	3	6	10
% Imputed	22%	21%	34%	32%	21%	13%	10%	15%
NM1BL (Total)	149	150	61	60	28	23	60	67
Observed	101	109	38	44	19	19	44	46
NA	489	41	23	16	9	4	16	21
% Imputed	32%	27%	38%	27%	32%	17%	27%	31%
NM2BL (Total)	149	150	61	60	28	23	60	67
Observed	96	116	36	39	16	20	44	57
NA	53	34	25	21	12	3	16	10
% Imputed	36%	23%	41%	35%	43%	13%	27%	15%

Table 14. Summary statistics for dental measures after imputation

		n	Mean	Stand. Dev.	Stand. Error	Min	Max	Geo. Mean	Coeff. Var.
XCMD	All sites								
	Males	159	8.12	0.39	0.03	6.51	9.18	8.11	4.80
	Females	154	7.89	0.48	0.04	6.43	8.83	7.88	6.05
	Central TN								
	Males	69	8.13	0.39	0.05	6.51	8.89	8.12	4.84
	Females	63	7.94	0.45	0.06	6.43	8.83	7.93	5.70
	Southern IL								
	Males	29	8.15	0.37	0.07	7.19	8.89	8.14	4.50
	Females	25	7.85	0.51	0.10	6.72	8.77	7.83	6.51
	Western KY								
	Males	61	8.10	0.40	0.05	7.31	9.18	8.09	4.96
	Females	66	7.87	0.49	0.06	6.50	8.74	7.85	6.26
XP3BL	All sites								
	Males	159	9.77	0.54	0.04	7.91	11.38	9.75	5.53
	Females	154	9.56	0.56	0.05	7.72	10.89	9.55	5.88
	Central TN								
	Males	69	9.75	0.60	0.07	7.98	11.38	9.73	6.19
	Females	63	9.61	0.60	0.08	7.72	10.89	9.59	6.21
	Southern IL								
	Males	29	9.86	0.54	0.10	8.75	10.67	9.84	5.51
	Females	25	9.52	0.59	0.12	8.49	10.66	9.50	6.23
	Western KY								
	Males	61	9.75	0.46	0.06	7.91	11.00	9.74	4.76
	Females	66	9.54	0.52	0.06	8.46	10.79	9.52	5.45
XP4BL	All sites								
	Males	159	9.61	0.52	0.04	8.09	11.28	9.59	5.46
	Females	154	9.28	0.55	0.04	6.80	10.29	9.27	5.88
	Central TN								
	Males	69	9.69	0.58	0.07	8.09	11.28	9.67	5.98
	Females	63	9.34	0.52	0.07	7.59	10.26	9.33	5.54
	Southern IL								
	Males	29	9.59	0.58	0.11	8.30	10.42	9.58	6.01
	Females	25	9.24	0.60	0.12	8.13	10.29	9.22	6.53
	Western KY								
	Males	61	9.52	0.42	0.05	8.20	10.70	9.51	4.36
	Females	66	9.24	0.55	0.07	6.80	10.26	9.322	5.99
XM1BL	All sites								
	Males	159	12.00	0.53	0.04	10.29	14.02	11.99	4.38
	Females	154	11.78	0.52	0.04	10.47	13.20	11.77	4.42
	Central TN								
	Males	69	11.99	0.60	0.07	10.29	14.02	11.98	4.96
	Females	63	11.83	0.56	0.07	10.73	13.16	11.82	4.77
	Southern IL								
	Males	29	11.97	0.55	0.10	10.86	13.16	11.96	4.61
	Females	25	11.81	0.39	0.08	10.87	12.67	11.80	3.31
	Western KY								
	Males	61	12.02	0.43	0.05	11.23	13.23	12.01	3.54
	Females	66	11.72	0.52	0.06	10.47	13.20	11.71	4.46

Table 14. Summary statistics for dental measures after imputation (continued)

		n	Mean	Stand. Dev.	Stand. Error	Min	Max	Geo. Mean	Coeff. Var.
XM2BL	All sites								
	Males	159	11.98	0.62	0.05	10.07	14.12	11.96	5.19
	Females	154	11.64	0.62	0.05	9.50	13.16	11.62	5.29
	Central TN								
	Males	69	12.02	0.68	0.08	10.07	14.12	12.00	5.63
	Females	63	11.66	0.69	0.09	9.50	13.13	11.64	5.92
	Southern IL								
	Males	29	12.00	0.68	0.13	10.18	13.10	11.98	5.69
	Females	25	11.66	0.65	0.13	10.34	13.16	11.65	5.56
	Western KY								
	Males	61	11.93	0.53	0.07	10.81	13.25	11.92	4.42
	Females	66	11.62	0.53	0.07	10.55	12.79	11.60	4.57
NCMD	All sites								
	Males	159	7.18	0.44	0.03	6.15	8.54	7.16	6.09
	Females	154	6.93	0.45	0.04	5.60	8.34	6.92	6.44
	Central TN								
	Males	69	7.20	0.49	0.06	6.15	8.54	7.19	6.84
	Females	63	6.95	0.45	0.06	5.60	7.91	6.93	6.46
	Southern IL								
	Males	29	7.19	0.38	0.07	6.32	8.00	7.18	5.24
	Females	25	7.03	0.50	0.10	6.23	8.34	7.02	7.10
	Western KY								
	Males	61	7.14	0.40	0.05	6.24	8.29	7.13	5.59
	Females	66	6.89	0.42	0.05	5.61	7.89	6.87	6.14
NP3BL	All sites								
	Males	159	8.24	0.45	0.04	6.90	9.38	8.23	5.50
	Females	154	8.01	0.51	0.04	6.79	9.22	7.99	6.37
	Central TN								
	Males	69	8.28	0.50	0.06	6.90	9.38	8.26	6.08
	Females	63	8.06	0.52	0.07	6.83	9.22	8.05	6.47
	Southern IL								
	Males	29	8.16	0.47	0.09	7.05	8.96	8.15	5.76
	Females	25	7.96	0.45	0.09	6.99	8.73	7.95	5.67
	Western KY								
	Males	61	8.23	0.38	0.05	7.42	9.05	8.22	4.63
	Females	66	7.98	0.52	0.06	6.79	9.15	7.96	6.55
NP4BL	All sites								
	Males	159	8.42	0.53	0.04	6.75	10.47	8.40	6.30
	Females	154	8.22	0.48	0.04	5.98	9.33	8.21	5.86
	Central TN								
	Males	69	8.48	0.57	0.07	6.75	9.89	8.46	6.71
	Females	63	8.25	0.38	0.05	7.34	8.92	8.24	4.63
	Southern IL								
	Males	29	8.46	0.49	0.09	7.14	9.51	8.45	5.81
	Females	25	8.26	0.54	0.11	7.37	9.33	8.24	6.59
	Western KY								
	Males	61	8.34	0.50	0.06	7.28	10.47	8.32	5.97
	Females	66	8.18	0.54	0.07	5.98	9.29	8.16	6.63

Table 14. Summary statistics for dental measures after imputation (continued)

		n	Mean	Stand. Dev.	Stand. Error	Min	Max	Geo. Mean	Coeff. Var.
NM1BL	All sites								
	Males	159	11.26	0.47	0.04	10.21	12.95	11.25	4.19
	Females	154	11.07	0.49	0.04	9.79	12.73	11.06	4.44
	Central TN								
	Males	69	11.30	0.52	0.06	10.21	12.95	11.29	4.59
	Females	63	11.11	0.50	0.06	9.79	12.39	11.10	4.54
	Southern IL								
	Males	29	11.28	0.55	0.10	10.29	12.48	11.27	4.90
	Females	25	11.04	0.41	0.08	10.13	12.07	11.04	3.73
	Western KY								
	Males	61	11.20	0.36	0.05	10.36	11.95	11.19	3.24
	Females	66	11.04	0.51	0.06	10.00	12.73	11.02	4.62
NM2BL	All sites								
	Males	159	10.97	0.54	0.04	9.35	12.53	10.96	4.95
	Females	154	10.73	0.58	0.05	9.13	12.31	10.72	5.41
	Central TN								
	Males	69	10.98	0.56	0.07	9.35	12.40	10.97	5.11
	Females	63	10.75	0.59	0.07	9.13	12.31	10.73	5.45
	Southern IL								
	Males	29	11.05	0.59	0.11	9.58	12.05	11.04	5.31
	Females	25	10.85	0.67	0.13	6.65	12.01	10.83	6.18
	Western KY								
	Males	61	10.93	0.50	0.06	9.79	12.53	10.92	4.61
	Females	66	10.67	0.54	0.07	9.16	11.91	10.66	5.04

Table 15. Coefficient of Variation for dental data set (observed and imputed)

	All sites		Central TN		Southern IL		Western KY	
	Males	Females	Males	Females	Males	Females	Males	Females
XCMD	4.80	**6.05**	4.84	**5.70**	4.50	**6.51**	4.96	**6.26**
XP3BL	5.53	**5.88**	**6.19**	5.21	5.51	**6.23**	4.76	**5.45**
XP4BL	5.46	**5.88**	**5.98**	5.54	6.01	**6.53**	4.36	**5.99**
XM1BL	4.38	**4.42**	**4.96**	4.77	**4.61**	3.31	3.54	**4.46**
XM2BL	5.19	**5.29**	5.63	**5.92**	**5.69**	5.56	4.42	**4.57**
NCMD	6.09	**6.44**	**6.84**	6.46	5.24	**7.10**	5.59	**6.14**
NP3BL	5.50	**6.37**	6.08	**6.47**	**5.76**	5.67	4.63	**6.55**
NP4BL	**6.30**	5.86	**6.71**	4.63	5.81	**6.59**	5.97	**6.63**
NM1BL	4.19	**4.44**	**4.59**	4.54	**4.90**	3.73	3.24	**4.62**
NM2BL	4.95	**5.41**	5.11	**5.45**	5.31	**6.18**	4.61	**5.04**
Number of variables for which each sex has greater CV values								
	1	**9**	**6**	4	4	**6**	0	**10**

Variables in order of least to most imputations made in that variable.
Bolded values represent the higher value between males and females.

Post-Cranial Results

The first table below (Table 16) provides summary statistics of post-cranial measures. For this table, individuals with missing data were removed for each variable. The table represents the number of observed values (a minimum number of individuals, then) for each variable.

Fifty-three females had a complete set of observations from the humerus, radius, femur, and tibia (left side only). Thirty-five females were excluded because they had no post-cranial remains. After the regression process (described above in Methods) there were 173 females for which all four bones were either observed or estimated (39 from the Black Earth site, 62 from the central Tennessee sites, and 72 from Indian Knoll). The same linear regression equation procedures were followed for males. 58 males had all four long bones of interest and they were used to generate the regression equations below. Thirty-eight males were excluded because they had no post-cranial skeleton observed. After estimating long bone lengths using the regression equations, 191 males had data for all four long bones (48 from Black Earth, 72 from central Tennessee sites, and 71 from Indian Knoll).

Table 19 provides summary statistics for long bone lengths after having completed side substitutions and regressions as required and outlined above. Table 20 provides the same for brachial, crural, and intermembral indices.

Table 16. Summary statistics for post-cranial measures (individuals with missing data points removed for each variable)

		n		Mean		Stand. Dev.		Stand. Error		Minimum		Maximum		Geo. Mean		Coeff. Var.	
		Left	Right	Left	Right	Left	Right	Left	Right	Left	Right	Left	Right	Left	Right	Left	Right
HXL	All sites																
	Males	128	142	319.70	318.45	13.91	14.87	1.23	1.25	285.00	283.00	359.00	367.00	319.40	318.10	4.35	4.67
	Females	115	133	294.07	298.21	12.64	13.46	1.18	1.17	265.00	254.00	327.00	347.00	293.80	297.91	4.30	4.51
	Central TN																
	Males	39	42	317.47	314.74	13.75	13.78	2.20	2.13	291.00	291.00	345.00	350.00	317.18	314.45	4.33	4.38
	Females	30	41	293.37	298.62	11.60	14.61	2.12	2.28	272.00	254.00	320.00	333.00	293.15	298.27	3.95	4.89
	Southern IL																
	Males	30	36	319.18	318.51	15.06	16.52	2.75	2.75	285.00	283.00	359.00	367.00	318.84	318.10	4.72	5.19
	Females	29	27	294.90	298.82	13.16	12.70	2.44	2.44	269.00	271.00	327.00	331.00	294.61	298.56	4.46	4.25
	Western KY																
	Males	59	64	321.42	320.84	13.40	14.30	1.74	1.79	291.00	290.00	351.00	346.00	321.15	320.53	4.17	4.46
	Females	56	65	294.02	297.69	13.09	13.20	1.75	1.64	265.00	271.00	327.00	347.00	293.73	297.41	4.45	4.43
RXL	All sites																
	Males	113	116	246.76	246.60	11.99	11.23	1.13	1.04	216.00	212.00	282.00	281.00	246.47	246.34	4.86	4.55
	Females	110	112	223.50	225.88	13.20	12.16	1.26	1.15	196.00	197.00	261.00	263.00	223.11	225.56	5.91	5.38
	Central TN																
	Males	39	28	247.29	246.30	13.15	11.90	2.11	2.25	223.00	221.50	282.00	281.00	246.96	246.03	5.32	4.83
	Females	31	30	223.60	224.32	15.62	13.55	2.81	2.47	196.00	197.00	261.00	261.00	223.08	223.93	6.99	6.04
	Southern IL																
	Males	30	38	246.10	246.50	12.14	11.59	2.22	1.88	216.00	212.00	272.00	274.00	245.81	246.23	4.93	4.70
	Females	25	22	223.64	228.27	12.28	10.34	2.46	2.20	205.00	209.00	245.00	247.00	223.32	228.05	5.49	4.53
	Western KY																
	Males	44	50	246.73	246.84	11.04	10.79	1.66	1.53	218.00	217.00	269.00	266.00	246.48	246.61	4.47	4.37
	Females	54	60	223.37	225.78	12.32	12.10	1.68	1.56	198.00	199.00	254.00	263.00	223.04	225.47	5.52	5.36
FXL	All sites																
	Males	148	152	443.10	440.88	20.36	20.49	1.67	1.66	400.00	401.00	494.00	494.00	442.64	440.40	4.60	4.65
	Females	130	126	414.12	413.31	19.36	19.22	1.70	1.71	360.00	360.00	478.00	475.00	413.68	412.87	4.67	4.65
	Central TN																
	Males	50	47	442.22	441.66	20.02	21.76	2.83	3.17	400.00	402.00	494.00	494.00	441.78	441.14	4.53	4.93
	Females	37	37	412.38	409.27	22.76	20.90	3.74	3.44	360.00	360.00	460.00	457.00	411.76	408.75	5.52	5.11
	Southern IL																
	Males	33	35	443.61	440.64	18.32	18.92	3.19	3.20	405.00	403.00	490.00	489.00	443.24	440.25	4.13	4.29
	Females	23	21	420.22	422.71	14.82	15.01	3.09	3.28	390.00	385.00	458.00	455.00	419.97	422.46	3.53	3.55
	Western KY																
	Males	65	70	443.52	440.47	21.84	20.64	2.71	2.47	402.00	401.00	490.00	484.00	442.99	439.99	4.92	4.69
	Females	70	68	413.04	412.60	18.58	18.72	2.22	2.27	379.00	381.00	478.00	475.00	412.64	412.19	4.50	4.54

Table 16. Summary statistics for post-cranial measures (individuals with missing data points removed for each variable) (continued)

		n		Mean		Stand. Dev.		Stand. Error		Minimum		Maximum		Geo. Mean		Coeff. Var.	
		Left	Right	Left	Right	Left	Right	Left	Right	Left	Right	Left	Right	Left	Right	Left	Right
TXL	All sites																
	Males	138	129	369.24	367.40	17.35	18.03	1.48	1.59	324.00	326.00	413.00	415.00	368.84	366.96	4.70	4.91
	Females	103	111	339.68	340.14	17.33	17.13	1.71	1.63	306.00	305.00	403.00	404.00	339.26	339.72	5.10	5.04
	Central TN																
	Males	48	41	368.89	366.29	18.09	18.61	2.61	2.91	324.00	326.00	413.00	415.00	368.45	365.83	4.90	5.08
	Females	27	31	337.31	339.02	17.22	15.73	3.31	2.83	306.00	305.00	378.00	373.00	336.90	338.66	5.10	4.64
	Southern IL																
	Males	30	32	372.30	370.97	16.85	16.31	3.08	2.88	337.00	339.00	403.00	404.00	371.93	370.62	4.53	4.40
	Females	15	17	348.53	345.65	13.38	15.70	3.45	3.81	320.00	320.00	375.00	370.00	348.29	345.31	3.84	4.54
	Western KY																
	Males	60	56	368.00	366.16	17.09	18.57	2.21	2.48	328.00	326.00	407.00	406.00	367.61	365.70	4.64	5.07
	Females	61	63	338.56	339.21	17.81	18.09	2.28	2.28	307.00	311.00	403.00	404.00	338.11	338.75	5.26	5.33

Table 17. Linear regression formulae (left females only, pooled sites)

Long bone	Regression formulae	R Square
Humerus	HXL = 78.021 + 0.639(TXL)	0.61
	HXL = 72.014 + 0.996(RXL)	0.70
	HXL = 67.897 + 0.868(RXL) + 0.096(TXL)	0.70
	HXL = 21.456 + 0.663(FXL)	0.73
	HXL = 21.921 + 0.073(TXL) + 0.602(FXL)	0.74
	HXL = 21.002 + 0.409(FXL) + 0.471(RXL)	0.78
	HXL = 18.584 + 0.745(RXL) + 0.545(FXL) – 0.339(TXL)	0.80
Radius	RXL = 0.965 + 0.540(FXL)	0.69
	RXL = 17.300 + 0.700(HXL)	0.70
	RXL = -7.212 + 0.381(HXL) + 0.287(FXL)	0.75
	RXL = 11.767 + 0.624(TXL)	0.78
	RXL = 4.479 + 0.553(TXL) + 0.077(FXL)	0.83
	RXL = -9.197 + 0.267(HXL) + 0.454(TXL)	0.87
	RXL = -2.868 + -0.125(FXL) + 0.528(TXL) + 0.335(HXL)	0.87
Femur	FXL = 124.637 + 1.284(RXL)	0.70
	FXL = 85.327 + 1.107(HXL)	0.73
	FXL = 74.993 + 0.597(RXL) + 0.689(HXL)	0.78
	FXL = 93.183 + 0.940(TXL)	0.79
	FXL = 90.547 + 0.226(RXL) + 0.799(TXL)	0.79
	FXL = 50.762 + 0.593(TXL) + 0.544(HXL)	0.86
	FXL = 47.815 + 0.738(TXL) + 0.629(HXL) - 0.320(RXL)	0.86
Tibia	TXL = 58.329 + 0.951(HXL)	0.61
	TXL = 59.310 + 1.252(RXL)	0.78
	TXL = -6.357 + 0.838(FXL)	0.79
	TXL = -8.226 + 0.087(HXL) + 0.780(FXL)	0.79
	TXL = 36.820 + 0.081(HXL) + 1.243(RXL)	0.83
	TXL = -7.140 + 0.400(FXL) + 0.811(RXL)	0.88
	TXL = -1.458 - 0.271(HXL) + 0.938(RXL) + 0.510(FXL)	0.89

Table 18. Linear regression formulae (left males only, pooled sites)

Long bone	Regression formulae	R Square
Humerus	HXL = 64.235 + 1.032(RXL)	0.67
	HXL = 63.357 + 0.696(TXL)	0.75
	HXL = 42.044 + 0.623(FXL)	0.76
	HXL = 37.498 + 0.435(RXL) + 0.474(TXL)	0.79
	HXL = 38.359 + 0.329(TXL) + 0.359(FXL)	0.79
	HXL = 18.697 + 0.441(RXL) + 0.430(FXL)	0.81
	HXL = 20.689 + 0.361(RXL) + 0.304(FXL) + 0.200(TXL)	0.82
Radius	RXL = 52.962 + 0.437(FXL)	0.60
	RXL = 59.502 + 0.512(TXL)	0.64
	RXL = 48.966 + 0.357(TXL) + 0.151(FXL)	0.66
	RXL = 41.529 + 0.646(HXL)	0.67
	RXL = 33.435 + 0.464(HXL) + 0.148(FXL)	0.68
	RXL = 35.273 + 0.382(HXL) + 0.245(TXL)	0.70
	RXL = 34.630 + 0.374(HXL) + 0.234(TXL) + 0.017(FXL)	0.70
Femur	FXL = 105.875 + 1.373(RXL)	0.60
	FXL = 54.653 + 1.225(HXL)	0.76
	FXL = 40.929 + 1.011(HXL) + 0.330(RXL)	0.77
	FXL = 69.620 + 1.022(TXL)	0.82
	FXL = 55.208 + 0.242(RXL) + 0.898(TXL)	0.83
	FXL = 37.581 + 0.506(HXL) + 0.670(TXL)	0.85
	FXL = 36.631 + 0.495(HXL) + 0.027(RXL) + 0.663(TXL)	0.85
Tibia	TXL = 56.417 + 1.260(RXL)	0.64
	TXL = 25.485 + 1.073(HXL)	0.75
	TXL = 6.479 + 0.777(HXL) + 0.458(RXL)	0.78
	TXL = 11.188 + 0.801(FXL)	0.82
	TXL = -5.107 + 0.560(FXL) + 0.388(HXL)	0.84
	TXL = -9.936 + 0.627(FXL) + 0.399(RXL)	0.84
	TXL = -14.693 + 0.517(FXL) + 0.254(HXL) + 0.287(RXL)	0.85

Table 19. Summary statistics for maximum long bone lengths
(left side only, observed and estimated individuals)

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
HXL	All sites								
	Males	191	318.76	13.22	0.96	285.00	359.00	318.49	4.15
	Females	173	295.10	13.86	1.05	260.14	338.37	294.77	4.70
	Central TN								
	Males	72	317.39	12.28	1.45	291.00	351.92	317.16	3.87
	Females	62	293.99	14.61	1.86	260.14	326.44	293.63	4.97
	Southern IL								
	Males	48	319.40	13.90	2.01	285.00	359.00	319.11	4.35
	Females	39	296.09	12.90	2.06	269.00	327.00	295.81	4.36
	Western KY								
	Males	71	319.73	13.74	1.63	289.13	351.00	319.43	4.30
	Females	72	295.51	13.83	1.63	265.00	338.37	295.20	4.68
RXL	All sites								
	Males	191	247.10	10.57	0.76	216.00	282.00	246.87	4.28
	Females	173	223.82	12.65	0.96	183.12	263.24	223.47	5.65
	Central TN								
	Males	72	246.74	10.58	1.25	223.00	282.00	246.52	4.29
	Females	62	222.99	14.32	1.82	183.12	261.00	222.54	6.42
	Southern IL								
	Males	48	246.74	11.00	1.59	216.00	272.00	246.50	4.46
	Females	39	225.01	10.52	1.68	205.00	245.00	224.77	4.67
	Western KY								
	Males	71	247.70	10.37	1.23	218.00	269.00	247.49	4.19
	Females	72	223.89	12.29	1.45	198.00	263.24	223.57	5.49
FXL	All sites								
	Males	191	443.38	18.79	1.36	400.00	494.00	442.98	4.24
	Females	173	413.13	18.50	1.41	360.00	478.00	412.72	4.48
	Central TN								
	Males	72	443.15	17.37	2.05	400.00	494.00	442.82	3.92
	Females	62	410.98	20.42	2.59	360.00	460.00	410.48	4.97
	Southern IL								
	Males	48	443.69	17.51	2.53	405.00	490.00	443.36	3.95
	Females	39	416.53	15.04	2.41	383.11	458.00	416.27	3.61
	Western KY								
	Males	71	443.39	21.13	2.51	402.00	490.00	442.89	4.77
	Females	72	413.14	18.42	2.17	379.00	478.00	412.75	4.46
TXL	All sites								
	Males	191	367.84	16.24	1.17	324.00	413.00	367.48	4.41
	Females	173	339.93	17.26	1.31	299.51	403.00	339.50	5.08
	Central TN								
	Males	72	367.28	16.12	1.90	324.00	413.00	366.93	4.39
	Females	62	338.70	18.62	2.36	299.51	386.08	338.20	5.50
	Southern IL								
	Males	48	368.36	15.72	2.27	337.00	403.00	368.03	4.27
	Females	39	343.11	14.58	2.34	315.97	375.00	342.80	4.25
	Western KY								
	Males	71	368.05	16.90	2.01	328.00	407.00	367.67	4.59
	Females	72	339.27	17.41	2.05	307.00	403.00	338.84	5.13

Table 20. Summary statistics for post-cranial computed measures of brachial, crural, and intermembral indices (left sides, observed and estimated individuals)

		n	Mean	Std. Dev.	Std. Error	Min	Max	Geo. Mean	Coeff. Var.
BRIND	All sites								
	Males	191	77.53	1.71	0.12	71.43	82.35	77.51	2.21
	Females	173	75.84	2.13	0.16	65.87	82.18	75.81	2.81
	Central TN								
	Males	72	77.74	1.43	0.17	73.62	81.27	77.73	1.85
	Females	62	75.82	2.13	0.27	65.87	81.56	75.79	2.81
	Southern IL								
	Males	48	77.27	1.80	0.26	72.93	82.35	77.25	2.32
	Females	39	76.01	1.82	0.29	69.38	79.03	75.98	2.39
	Western KY								
	Males	71	77.50	1.90	0.23	71.43	82.32	77.48	2.46
	Females	72	75.77	2.31	0.27	70.69	82.18	75.73	3.05
CRIND	All sites								
	Males	191	82.97	1.64	0.12	78.72	87.65	82.96	1.97
	Females	173	82.28	1.77	0.13	77.95	88.02	82.26	2.15
	Central TN								
	Males	72	82.88	1.57	0.19	79.66	87.47	82.86	1.90
	Females	62	82.41	1.69	0.21	78.75	87.27	82.39	2.05
	Southern IL								
	Males	48	83.03	1.57	0.23	79.52	86.88	83.01	1.89
	Females	39	82.37	1.54	0.25	77.98	86.17	82.35	1.87
	Western KY								
	Males	71	83.03	1.76	0.21	78.72	87.65	83.01	2.12
	Females	72	82.12	1.96	0.23	77.95	88.02	82.09	2.38
INTERMEM INDEX	All sites								
	Males	191	69.77	1.19	0.09	66.06	73.37	69.76	1.71
	Females	173	68.91	1.04	0.08	64.39	72.24	68.90	1.50
	Central TN								
	Males	72	69.62	0.96	0.11	67.32	71.61	69.61	1.37
	Females	62	68.95	1.00	0.13	64.39	71.59	68.95	1.45
	Southern IL								
	Males	48	69.72	1.31	0.19	66.06	73.37	69.71	1.88
	Females	39	68.58	0.99	0.16	65.85	70.38	68.58	1.44
	Western KY								
	Males	71	69.96	1.32	0.16	66.75	72.84	69.94	1.89
	Females	72	69.03	1.07	0.13	67.25	72.24	69.03	1.55

As for the cranial and dental data, the coefficient of variation from the observed and estimated (complete) post-cranial data set were isolated below to get a crude estimate of the relative variation in each of the measures, in each subsample. Below are only the coefficient of variations (CV) for the maximum long bone lengths and computed indices (Table 21).

For the pooled data set of males and females from all sites, females have higher coefficients of variation (CV) for all measured and computed variables except the intermembral index. Breaking down the samples into geographic regions shows a different pattern between male and female CV values. No variables showed higher male CV in the central TN sample. Females had higher CV values for all seven post-cranial observed and calculated variables. The pattern was similar for the western KY sample. Females had higher CV values in five of the seven variables. The sample from southern IL showed a more balanced distribution of CV values across the post-cranial variables. Four of the seven variables had higher CV values for males rather than females.

Table 22 provides a very crude summary of the overall variation across the cranial, dental, and post-cranial data sets as measured by CV values. This summarized view of variation shows females have higher CV values than males in the majority of instances. The pattern seen in the sample from southern Illinois is the opposite, though – males are more variable than females but the balance is much closer than what is observed at the other sites.

Table 21. Coefficient of Variation for full post-cranial data set (observed and estimated)								
	All sites		Central TN		Southern IL		Western KY	
	Males	Females	Males	Females	Males	Females	Males	Females
HXL	4.15	**4.70**	3.87	**4.97**	4.35	**4.36**	4.30	**4.68**
RXL	4.28	**5.65**	4.29	**6.42**	4.46	**4.67**	4.19	**5.49**
FXL	4.24	**4.48**	3.92	**4.97**	**3.95**	3.61	**4.77**	4.46
TXL	4.41	**5.08**	4.39	**5.50**	**4.27**	4.25	4.59	**5.13**
BRACHIAL INDEX	2.21	**2.81**	1.85	**2.81**	2.32	**2.39**	2.46	**3.05**
CRURAL INDEX	1.97	**2.15**	1.90	**2.05**	**1.89**	1.87	2.12	**2.38**
INTERMEMB INDEX	**1.71**	1.50	1.37	**1.45**	**1.88**	1.44	**1.89**	1.55
Number of variables for which each sex has greater CV values								
	1	**6**	0	**7**	**4**	3	2	**5**
Bold values represent the higher value between males and females								

Table 22. Summary of number of variables for which each sex had higher CV values								
	All sites		Central TN		Southern IL		Western KY	
	Males	Females	Males	Females	Males	Females	Males	Females
Cranial	**9**	4	3	**10**	**8**	5	**10**	3
P-C	1	**6**	0	**7**	**4**	3	2	**5**
Dental	1	**9**	**6**	4	4	6	0	**10**
Sum	11	**19**	9	**21**	**16**	14	12	**18**

Multivariate Results

Principal Component Analysis

Principal component analyses were performed using the var-covar matrix rather than the correlation matrix because the chosen variables are all measured on the same scale. The color key for the PCA graphs is given in Table 23 below.

Cranial Principal Component Analyses

Principal Component Analysis of cranial variables consists of all sites, pooled sexes, and raw data (including imputations made for missing data) (Tables 24-25). The first principal component (PC1) accounts for just over 52% of the variance. All variables are positively loaded on the first axis. The greatest three loadings on PC1 are from Bi-zygomatic Breadth (0.4568), Bi-asterionic Breadth (0.4456), Bi-auricular Breadth (0.3849). The pattern of 95% confidence ellipses are interesting for the first two components. There is good separation between males and females along PC1, indicative that females are smaller than males as a group (Figure 7). The angle of the ellipses are different between the sexes, though. Southern Illinois and central Tennessee females have a positive “slope” through their ellipses while the western Kentucky sample is nearly flat. The situation is somewhat reversed in the males. Western Kentucky and central Tennessee males have a nearly flat orientations paralleling PC1 while southern Illinois males would have a negative “slope.” Southern Illinois males and females occupy opposite ends of PC1, as well. Both ellipses for those subgroups are also larger than the other two subgroups.

Table 23. Color codes for Principal Components Analyses

Group	Color in PCAs
Black Earth Males	Purple
Black Earth Females	Pink
Central TN Males	Dark green
Central TN Females	Light green
Western KY Males	Dark blue
Western KY Females	Light blue

Table 24. Cranial raw data eigenvalues and contribution to variance for pooled sexes and all sites

PC	Eigenvalue	% variance
1	155.196	52.073
2	42.2428	14.174
3	22.8762	7.6757
4	19.1754	6.434
5	16.3153	5.4743
6	11.4305	3.8353
7	8.2723	2.7756
8	6.74314	2.2625
9	4.18533	1.4043
10	3.8601	1.2952
11	2.97052	0.9967
12	2.01295	0.67541
13	1.58816	0.53288
14	1.16615	0.39128

Table 25. Cranial raw data loadings on the first three PC axes for pooled sexes and all sites

	Axis 1	Axis 2	Axis 3
BZB	0.4568	0.1788	-0.4051
BAB	0.4456	-0.5159	0.146
BAUR	0.3849	-0.06894	-0.3296
XCB	0.3151	-0.2221	-0.02934
XCL	0.2999	0.5855	0.4381
FB	0.2440	-0.3807	0.4033
CBL	0.2353	0.2425	-0.09632
FH	0.2292	0.172	0.1631
BPL	0.1880	0.2372	-0.1642
MXAB	0.1436	0.005633	-0.1668
OC	0.1252	0.09472	0.5069
FML	0.09732	0.07897	0.03908
FMB	0.06059	0.01103	-0.03044
NB	0.05614	-0.0006145	0.01836

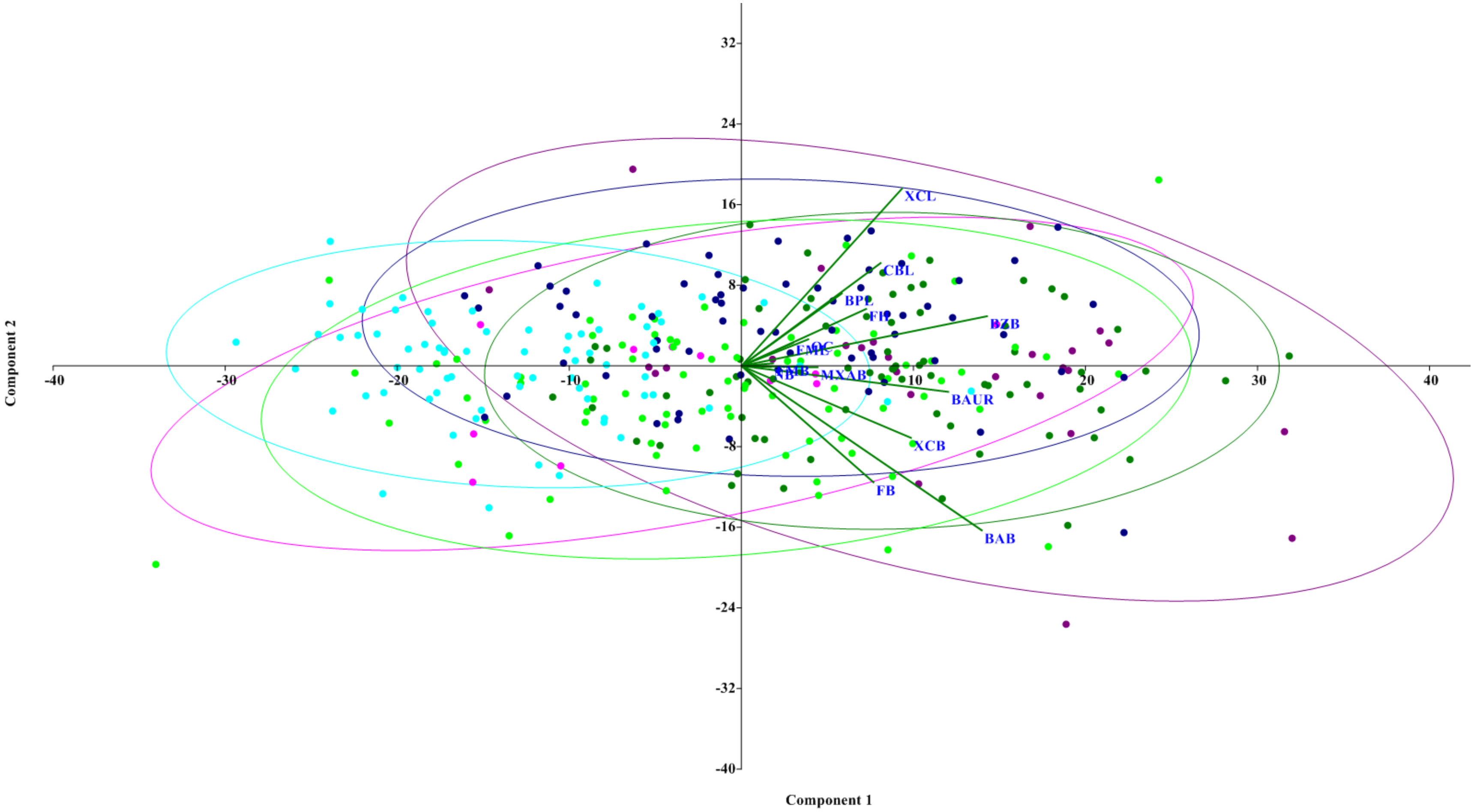

Figure 7. Cranial raw data. PC1 x PC2

Graphing PC2 on PC3 produces another interesting graph of the variation in these cranial data (Figure 8). Southern Illinois males encompass all of the variation seen in all other groups within their 95% confidence ellipse. The angle of their ellipse is also markedly shifted while the others are rather flat along PC2. The greatest loadings contributing to this pattern along PC2 and PC3 are the Maximum cranial length (0.5855 on PC2) and Bi-asterionic Breadth (-0.5159 on PC2). PC3 is driven mostly by the Occipital chord (0.5069 on PC3). Females form somewhat of a cluster towards the negative end of PC2 while the males occupy the other end. All groups (except for southern Illinois males) are nearly the same shape and distribution across PC3 especially.

To remove size from the cranial variables, the data set was standardized by the area of the foramen magnum (FML x FMB) and the PCA's were run again (Tables 26-27). This time PC1 accounts for almost 69% of the variance, loaded mostly by Maximum cranial length (0.5968). Graphing PC1 on PC2 shows clusters by geographic sub-group (Figure 9). The western Kentucky males and females have nearly identical 95% confidence ellipses (with the females occupying an area smaller than the males). The central Tennessee samples look similar with the females being subsumed within the male ellipse completely. The southern Illinois sample is again an outlier. Females from southern Illinois have a skewed orientation to their ellipse (what would be a negative "slope"), while the males encompass all the variation along PC2. The pattern of male versus female ellipses for the southern Illinois subgroup is not at all congruent like the other two geographic groups.

PC2 on PC3 gives fairly good separation between groups (Figure 10). These two axes account for just over 18% of the variance when combined. Southern Illinois males lay across PC2 again but do not have much variation along PC3. Females tend to cluster towards the negative half of PC3 axis more so than males. The greatest loading to PC3 is from Bi-zygomatic Breadth (0.6794).

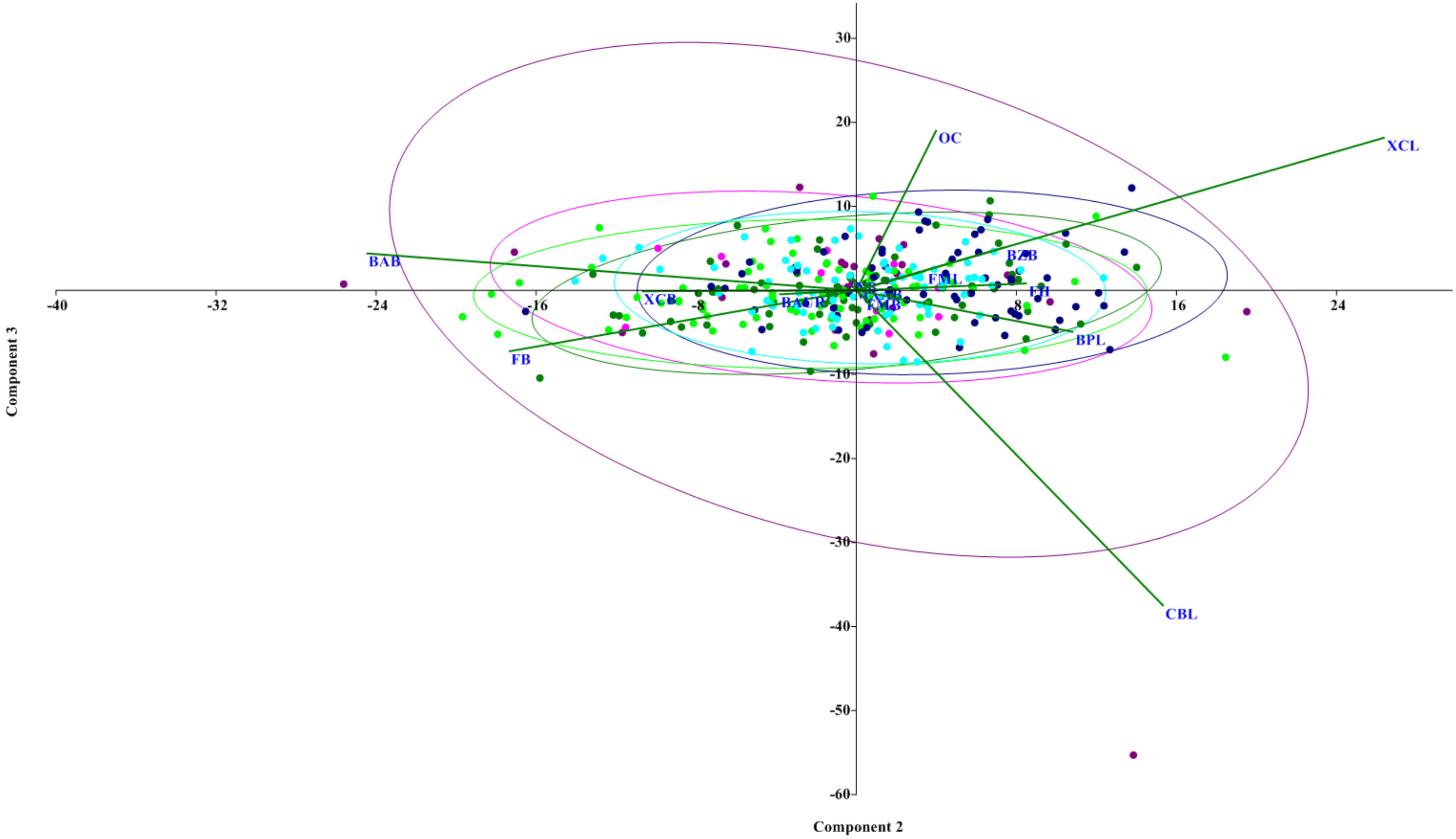

Figure 8. Cranial raw data. PC2 x PC3

Table 26. Cranial standardized data for pooled sexes and all sites

PC	Eigenvalue	% variance
1	18.1694	68.946
2	3.31594	12.583
3	1.52077	5.7707
4	1.11732	4.2398
5	0.677587	2.5712
6	0.499542	1.8956
7	0.378609	1.4367
8	0.312147	1.1845
9	0.194356	0.7375
10	0.100682	0.38205
11	0.0626884	0.23788
12	0.00422812	0.016044

Table 27. Cranial standardized data loadings on the first three PC axes for pooled sexes and all sites

	Axis 1	Axis 2	Axis 3
XCL	0.5968	-0.6628	-0.1231
FB	0.2121	0.2429	-0.4899
XCB	0.408	0.3028	-0.09526
BAB	0.2876	0.5263	-0.2931
BAUR	0.2681	0.2756	0.3246
OC	0.2019	-0.09853	-0.233
NB	0.01174	0.0024	-0.003252
MXAB	0.07853	0.03101	0.06084
CBL	0.1739	-0.05253	0.1112
BZB	0.3248	0.1749	0.6794
FH	0.2444	-0.08406	-0.0197
BPL	0.1874	-0.07703	0.1101

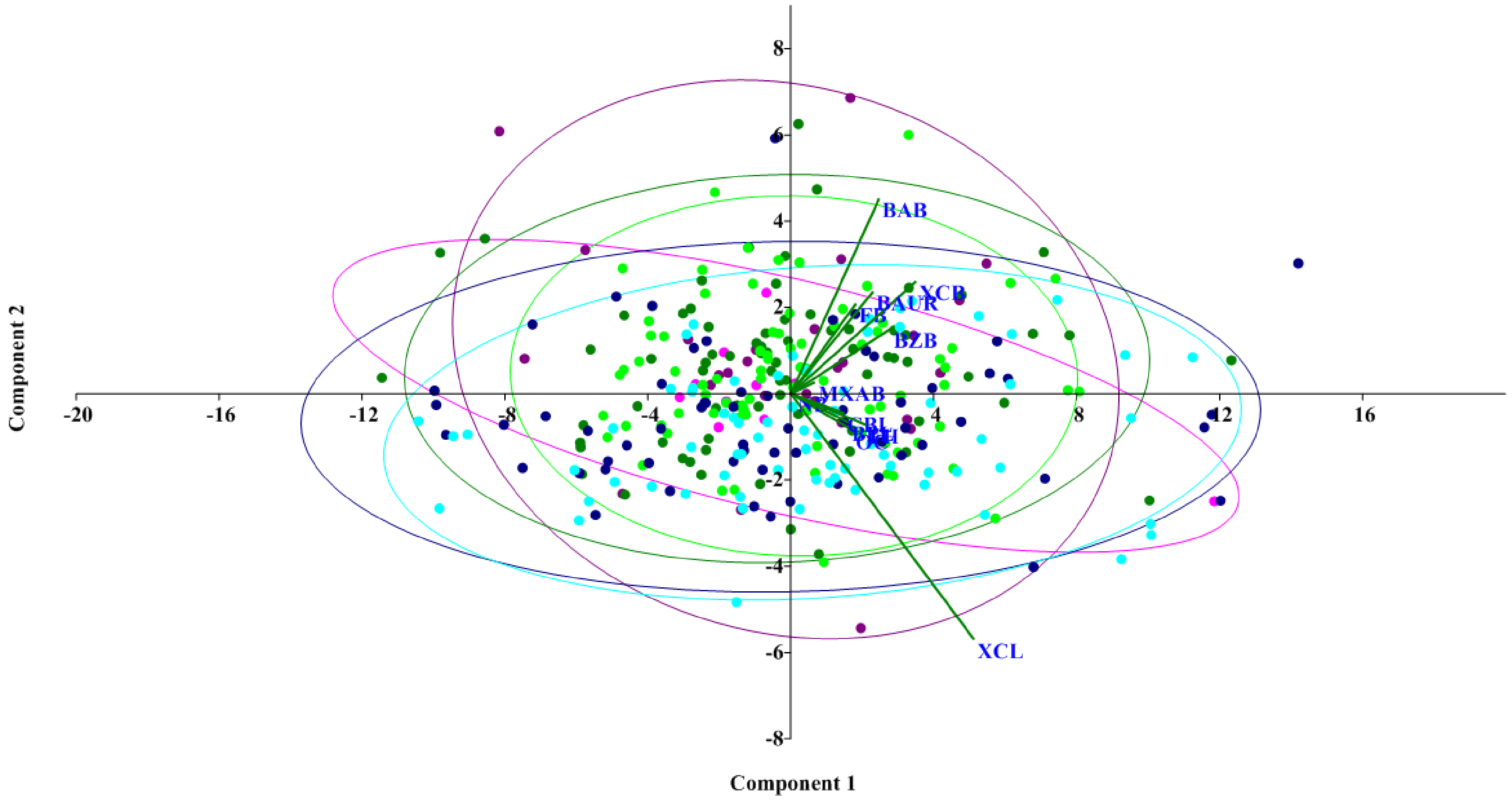

Figure 9. Cranial standardized data. PC1 x PC2

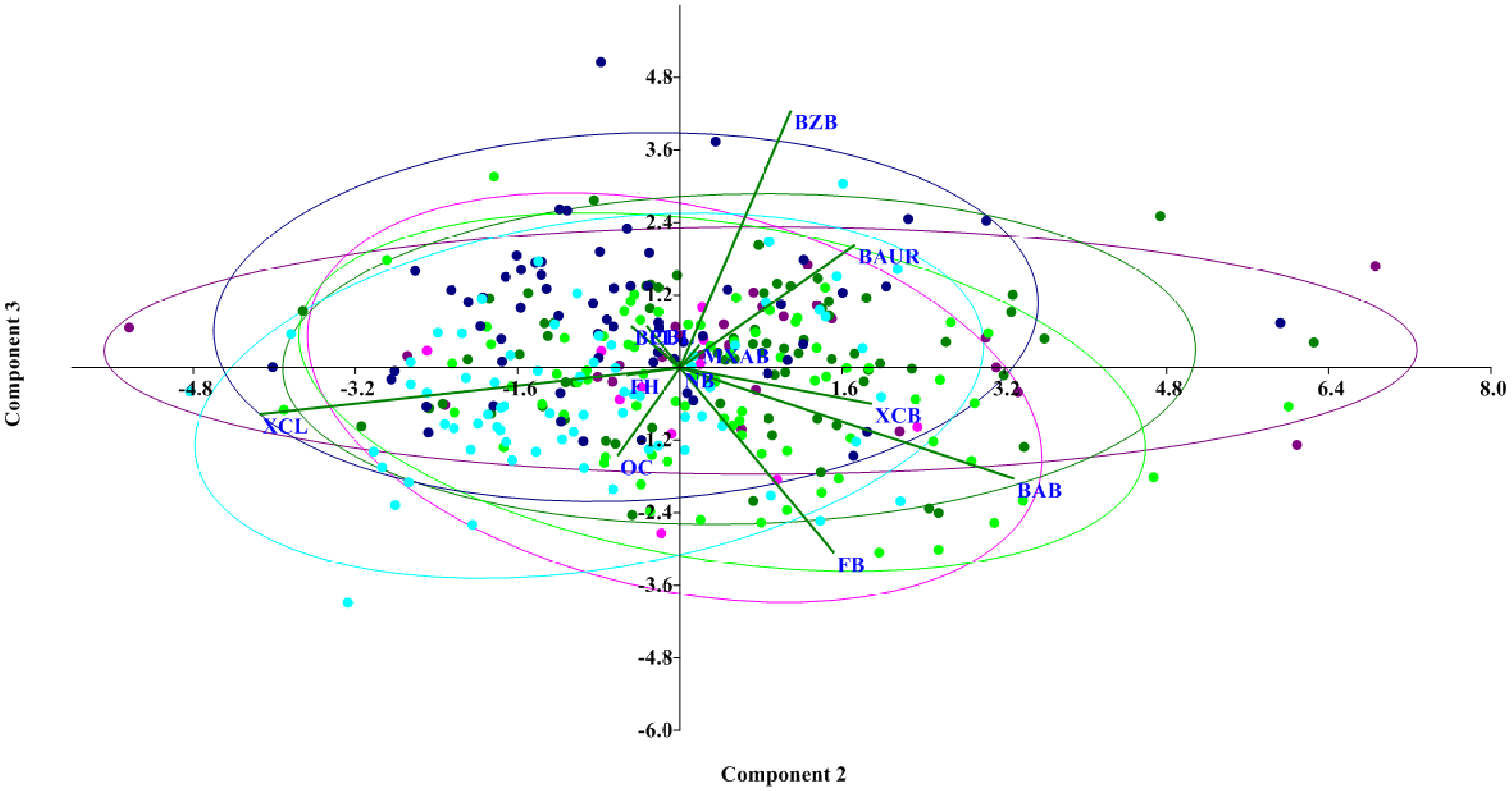

Figure 10. Cranial standardized data. PC2 x PC3.

Dental Principal Component Analyses

The following principal components analys3s (Tables 28-29) were performed on untransformed (raw) dental maxillary and mandibular dimensions from all individuals from all sites (and this set includes observed and imputed data).

The first component accounts for 62.43% of the variance with good separation on the first axis between males and females. Females are smaller on PC1 and have a greater dispersion on the second axis than do males (Figure 11). Components 2 and 3 account for 16.33% of the variation (Figure 12). Female 95% ellipses encompass the three male ellipses nearly completely. Southern Illinois females have the greatest variation in dental metrics.

Tables 30-31 below report the results of principal component analyses on size-standardized dental data (see Methods). PC1 (28.70% of the variance) and PC2 (19.03% of the variance) show little separation of males, females, or sites (Figure 13). Tooth types still group together based on loadings (maxillary and mandibular premolars cluster together, canines cluster together, and the molars each constitute their own groups). Southern Illinois females encompass nearly all of the variation in their 95% ellipses on both PC1 and PC2. This could be a sample size issue, though they do follow the general trend of females being more variable than males for each geographic area.

PC2 vs PC3 also shows little separation of groups or sexes (Figure 14). The graph of these two principal component axes also shows clusters of loadings on both the second and third axes. The premolars, molars, and canines each group together (as would be expected since these are raw, untransformed data). There is a great deal of overlap in the 95% ellipses plotted on PC 2 and 3. Females seem to have slightly greater variation (they occupy more of PC2 in both directions – driven most directly by premolar size). Southern Illinois females have the largest 95%

confidence ellipse, and therefore the greatest relative variance, but this could be influenced by the sample size of this subset of the data.

Table 28. Odonotometric raw data eigenvalues and contribution to variance for pooled sexes and all sites

PC	Eigenvalue	% variance
1	1.75512	62.43
2	0.264717	9.416
3	0.194299	6.9113
4	0.149822	5.3292
5	0.107109	3.8099
6	0.100519	3.5755
7	0.0765268	2.7221
8	0.0669423	2.3812
9	0.0560638	1.9942
10	0.040225	1.4308

Table 29. Odontometric raw data loadings on the first three PC axes for pooled sexes and all sites

	Axis 1	Axis 2	Axis 3
XCMDL	0.2006	0.1861	0.6722
XP3BLL	0.3466	-0.4027	0.144
XP4BLL	0.3393	-0.4414	-0.05368
XM1BLL	0.3266	0.3327	-0.1661
XM2BLL	0.4374	0.1554	-0.2628
NCMDL	0.2306	0.2916	0.5464
NP3BLL	0.2806	-0.2891	0.02603
NP4BLL	0.3049	-0.3213	0.06918
NM1BLL	0.2757	0.3879	-0.1293
NM2BLL	0.3546	0.2263	-0.3274

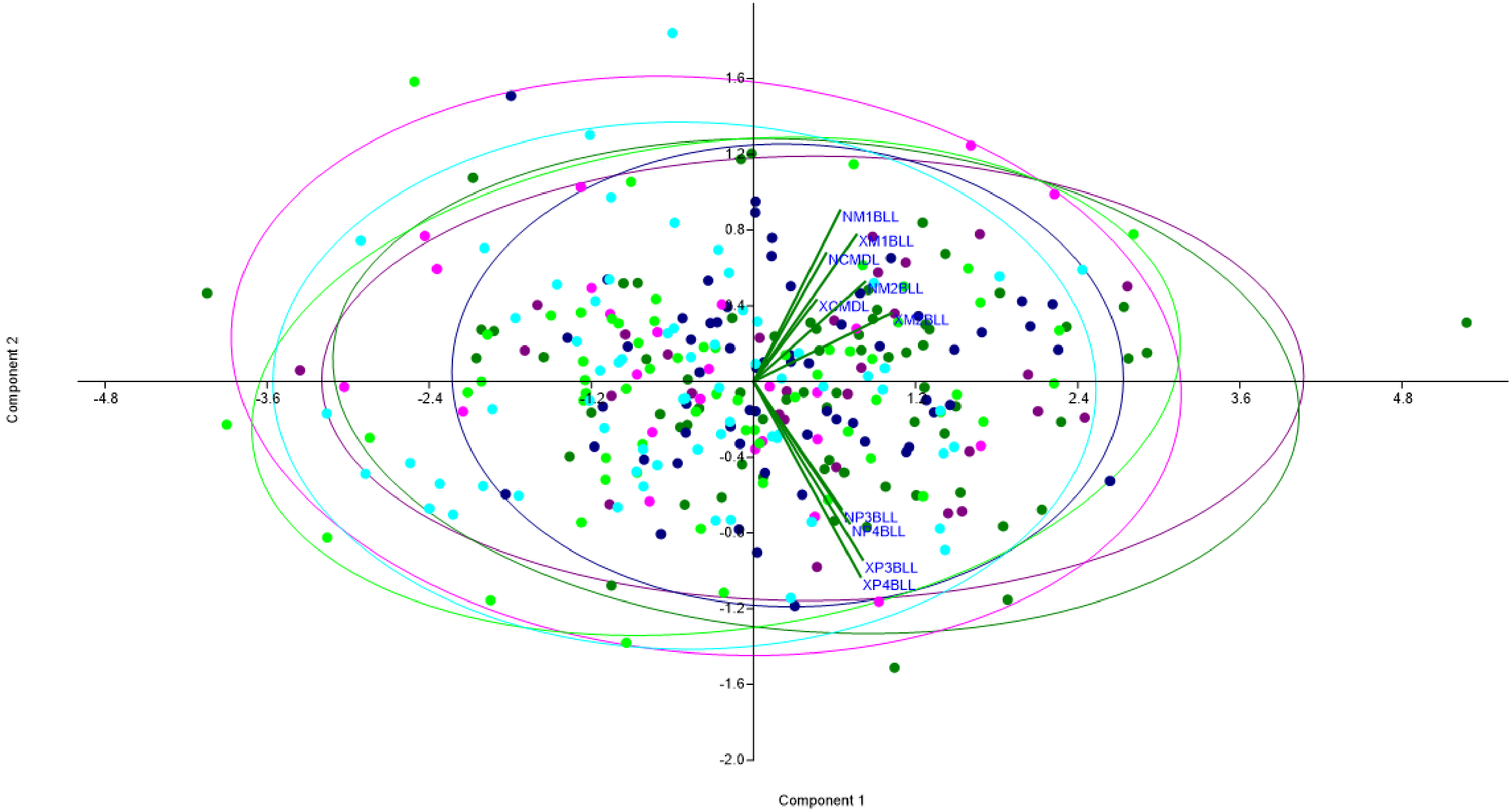

Figure 11. Odontometric raw data. PC1 x PC2

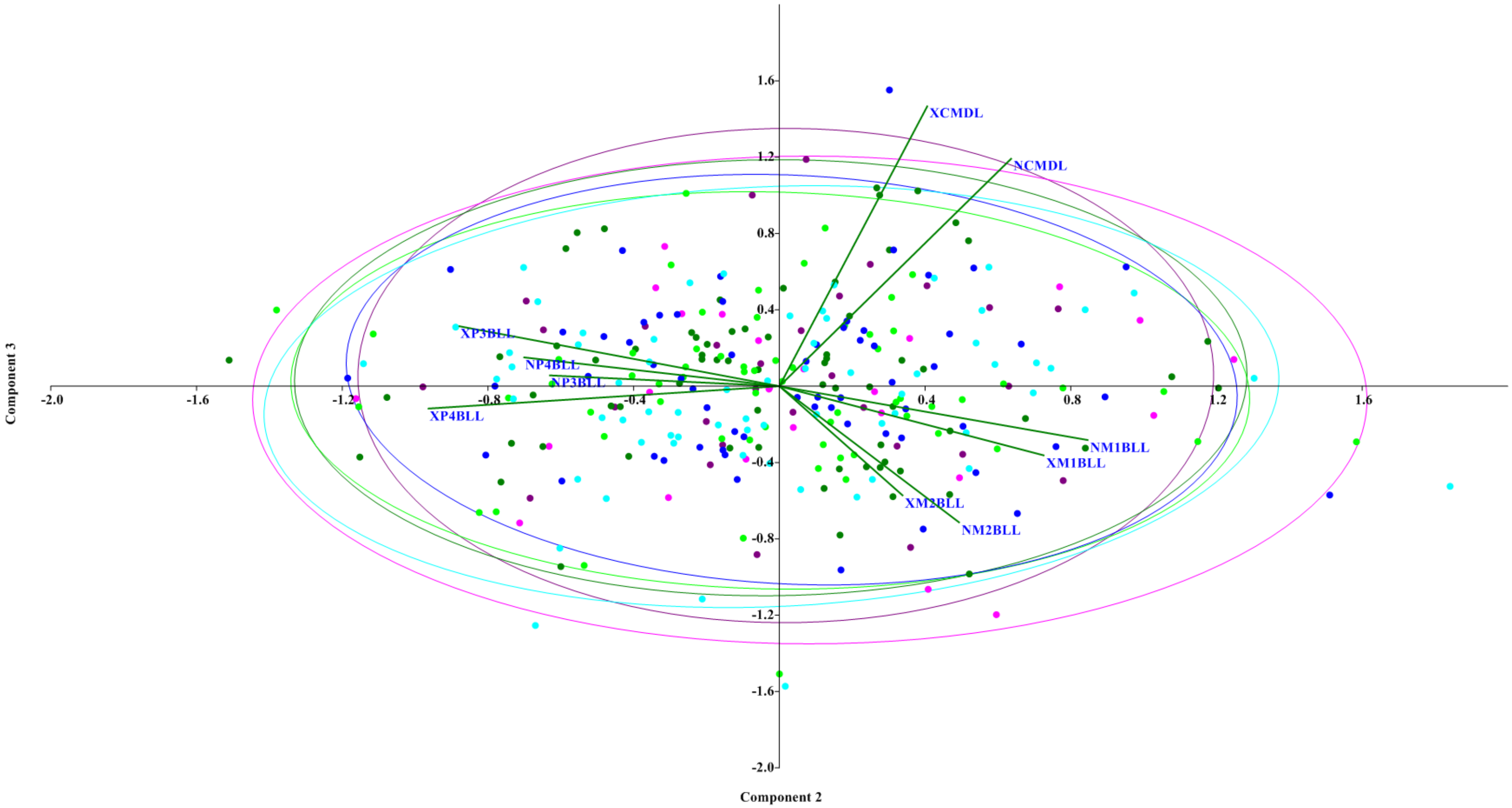

Figure 12. Odontometric raw data. PC2 x PC3.

Table 30. Odontometric standardized data eigenvalues and contribution to variance for pooled sexes and all sites

PC	Eigenvalue	% variance
1	2.87015	28.702
2	1.90333	19.033
3	1.26056	12.606
4	1.15222	11.522
5	0.823965	8.2397
6	0.723141	7.2314
7	0.68225	6.8225
8	0.523891	5.2389
9	0.0604889	0.60489
10	7.68278E-20	7.6828E-19

Table 31. Odontometric standardized data loadings on the first three PC axes for pooled sexes and all sites

	Axis 1	Axis 2	Axis 3
% variance	28.702%	19.033%	12.606%
XCMDLC	0.3668	0.2247	0.04127
XP3BLLC	-0.3274	-0.2192	0.3009
XP4BLLC	-0.3948	-0.01349	0.1268
XM1BLLC	0.3285	-0.4197	0.3255
XM2BLLC	-0.1414	0.5088	0.3954
NCMDLC	0.4534	0.1665	0.1993
NP3BLLC	-0.2232	-0.2434	0.03111
NP4BLLC	-0.2982	-0.1615	-0.4497
NM1BLLC	0.3600	-0.3199	-0.4079
NM2BLLC	-0.02499	0.5008	-0.4692

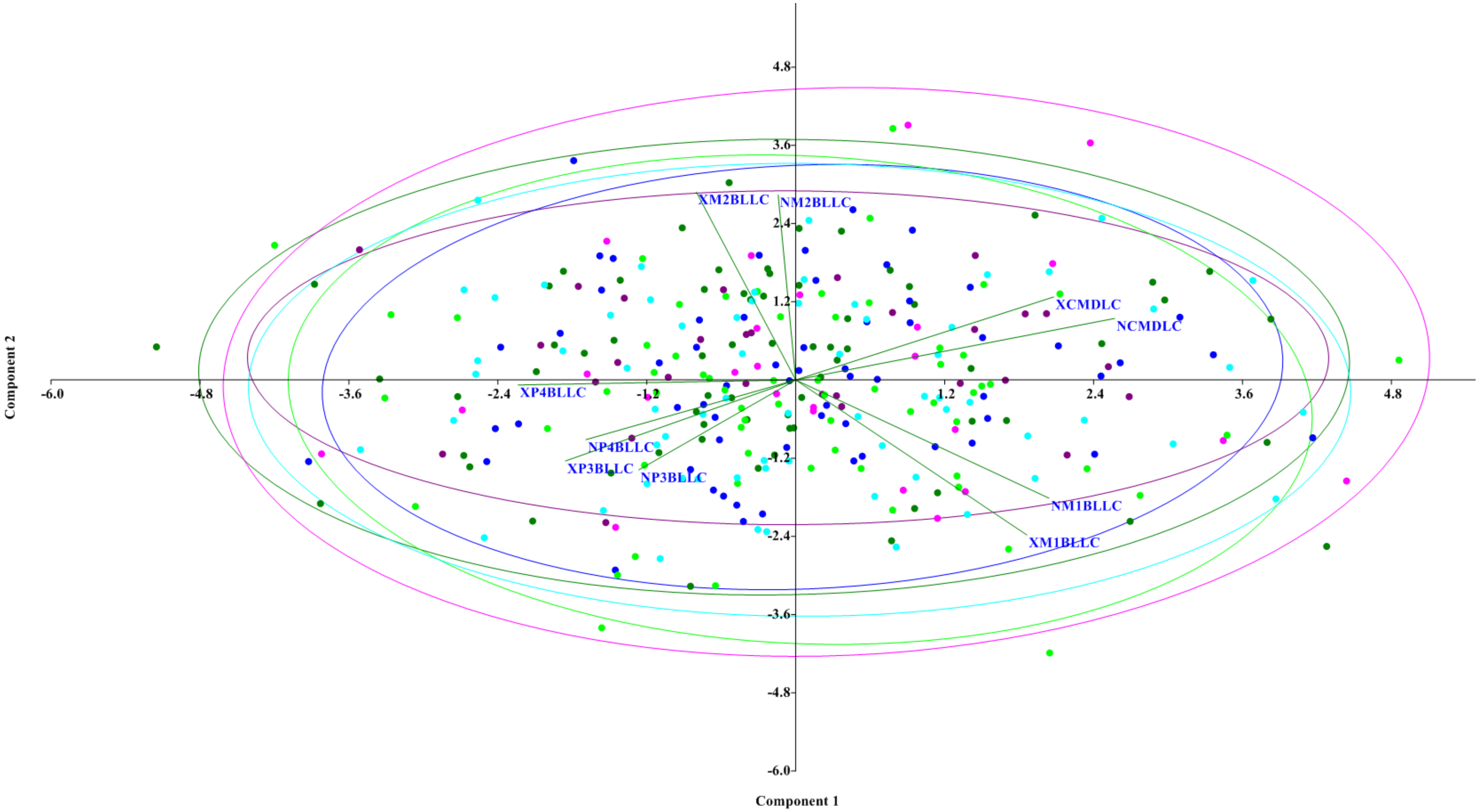

Figure 13. Odontometric standardized data. PC1 x PC2.

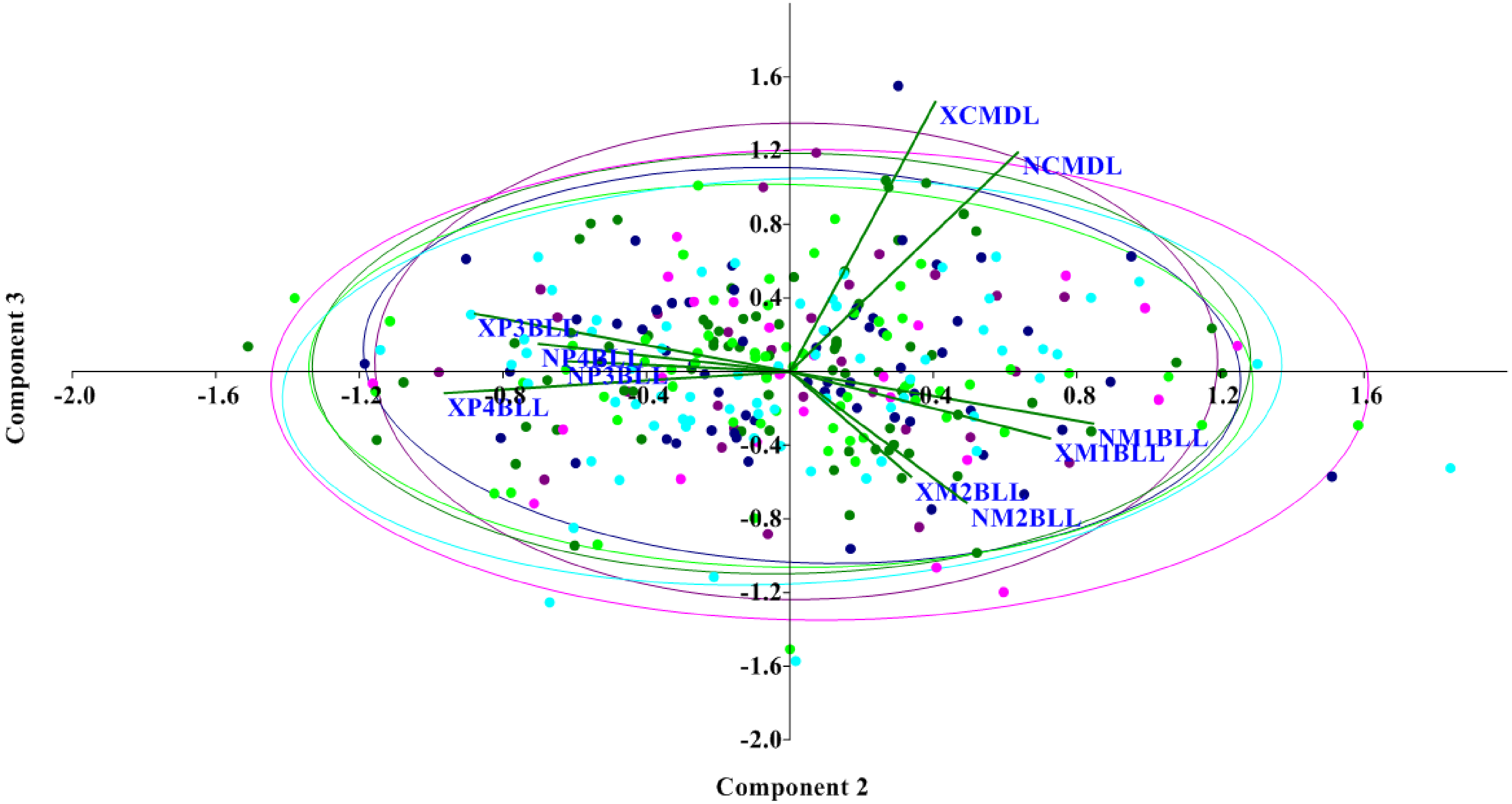

Figure 14. Odontometric standardized data. PC2 x PC3.

Post-Cranial Principal Component Analyses

Female Long Bones. The following principal components analyses (Tables 32-33) were preformed on untransformed (raw) left female humerii, radii, femora, and tibiae maximum lengths from all sites. The first principal component accounts for 92.64% of the variance. Size is typically the biggest driver of PC1 and that is certainly the case for these raw measures. All long bones have positive loadings on the first principal component, in order of their relative lengths (femur, tibia, humerus, radius) (Figure 15). The proximal and distal elements contribute in opposite ways on the second PC axis (just only 4% of the variance) (HXL and FXL are negative while RXL and TXL are positive). Comparing PC2 and PC3 removes size that is loading so heavily on PC1 (Figure 16). These two components only account for 6.36% of the variance together. Each long bone occupies a quadrant of the graph and western Kentucky (females, in this case) encompass the other two groups (and are therefore more variable).

Table 32. Post-cranial raw data eigenvalues and contribution to variance for females from all sites

PC	Eigenvalue	% variance
1	914.219292	92.63696
2	42.304864	4.286711
3	20.562750	2.083604
4	9.797031	0.9927237

Table 33. Post-cranial raw data loadings on the first four PC axes for females from all sites

	Axis 1	Axis 2	Axis 3	Axis 4
HXLL	0.4338	-0.4021	0.7334	-0.3351
RXLL	0.3945	0.4749	0.3491	0.705
FXLL	0.5929	-0.5449	-0.5165	0.291
TXLL	0.5519	0.562	-0.2711	-0.5532

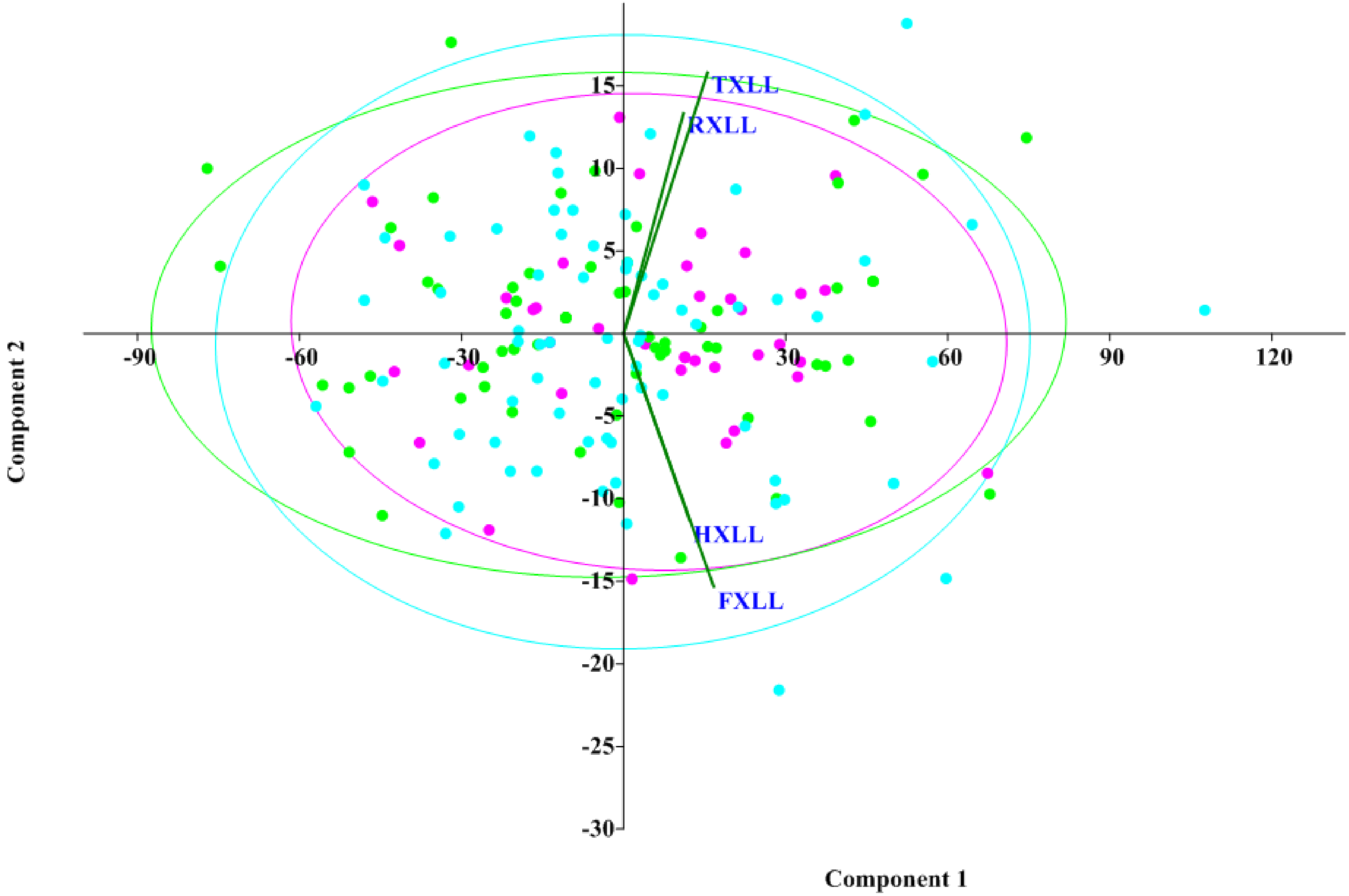

Figure 15. Post-cranial raw data for females only. PC1 x PC2.

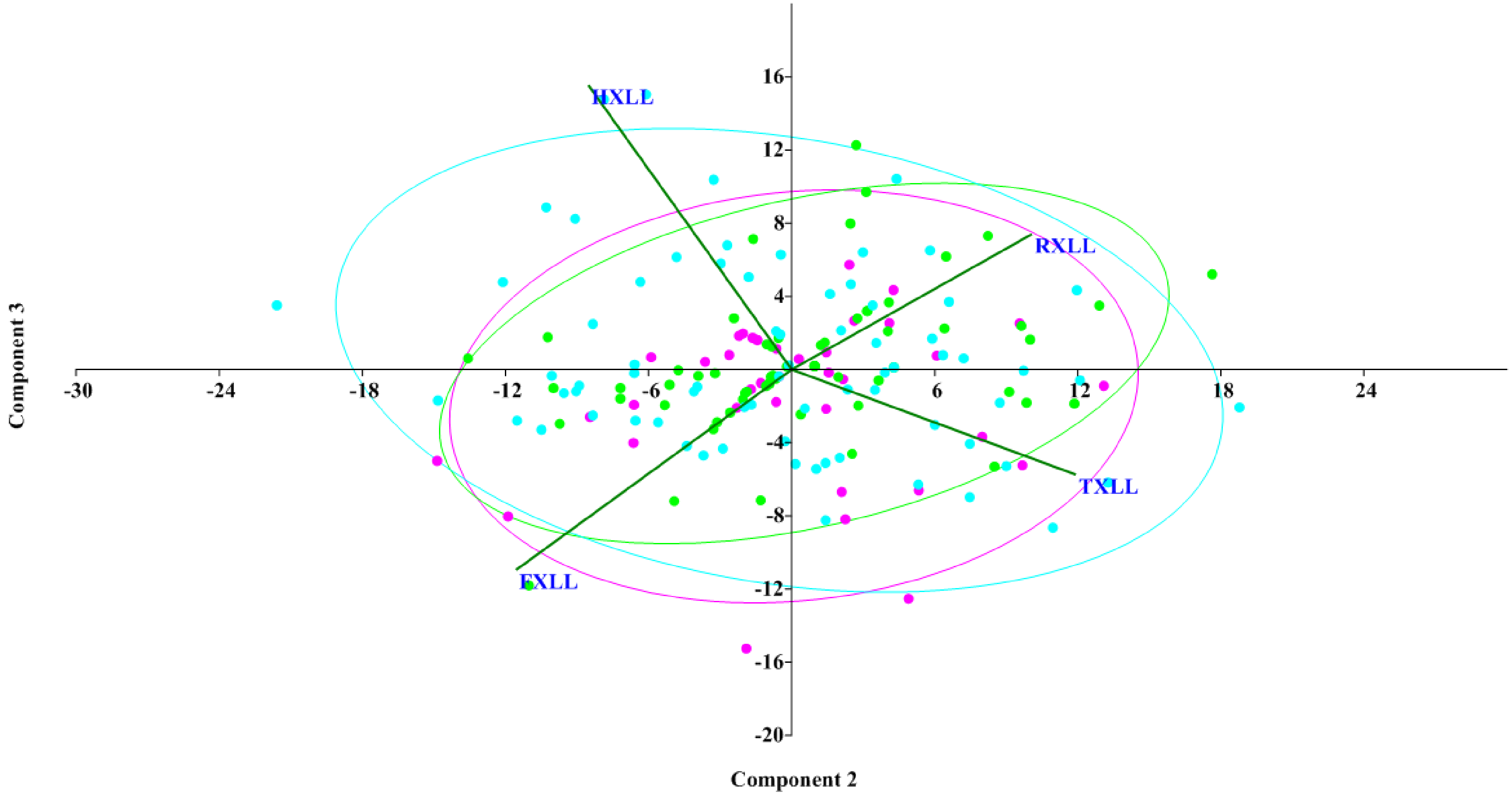

Figure 16. Post-cranial raw data for females only. PC2 x PC3

Male Long Bones. The following principal component analyses (Tables 34-35) were run on male left maximum lengths of the humerus, radius, femur, and tibia. Like the females, PC1 accounts for just over 91% of the variance, which is interpreted as reflecting size. All four long bones have positive loadings, then, on PC1, and again in the order of their lengths (femur, tibia, humerus, radius) (Figure 17). PC2 vs PC3 shows all four bones contributing in opposite ways for their loadings but these two axes account for only 7% of the variance combined (Figure 18).

Pooled Sexes Long Bone Lengths. The PCAs below (Tables 36-37) were performed on raw (untransformed) from all sites and males and females combined (left sides only). These results are highly skewed by size with over 95% of the variance being accounted for on the first principal component. Males and females clearly separate on this axis and females are smaller than males (Figure 19). Given the large contribution of the first principal component in these data, and that patterns of PC2 vs PC3 and PC1 vs PC3 look similar to those presented above for females and males separately, they are not presented here for these pooled data.

Female Indices. Below are the PCA results (Tables 38-39) for female brachial, crural, and intermembral indices. The first principal component accounts for just over 79% of the variance. All loadings on the first PC axis are positive. Brachial index has a loading of 0.80 and the crural index has a loading of 0.59. A graph of PC1 and PC2 shows all three groups of females with similar shaped 95% ellipses (western Kentucky again encompasses the other three) (Figure 20). PC2 vs PC3 accounts for nearly 21% of the variance (Figure 21). Here the orientation of central Tennessee females is different from the southern Illinois and western Kentucky samples.

Male Indices. Like females above, these data are from male computed indices for the arm, leg, and limbs (Tables 40-41). PC1 accounts for just over 50% of the variance. The brachial index has a loading of 0.77 on this axis while the crural index loading on PC1 was 0.62. Ellipses representing 95% confidence intervals show close congruity between western Kentucky and central Tennessee males while southern Illinois males have a different orientation (Figure 22). PC2 accounts for just over 30% of the variance while PC3 accounts for 19%. Plotting the two against one another shows central Tennessee males with a more constricted 95% confidence ellipse that is oriented differently from the other two (Figure 23).

Pooled Sexes Indices. Males and females from all sites were pooled together in a Principal Components Analysis of their computed indices (Tables 42-43). Like the PCAs above, the first principal component axis accounts for a significant portion of the variance (64.28%). There is good separation between females and males along this axis (Figure 24). Brachial and crural indices are the largest and second largest loadings on the first PC axis (0.82 and 0.55 respectively). Plotting PC2 against PC3 ignores the influence of size that is driving the first PC axis (Figure 25). PC2 accounts for 20.79% of the variance while PC3 accounts for 14.94%. In this graph, females are wholly within the 95% ellipses generated for the males.

Table 34. Post-cranial raw data eigenvalues and contribution to variance for males from all sites

PC	Eigenvalue	% variance
1	822.89	91.107
2	35.0346	3.8789
3	28.9647	3.2069
4	16.3223	1.8071

Table 35. Post-cranial raw data loadings on the first four PC axes for males from all sites

	Axis 1	Axis 2	Axis 3	Axis 4
HXLL	0.4349	0.1982	0.6443	-0.5971
RXLL	0.3313	0.5627	0.262	0.7107
FXLL	0.6367	-0.7239	0.03657	0.2629
TXLL	0.5438	0.3465	-0.7176	-0.2632

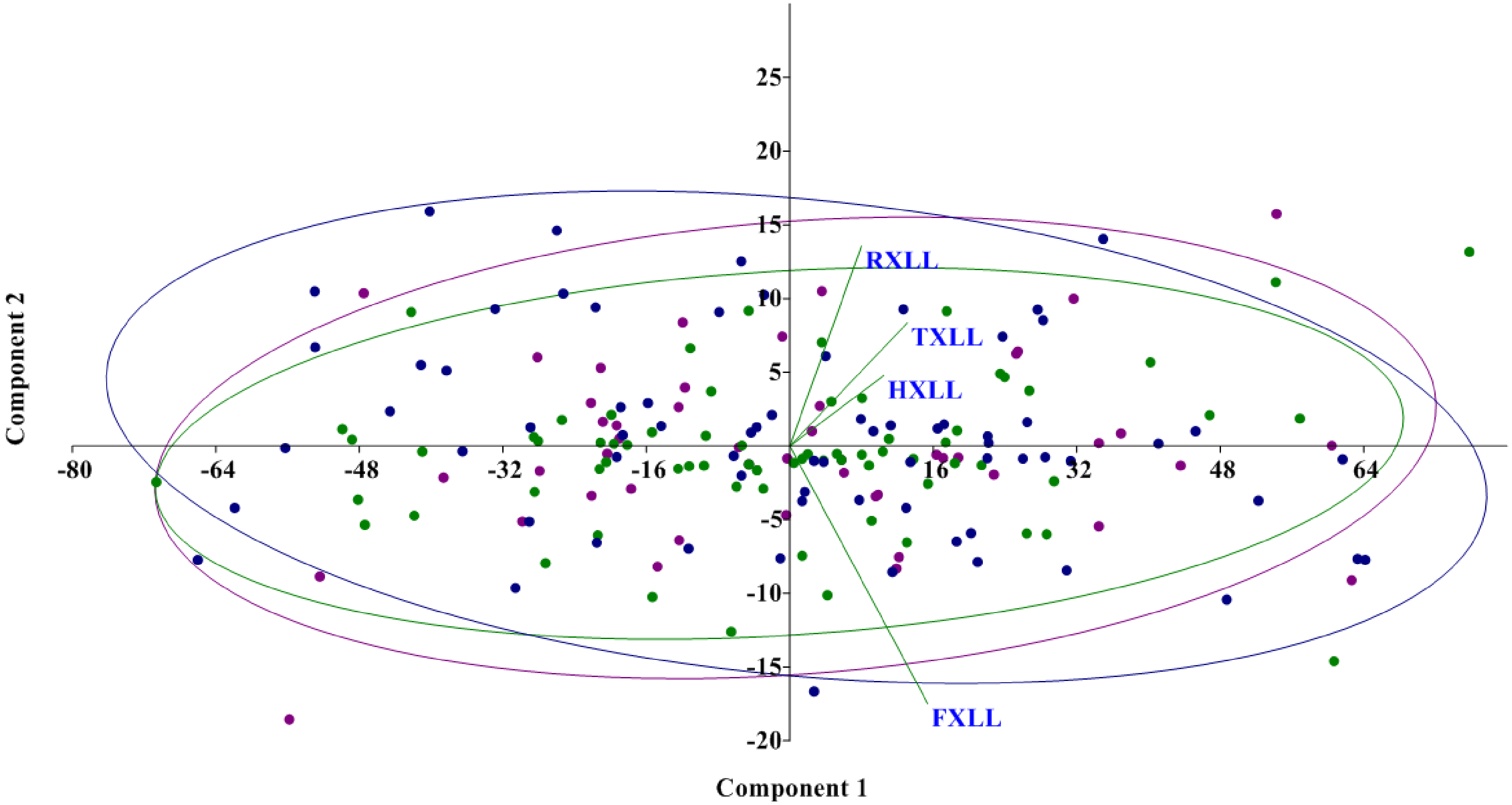

Figure 17. Post-cranial raw data for males only. PC1 x PC2.

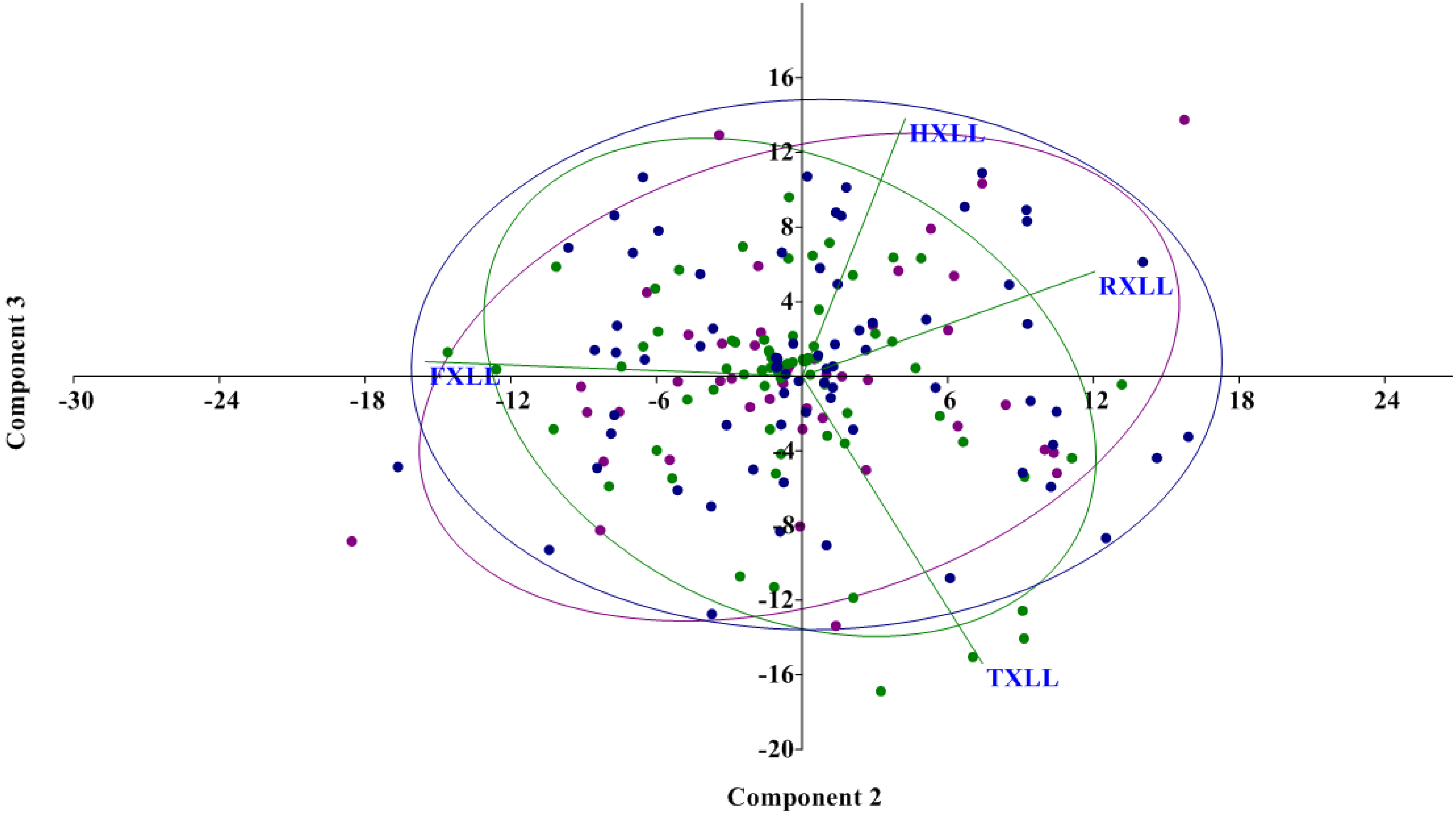

Figure 18. Post-cranial raw data for males only. PC2 x PC3.

Table 36. Post-cranial raw data eigenvalues and contribution to variance for pooled sexes and all sites

PC	Eigenvalue	% variance
1	1561.09	95.062
2	39.2512	2.3902
3	27.2955	1.6621
4	14.5463	0.88579

Table 37. Post-cranial raw data loadings on the first four PC axes for pooled sexes and all sites

	Axis 1	Axis 2	Axis 3	Axis 4
HXLL	0.4412	-0.1643	0.7112	-0.5221
RXLL	0.3987	0.5624	0.3488	0.6349
FXLL	0.596	-0.6689	-0.2594	0.3607
TXLL	0.5397	0.4575	-0.5525	-0.4406

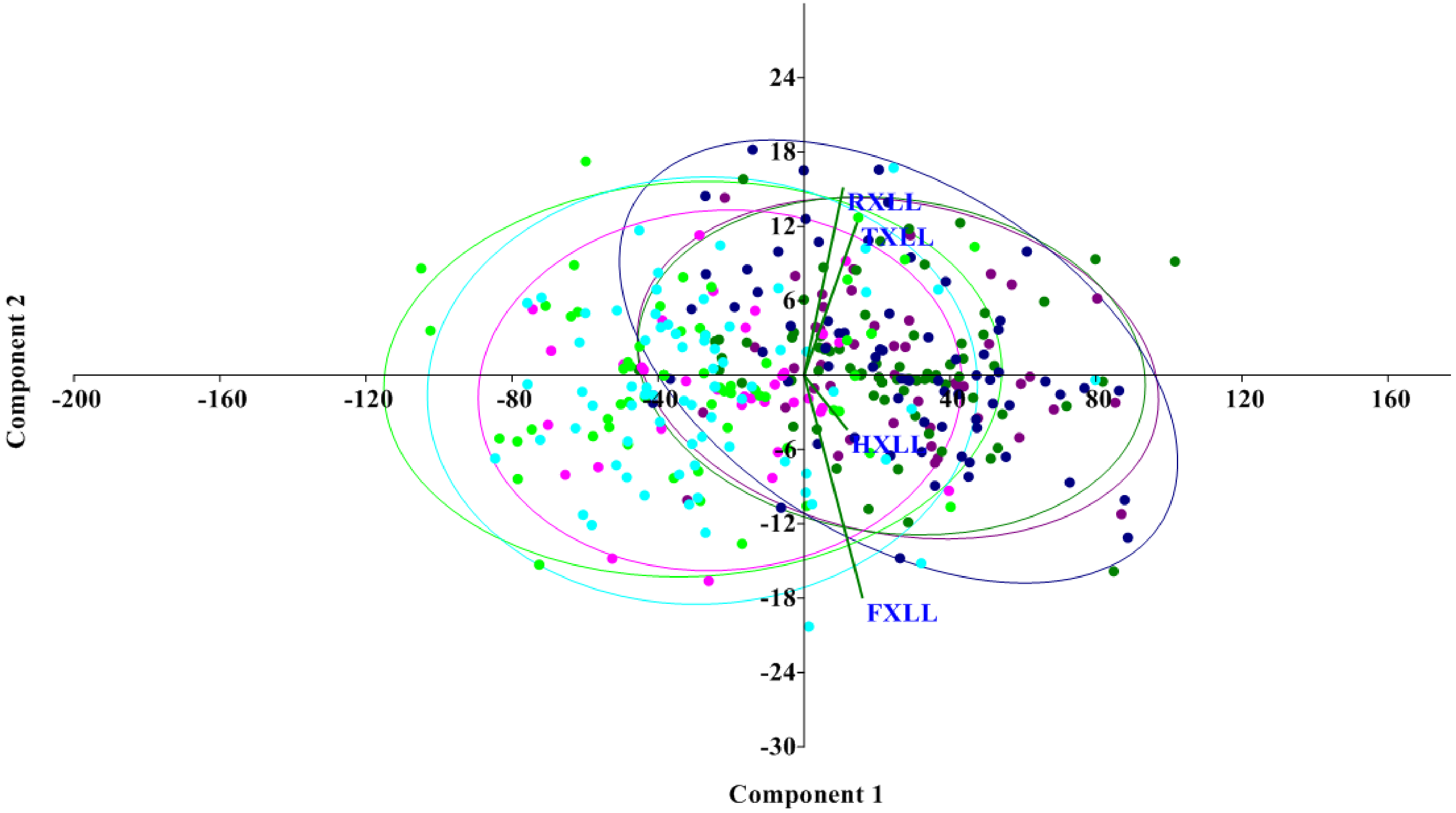

Figure 19. Post-cranial raw data for pooled sexes and all sites. PC1 x PC2.

Table 38. Post-cranial indices eigenvalues and contribution to variance for females from all sites		
PC	Eigenvalue	% variance
1	9.38671	79.211
2	1.41488	11.94
3	1.04865	8.8492

Table 39. Post-cranial indices loadings on the first three PC axes for females from all sites			
	Axis 1	Axis 2	Axis 3
Brachial Index	0.8032	-0.5876	0.09794
Crural Index	0.5942	0.7789	-0.2006
Intermembral Index	0.0416	0.2193	0.9748

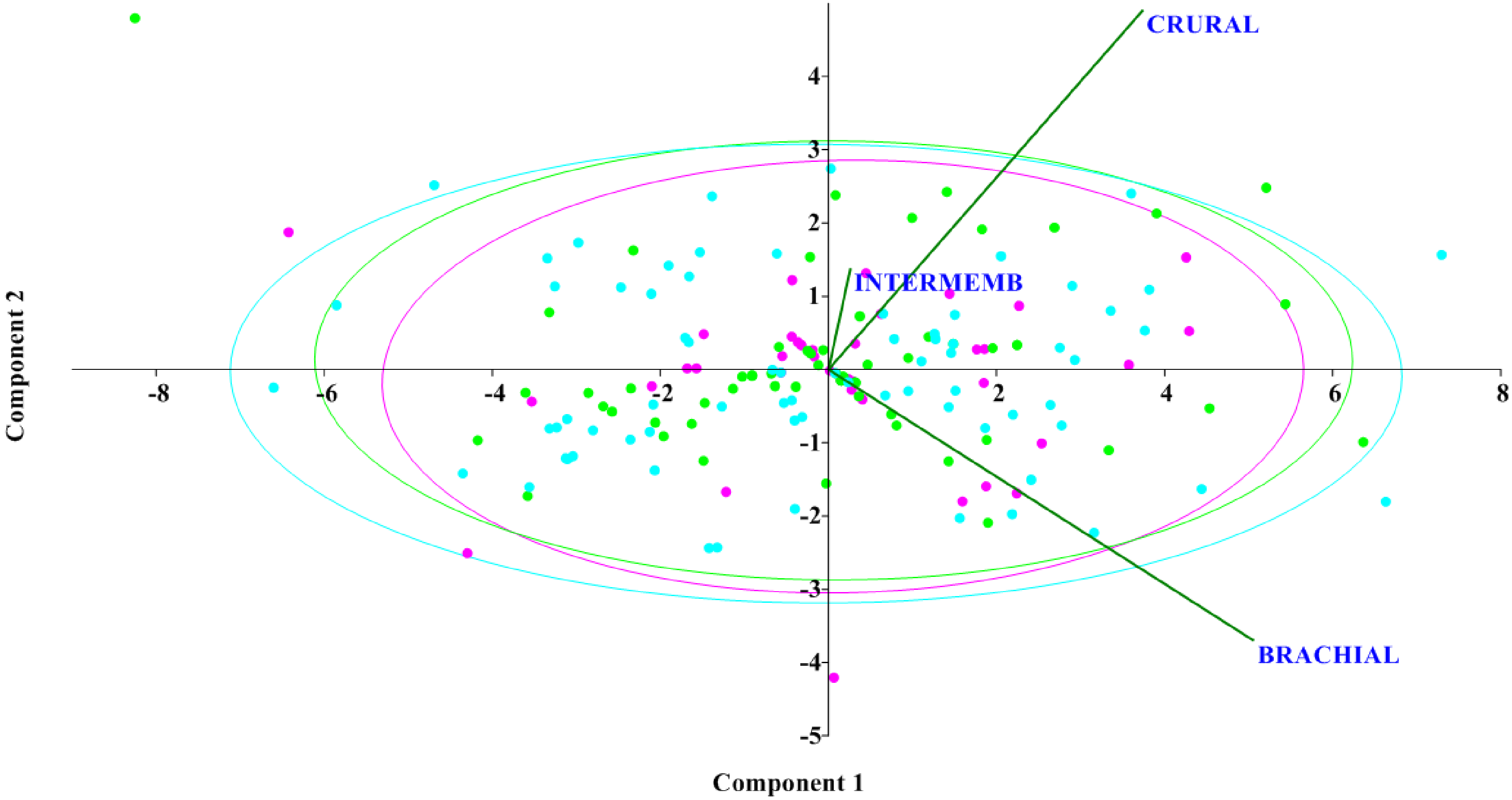

Figure 20. Post-cranial indices for females only. PC1 x PC2.

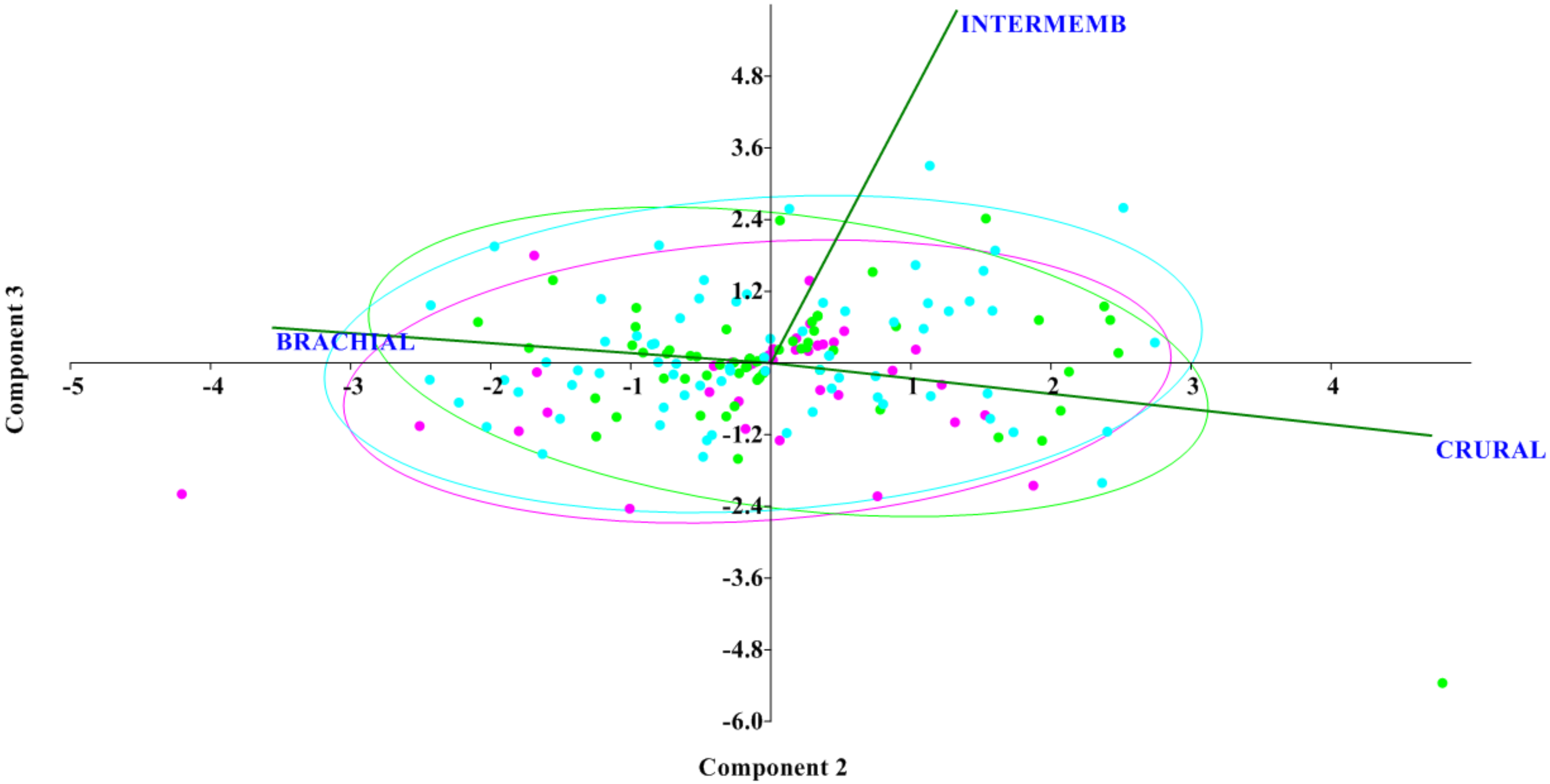

Figure 21. Post-cranial indices for females only. PC2 x PC3.

Table 40. Post-cranial indices eigenvalues and contribution to variance for males from all sites

PC	Eigenvalue	% variance
1	3.54172	50.297
2	2.14364	30.443
3	1.35623	19.260

Table 41. Post-cranial indices loadings on the first three PC axes for males from all sites

	Axis 1	Axis 2	Axis 3
Brachial Index	0.7726	0.5922	-0.2288
Crural Index	0.6196	-0.7819	0.06878
Intermembral Index	0.1382	0.1949	0.971

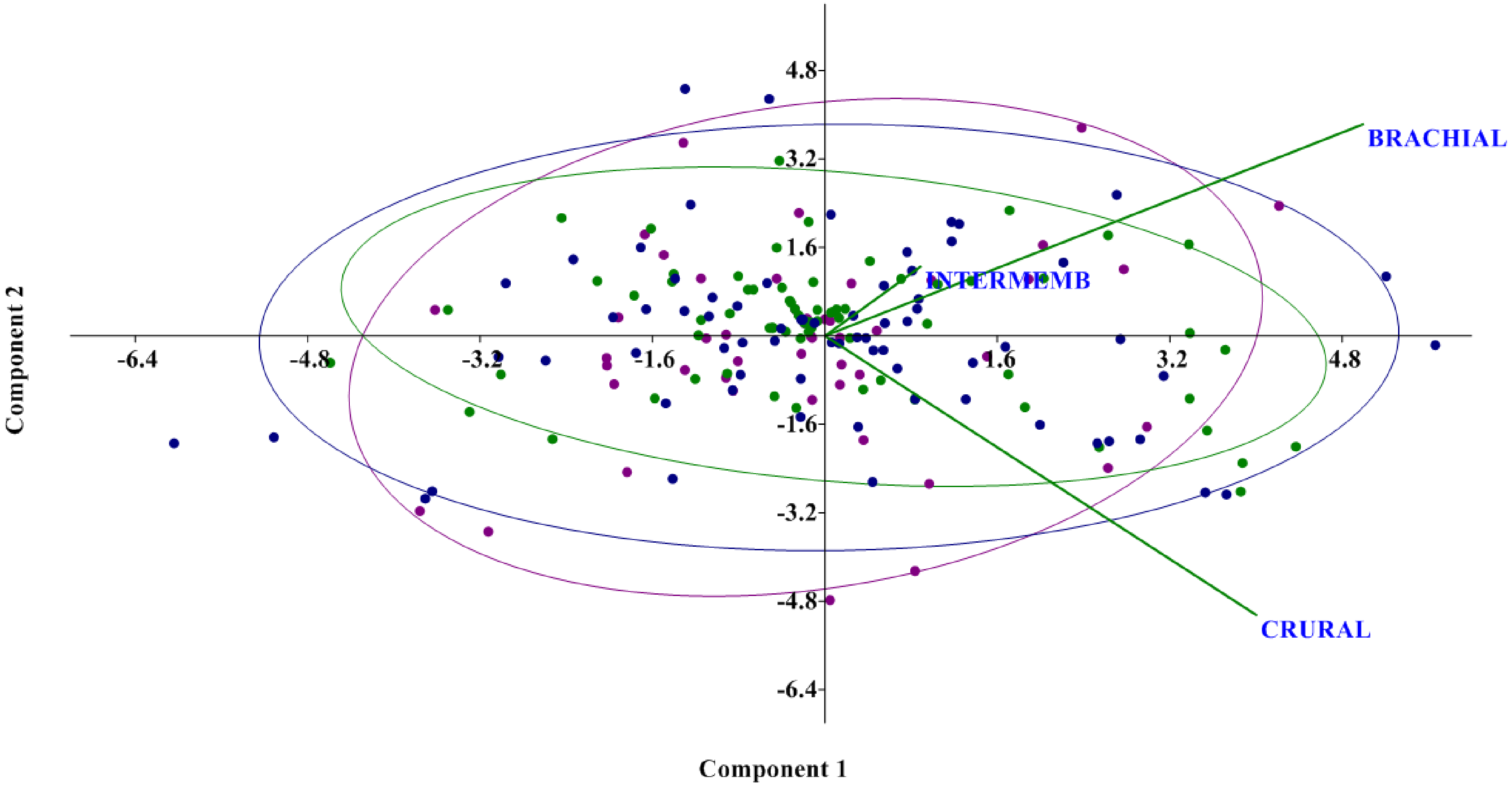

Figure 22. Post-cranial indices for males only. PC1 x PC2.

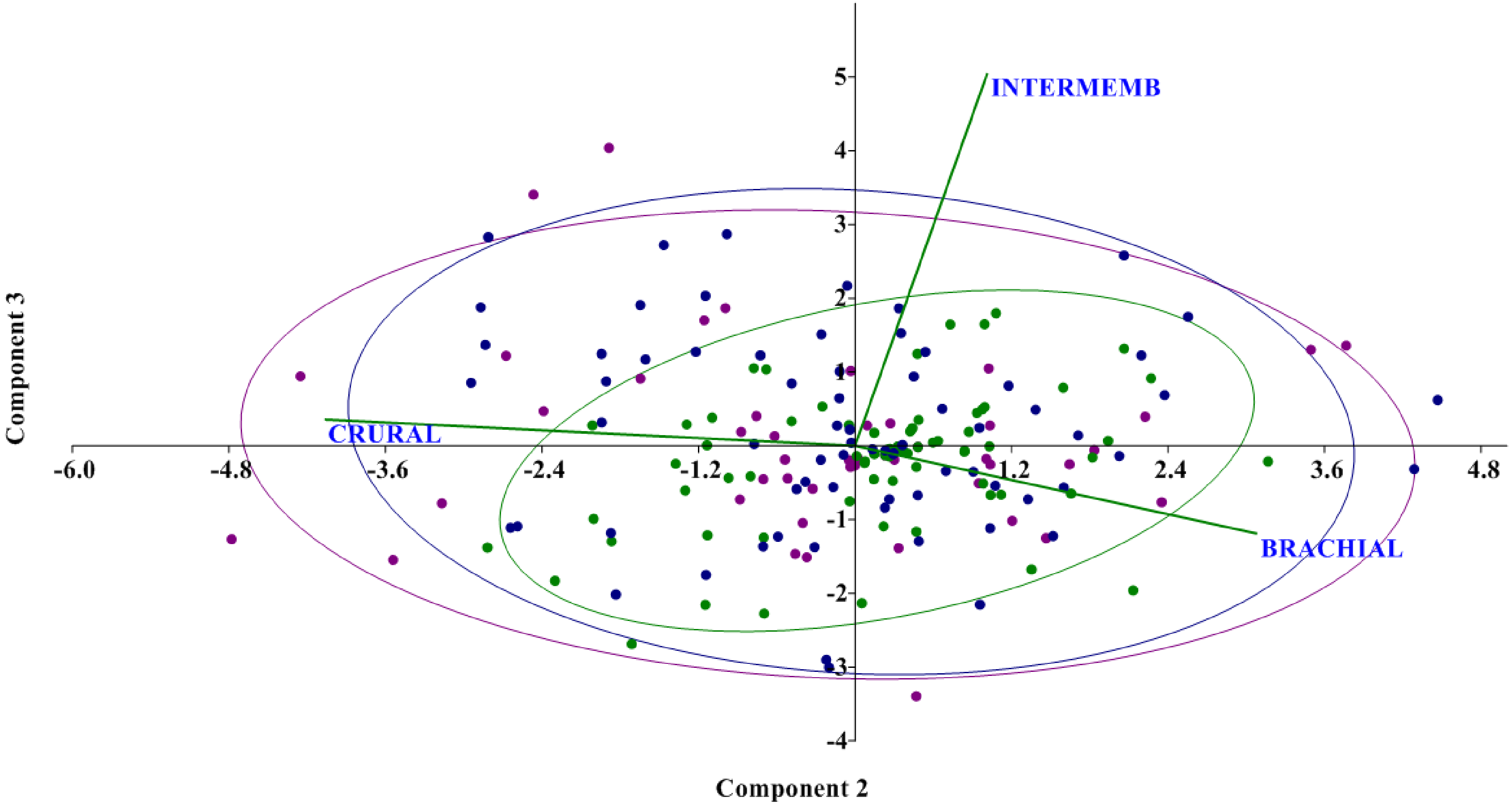

Figure 23. Post-cranial indices for males only. PC2 x PC3.

Table 42. Post-cranial indices eigenvalues and contribution to variance for pooled sexes and all sites

PC	Eigenvalue	% variance
1	5.69497	64.276
2	1.84159	20.785
3	1.32363	14.939

Table 43. Post-cranial indices loadings on the first three PC axes for pooled sexes and all sites

	Axis 1	Axis 2	Axis 3
Brachial Index	0.8212	-0.5206	-0.2336
Crural Index	0.5503	0.8308	0.08324
Intermembral Index	0.1507	-0.1969	0.9688

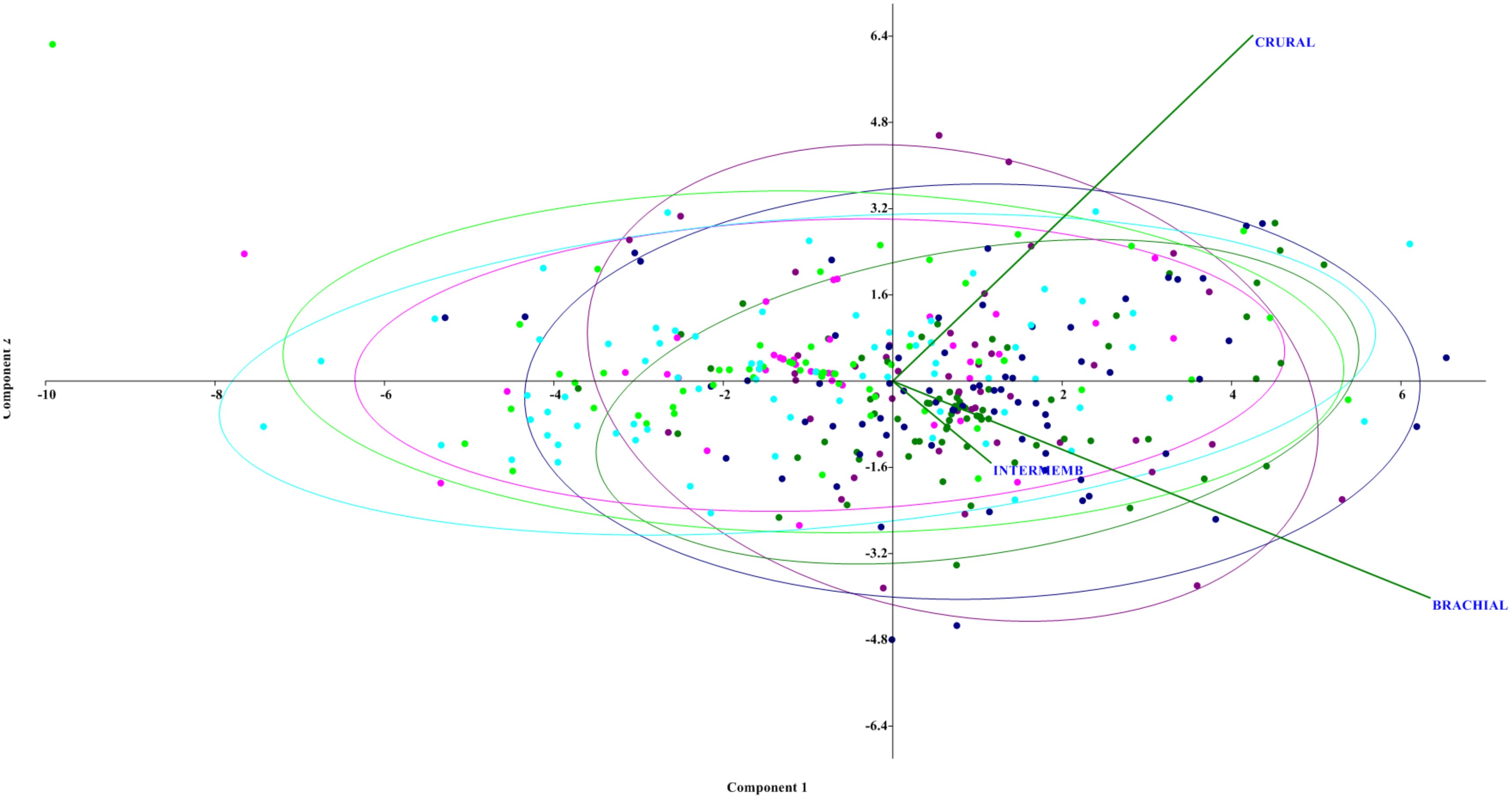

Figure 24. Post-cranial indices for pooled sexes. PC1 x PC2.

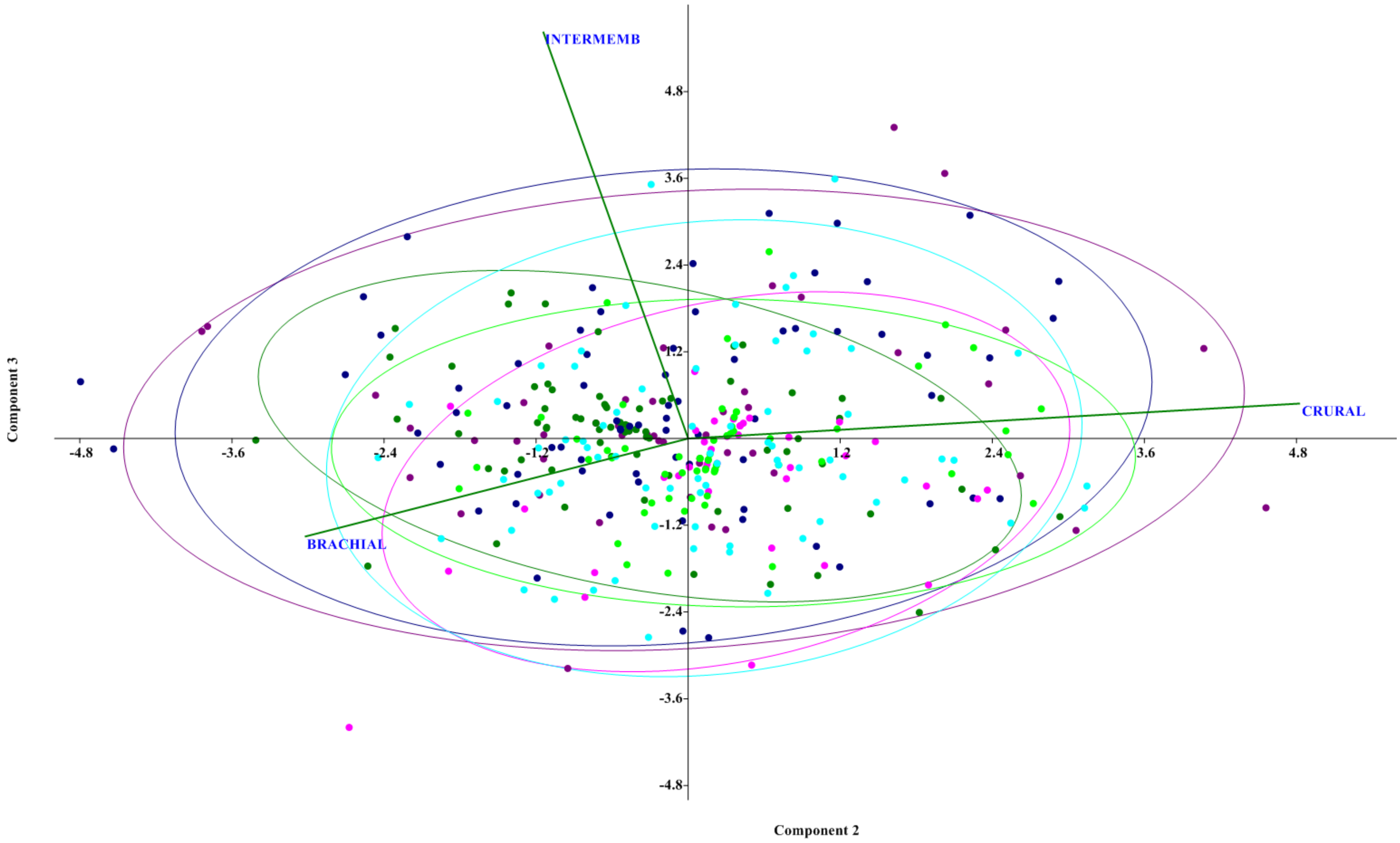

Figure 25. Post-cranial indices for pooled sexes. PC2 x PC3.

Mahalanobis Distance

Biological Distance Based on Craniometrics

The following results are from cranial data (average of five imputation runs) from all individuals from all sites. Six groups went into the analysis: males and females from each of the three geographic sub-regions. All observations were divided by the area of the foramen magnum (FMB x FML) to minimize the influence of size (see Methods above). The table below is the pairwise Mahalanobis distance between group means (Table 44).

Comparing sexes within each sub-region shows southern Illinois males and females have a distance of 1.96, central Tennessee males and females are 1.48 apart, and western Kentucky males and females have a distance score of 2.45. Western Kentucky has the greatest distances between sexes while central Tennessee has the least.

Looking at distances between males from different sub-regions, southern Illinois males have a distance of 1.06 to males in central Tennessee and 1.93 with males in western Kentucky. Central Tennessee males and western Kentucky males have a D score of 2.39. Females from southern Illinois have a distance of 0.69 to females in central Tennessee and 2.09 to females in western Kentucky. Central Tennessee females and western Kentucky females have a D score of 2.14. For both sexes, southern Illinois and central Tennessee groups are closest to one another. Western Kentucky and central Tennessee have the highest distances for both sexes.

For descriptive and graphical purposes only, the Mahalanobis D distance scores presented above for the cranial data set were plotted as first as linear distances between sexes within each

Table 44. Mahalanobis distance (D) between group means for standardized cranial data including pooled sexes from all sites

	SOILM	SOILF	CTNM	CTNF	WKYM	WKYF
SOILM		1.9624284	1.055185	1.7454018	1.931221	2.303490
SOILF			1.469998	0.6945097	3.240275	2.092338
CTNM				1.4772643	2.389636	2.491458
CTNF					3.213198	2.143082
WKYM						2.449214
WKYF						

site (Figure 26), then as triangles – one for males and one for females – with the points of the triangles as the archaeological sites (Figure 27). For the distances between sexes within sites the D scores were converted to millimeters then inches (because that is what Microsoft Word uses for measurements). The D scores for distances between sites (males and females separate) were just converted to millimeters (i.e. a distance/D score of 2.14 between Central Tennessee and Western Kentucky females, for instance, is represented as 214 mm in the triangle below). Those triangles were drawn by hand then scanned as images for importation to Word. For all such triangles presented here, central Tennessee is always in the bottom left, western Kentucky is always in the bottom right, and southern Illinois always occupies the top spot (this approximates actual geographic orientations as best as can be portrayed). The images have not been scaled, stretched, or reduced in this document in any way so they should be comparable on a one-to-one basis.

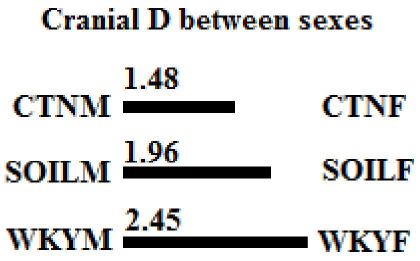

Figure 26. Graphical representations of Mahalanobis D for cranial data between sexes at each site.

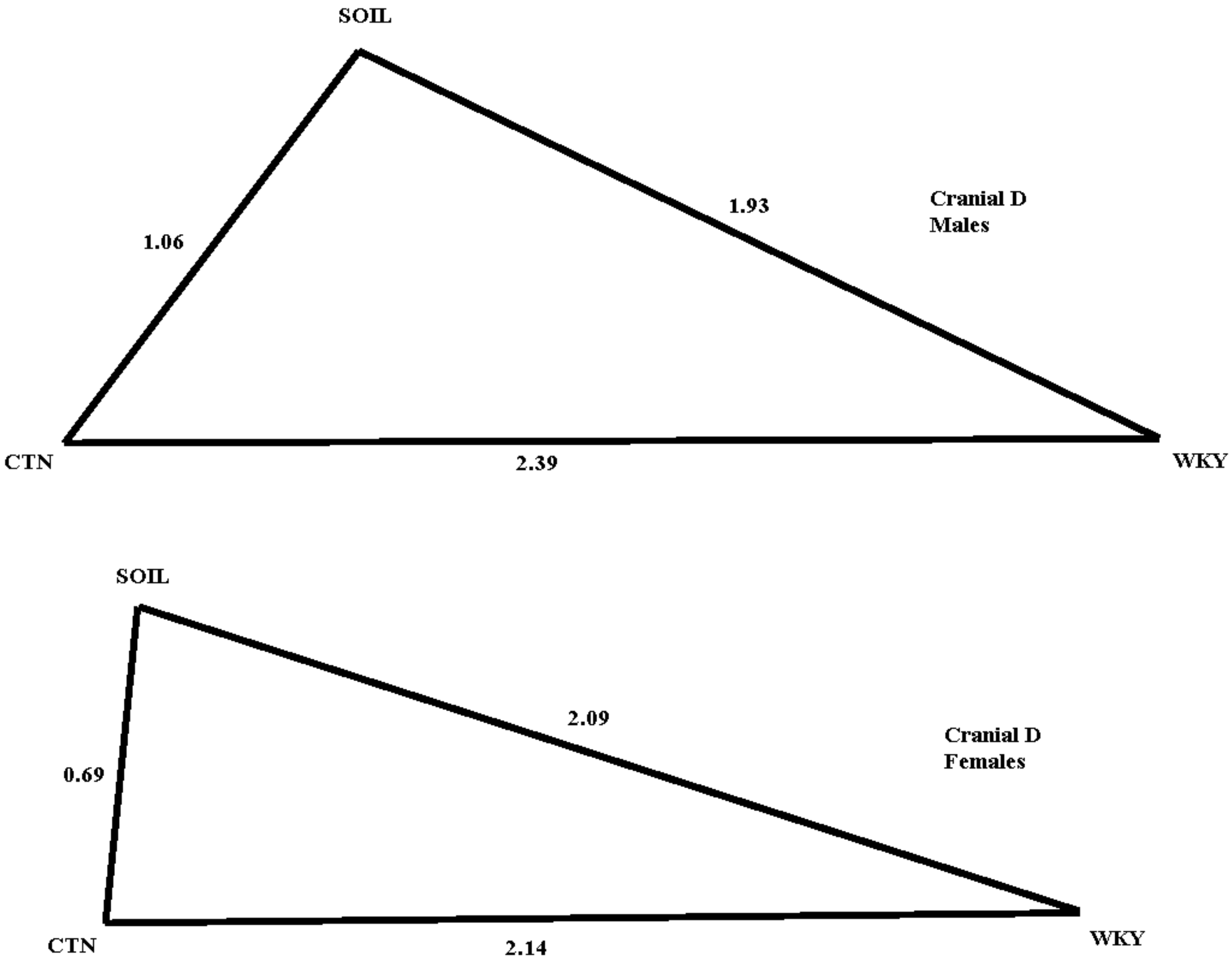

Figure 27. Graphical representations of Mahalanobis D for cranial data from males (top) and females (bottom*)*.

Biological Distance Based on Odontometrics

The Mahalanobis distances given in Tables 45-47 below were calculated on the C-score transformed odontometrics. Table 45 is for maxillary teeth only, Table 46 is for mandibular teeth only, and the last one, Table 47 is for alternating antagonists including both canines (XCMDLC, XP3BLLC, XM1BLLC, XCMDLC, NP4BLLC, NM2BLLC).

The first thing to notice about the Mahalanobis D scores for the C-Score transformed dental data, is that all distances are rather small. The distances given above for post-cranial indices and for the cranial data are also rather small, but the D scores for the dental data are the smallest. The size and morphology of human dentition is biologically conservative so perhaps it is not surprising these D scores are small.

The pattern across the three distance matrices (maxillary, mandibular, and alternating antagonists) are not the same.

Let us begin by looking at distances between the sexes within each sub-region. Southern Illinois males and females have distances of 0.67 for maxillary teeth, 0.27 for mandibular teeth, and 0.58 for the alternating antagonists. In the central Tennessee sub-region, males and females have distances of 0.62 for the maxillary teeth, 0.66 for mandibular teeth, and 0.64 for the antagonists. The western Kentucky males and females have distances of 0.40 for the maxillary teeth, 0.42 for the mandibular teeth, and 0.30 for the alternating antagonist teeth. At least the central Tennessee and western Kentucky distances between sexes are somewhat similar.

In a general trend, males and females are closer (smaller D) in the western Kentucky sample than the other two sub-regions. Central Tennessee males and females D ranges from 0.62 to 0.66 and have consistently higher D than the other two. The dental data from southern Illinois

Table 45. Mahalanobis distance (D) between group means for standardized odontometrics data (maxillary dentition only) including pooled sexes from all sites

	SOILM	SOILF	CTNM	CTNF	WKYM	WKYF
SOILM		0.6725698	0.436699	0.4541854	0.2018739	0.4174741
SOILF			0.7418874	0.5634967	0.645938	0.5342596
CTNM				0.6188646	0.3823741	0.5645409
CTNF					0.3064737	0.4456446
WKYM						0.3980173
WKYF						

Table 46. Mahalanobis distance (D) between group means for standardized odontometrics data (mandibular dentition only) including pooled sexes from all sites

	SOILM	SOILF	CTNM	CTNF	WKYM	WKYF
SOILM		0.2725326	0.7929868	0.450617	0.1239808	0.4376649
SOILF			0.623522	0.4062691	0.1848681	0.294454
CTNM				0.6599404	0.6894304	0.793767
CTNF					0.4329126	0.5347319
WKYM						0.4174305
WKYF						

Table 47. Mahalanobis distance (D) between group means for standardized odontometrics data (alternating antagonists only) including pooled sexes from all sites

	SOILM	SOILF	CTNM	CTNF	WKYM	WKYF
SOILM		0.5770178	0.5464177	0.376085	0.1611264	0.2417213
SOILF			0.9106938	0.5415353	0.4531271	0.5751027
CTNM				0.6365508	0.6323619	0.6480467
CTNF					0.2956034	0.4227101
WKYM						0.302699
WKYF						

males and females varies whether we consider the maxillary, mandibular, or antagonist teeth. The set for maxillary teeth (0.67) and alternating antagonists (0.58) are on par or slightly smaller than the central Tennessee males and females. The mandibular teeth from southern Illinois males and females have a D of only 0.27. They are extremely close.

Let us turn now to the distances between males at each sub-region, and then to females in each sub-region. Southern Illinois males have a D of 0.44 with central Tennessee males, and a D of 0.20 with western Kentucky males for maxillary teeth. For mandibular teeth southern Illinois males have a D of 0.79 with central Tennessee males and 0.12 with western Kentucky males. For the alternating antagonists southern Illinois males have a D of 0.55 with central Tennessee males and 0.16 with western Kentucky males. Central Tennessee and western Kentucky males have D of 0.38 for maxillary teeth, 0.69 for mandibular teeth, and 0.63 for alternating antagonists.

Southern Illinois males have dental D scores ranging from 0.44 to 0.79 with central Tennessee males. The D scores from southern Illinois to western Kentucky males range from 0.12 to 0.20, quite low. The western Kentucky and central Tennessee males have D scores that range from 0.38 to 0.69. The general trend in the male dental data is that southern Illinois and western Kentucky are more similar (lower D scores) and that the distances between southern Illinois and central Tennessee, as well as between western Kentucky and central Tennessee males are similar.

Southern Illinois females have a D score of 0.56 with central Tennessee females, and 0.53 with western Kentucky females for maxillary teeth. For the mandibular dentition southern Illinois females have a D score of 0.41 with central Tennessee females, and 0.29 with females from western Kentucky. For the data set of alternating antagonists, southern Illinois females have D scores of 0.54 with central Tennessee females, and 0.58 for western Kentucky females.

Females from central Tennessee and western Kentucky have D scores of 0.45 for maxillary teeth, 0.53 for mandibular teeth, and 0.42 for the alternating antagonist data.

Distances between southern Illinois females and females from central Tennessee range from 0.41 to 0.56, while the range when they are compared with females from western Kentucky is 0.29 to 0.58, depending upon which set of dental data are used. As given above, central Tennessee females and western Kentucky females range from 0.42 to 0.53 depending upon the dental data set used. Females are quite similar to one another for dental data.

As for the cranial data presented above, the Mahalanobis D scores are represented graphically below for odontometric data (Figure 28 distances between sexes within sites, Figure 29 for male distances between sites, Figure 30 for female distances between sites, Figure 31 combines the male and female triangles but is scaled to fit onto one page).

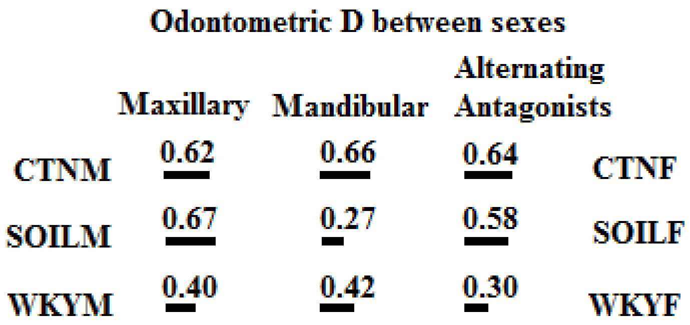

Figure 28. Graphical representations of Mahalanobis D for maxillary (left), mandibular (middle), and alternating antagonists (right) between sexes at each site.

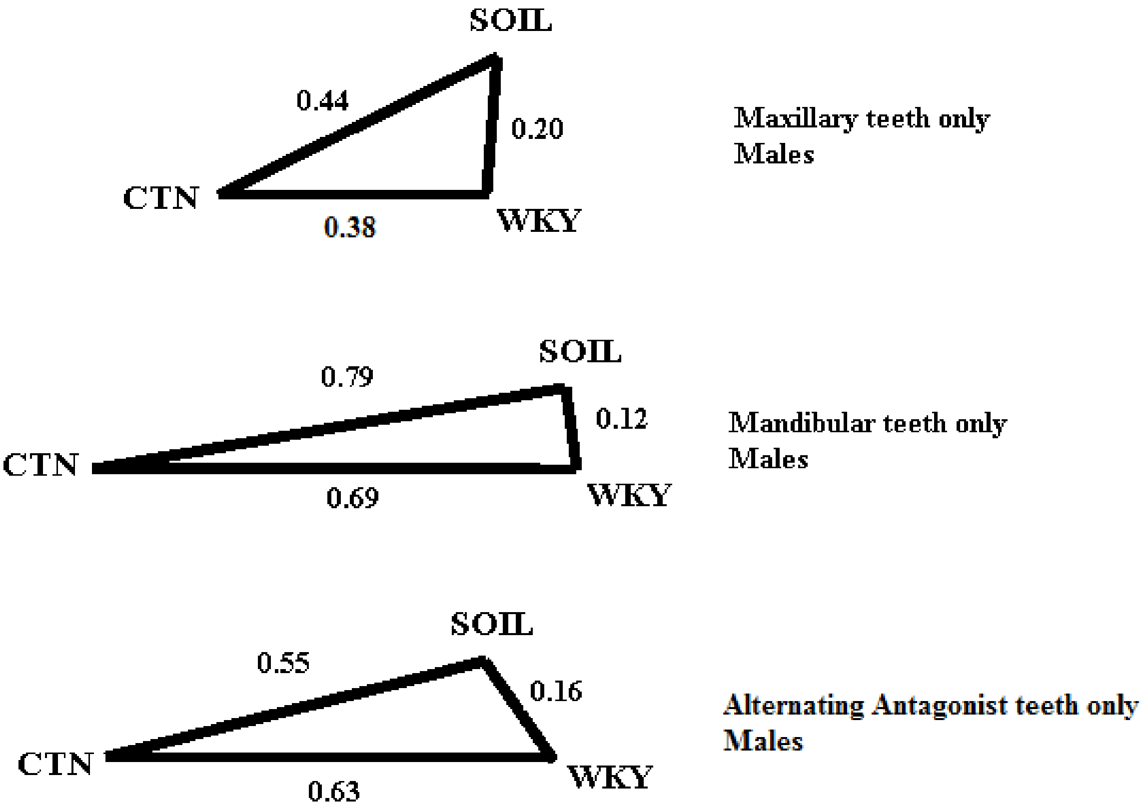

Figure 29. Graphical representations of Mahalnobis D for maxillary (top), mandibular (middle), and alternating antagonists (bottom) for males only.

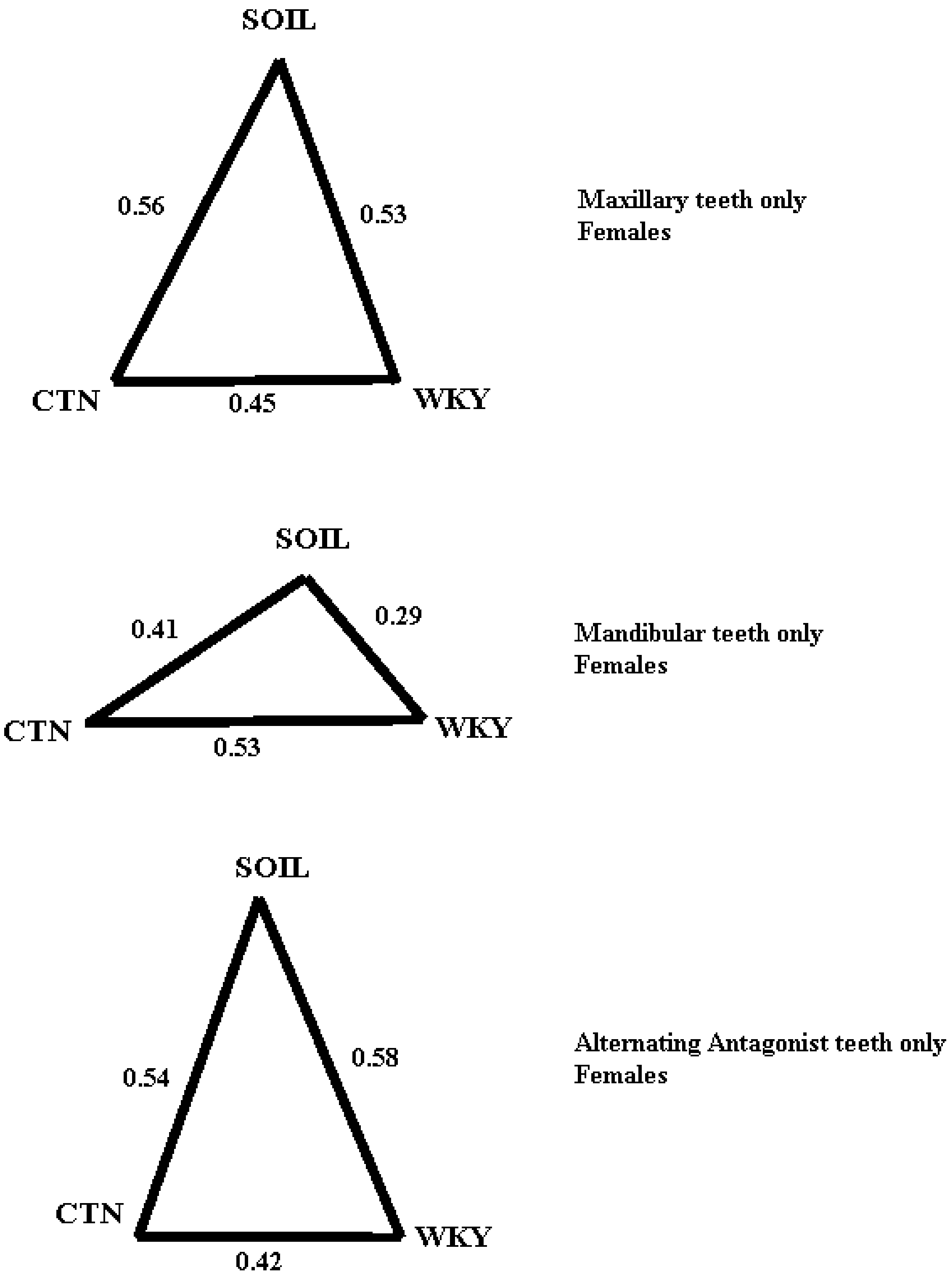

Figure 30. Graphical representations of Mahalnobis D for maxillary (top), mandibular (middle), and alternating antagonists (bottom) for females only.

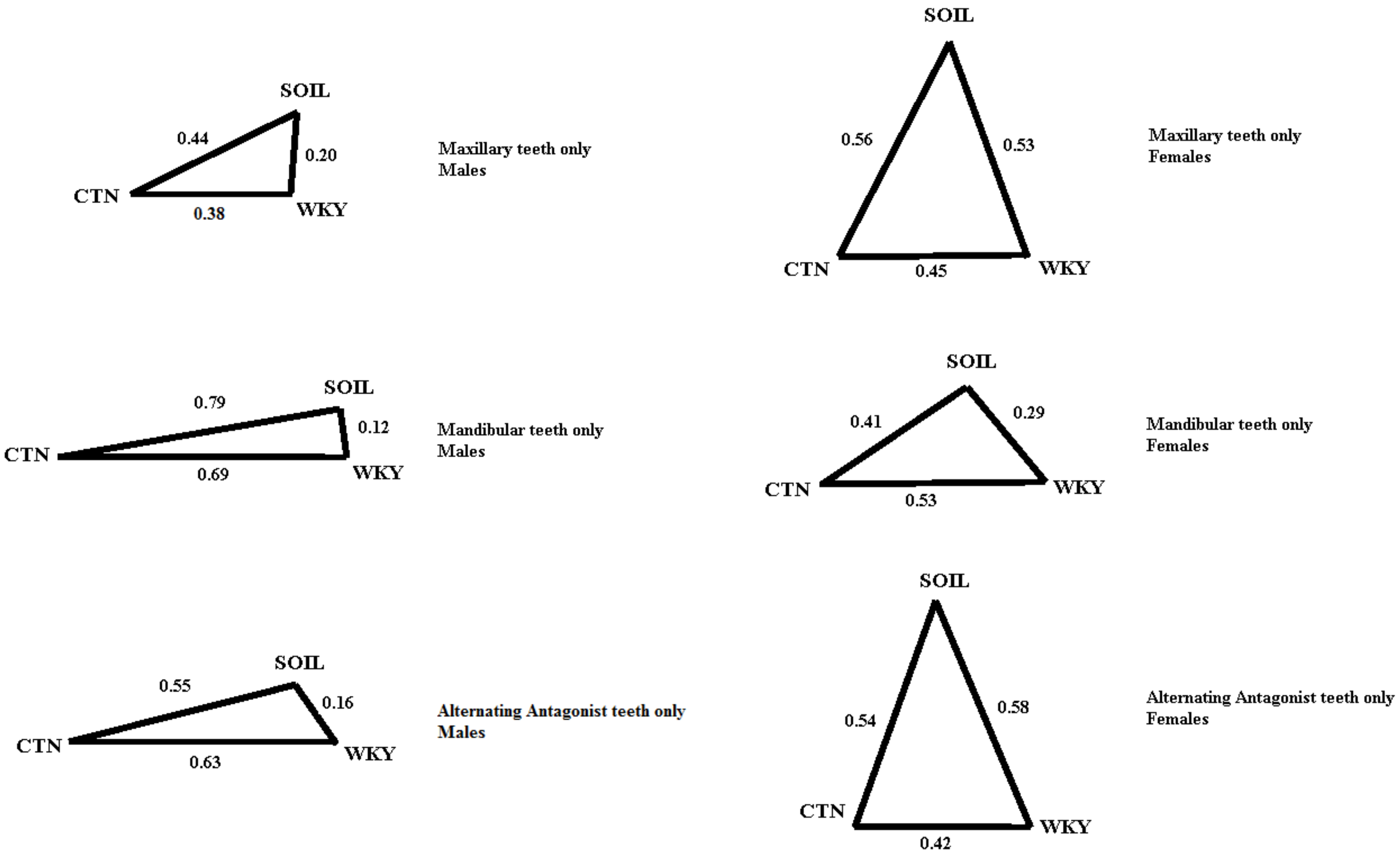

Figure 31. Graphical representations of Mahalanobis D for odontometrics data for males (left) and females (right). Triangles are identical to those presented in Figures 30 and 31 except now they are side by side allowing for ease of comparison between male and females patterns of distance. The image was scaled to fit on one page but the numbers (D) are the same as those above.

Biological Distance Based on Post-Cranial Indices

The data below (Table 48) presents Mahalanobis distance (D) from post-cranial indices for all sites and pooled sexes.

Of particular interest are the relationships between males and females at each geographic sub-region. The Mahalanobis Distance measure between males and females in southern Illinois is 2.00, between the same at central Tennessee is 1.53, and at western Kentucky the distance between males and females is 1.81. The distance between sexes within each sub-region is therefore greatest in the southern Illinois sample and the least at the central Tennessee sites.

Also of interest is how each sex compares to the others in different sub-regions. Males from southern Illinois are 0.48 from central Tennessee males, and 0.32 from western Kentucky males. Central Tennessee males and western Kentucky males have a D score of 0.59. Females from southern Illinois are 0.67 from central Tennessee females and 0.56 from western Kentucky females. Central Tennessee females and western Kentucky females have a D score of 0.32.

As for the cranial and dental data sets presented above, the D scores are represented graphically below as linear distances between sexes within each site (Figure 32), and as triangles between sites (each geographic location occupies a point of the triangle) (Figure 33). No scaling of the image was performed in this document.

Table 48. Mahalanobis distance (D) between group means for post-cranial indices including pooled sexes from all sites.

	SOILM	SOILF	CTNM	CTNF	WKYM	WKYF
SOILM		2.0020348	0.4792013	1.5152716	0.3238512	1.8059473
SOILF			1.8865332	0.6731495	1.9864652	0.5596247
CTNM				1.5256938	0.5889149	1.8238381
CTNF					1.5502629	0.3221457
WKYM						1.8115642
WKYF						

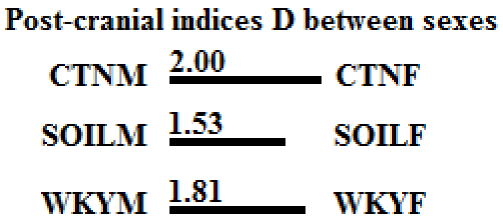

Figure 32. Graphical representations of Mahalanobis D between sexes for post-cranial indices within each site

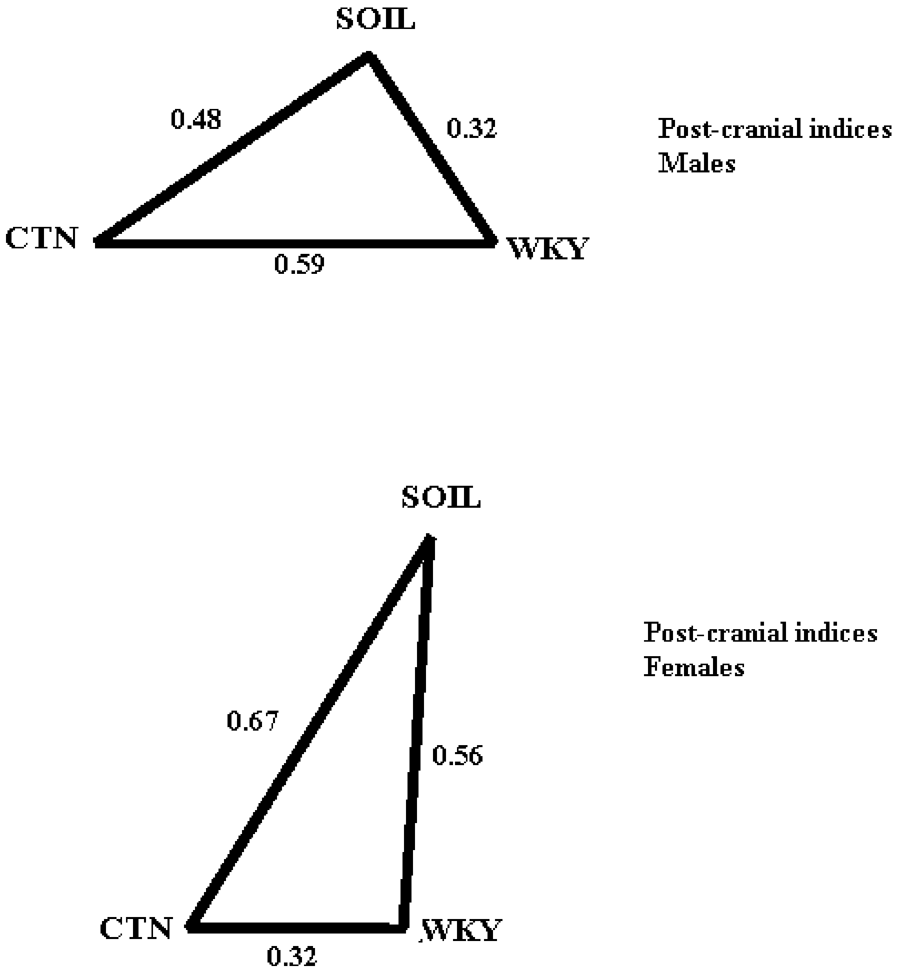

Figure 33. Graphical representations of Mahalanobis D for post-cranial indices for males (top) and females (bottom)

Distance Triangle Based on Geographic Distance

As a comparison to the biological distances represented in the three data sets above, a similar triangle representing straight-line geographical distances is presented below (Figure 34). Since the triangles above used millimeters to represent the D scores, the geographic distances shown below are also represented in millimeters, though the actual distances were measured in kilometers. The scale of the triangle below (geographic distance) would then be 1,000,000 times the size of the biological distances represented above in millimeters.

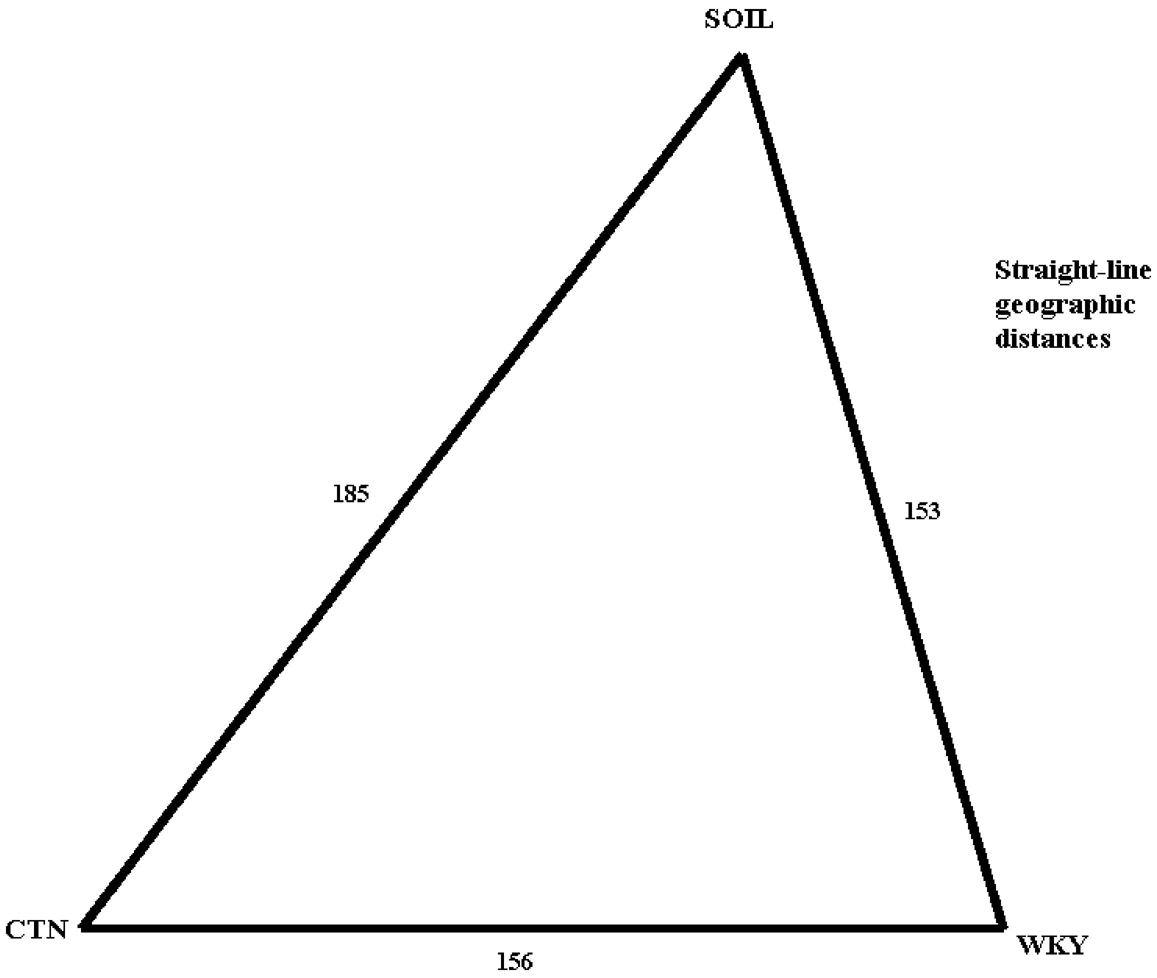

Figure 34. Straight-line geographical distances for comparison with biological Mahalanobis D triangles.

Mantel Tests

With an overall pattern of biological distance established via Mahalanobis D matrices, a Mantel test was performed to test the correlation between various data matrices (Hammer, 2015) including geographic distance. Five-thousand permutations were run for each Mantel comparison. The resultant p-values are one-tailed. Table 49 summarizes the correlation and statistical significance for the Mantel tests between geographic distance and the biological distance matrices. None of the Mahalanobis distance matrices are significantly correlated with geographic distance.

Table 49. Mantel test for correlation between Mahalanobis distance matrices and geographic distance

	Males		Females	
	R	p	R	p
Geographic distance x craniometrics	-0.9091	0.8282	-0.9933	0.841
Geographic distance x maxillary odontometrics	0.118	0.5059	0.6281	0.3213
Geographic distance x mandibular odontometrics	0.6837	0.1674	0.04498	0.4929
Geographic distance x alternating antagonists odontometrics	0.4228	0.4881	0.2255	0.6677
Geographic distance x post-cranial indices	0.183	0.5029	0.6897	0.3365

CHAPTER 6

DISCUSSION

The final chapter is a discussion of the results presented along with interpretations as to how these data fit the hypotheses regarding mate exchange and patterns of post-marital residence. First I review the results of the current research. Next I will provide context for the groups represented by the samples used here by discussing who their predecessors were and how they may have arrived in the mid-South. Lastly, I will summarize the present findings and discuss areas for future work.

Results from the Present Work

The results discussed below describe the general pattern of biological variation seen in the present data. What follows is a distillation and reduction of the myriad of details presented previously – a fact which cannot be overstated. The three sets of data used in this study (post-cranial indices, craniometrics, and odontometrics) also do not carry equal weight in the consideration and interpretation of results. Cranial and dental results are more useful for purposes of estimating biological distance. Therefore, they are given more weight in interpretation.

Biological Distance Based on Cranial Remains

Looking only at the univariate measure of Coefficient of Variation for the craniometric data set, males have higher CV values for more variables than females do in a pooled sample of all sites. Within sub-regions, though, interesting patterns of CV developed. Females have higher CV values for the vast majority of cranial variables in the sample from central Tennessee. The exact opposite pattern is seen in western Kentucky, where males had higher CV values for the majority of variables. Southern Illinois is intermediate (males had higher CV values in a few more variables but the split is more even between the sexes).

Like the dentition, cranial remains should provide a strong signal of biological distance. The pattern of biological distance based on cranial morphology is the same for males and females. Males at central Tennessee sites are the furthest (have the greatest D scores) from western Kentucky males. The same pattern is true for females – central Tennessee and western Kentucky females are the most distant. The greatest degree of similarity (the lowest D score) is between southern Illinois males and males from central Tennessee. The same pattern is also true here for females – southern Illinois females are closest to central Tennessee females. Within each sub-region the greatest distance between the sexes is found in the western Kentucky sample (the opposite is true for the dental data presented below). The closest distance between the sexes was found in the central Tennessee sample. These data suggest that both sexes have greater biological affinity between southern Illinois and central Tennessee, while the Green River region of western Kentucky is most different from the other two.

As discussed in Chapter 2 above, the morphological similarity of his Indian Knoll cranial series led Snow to describe them as inbred or isolated (Snow, 1948). The data for both males and females in the present study would support at least that the western Kentucky sample (Indian

Knoll individuals only) are most distant from groups in southern Illinois and central Tennessee based on cranial morphology. Herrmann (2002) found females had greater variation in cranial non-metric traits, which he interpreted as patrilineal or patrilocal post-marital residence pattern. Geography (Sciulli, 1979; Herrmann, 2002) and cultural differences due to different ancestry (Sassaman, 2010) may have played a large role in keeping these groups rather cohesive.

Biological Distance Based on Dental Remains

The pattern of female versus male variation in odontometric data is interesting. When all sites in the current analysis are pooled, females are more variable (have higher CV values) for all but one dental metric. Within each sub-region, though, the pattern of male versus female variation breaks down quite differently. Western Kentucky females are more variable than males for all dental metrics. The sexes are more evenly distributed though, in the central Tennessee sites and in southern Illinois (males have higher CV scores for slightly more variables than females in central Tennessee while the exact opposite is true in southern Illinois).

Patterns of biological distance based on odontometric data vary depending upon which dental data set used (maxillary, mandibular, or alternating antagonists) and all sets resulted in low biological distance scores in general. To summarize, the general pattern is that males and females are closest to one another in the western Kentucky sample while the within-sex distances between central Tennessee and southern Illinois males and females are about the same within each sub-region. Looking only at males, southern Illinois males are closest to western Kentucky (the same as is shown by the post-cranial indices reviewed below). They are in fact very close (the lowest D scores produced in the present data set). The distances between southern Illinois and central Tennessee males, as well as between western Kentucky and central Tennessee males, are similar to one another. Among females, the distances between the three sub-regions are relatively the same. Females of one site are not necessarily closer or further away from females at the two other sites. These data suggest again, that females were perhaps the ones moving more so than males in the mid-South Archaic.

Lewis and Lewis (1961) noted interesting patterns in dental and maxillary bone morphology among the Eva site (the principal site in the central Tennessee sample used here). They mention a high frequency of displacement of teeth in the maxilla and particularly large canines, principally among males. Compared to parabolic or hyperbolic maxillary arch shapes seen in Indian Knoll, they noted elliptical or U-shaped maxillae at Eva. Shovel shaped incisors were also less common at Eva than at Indian Knoll (Lewis and Lewis, 1961). These differences in morphology were found across strata at Eva, which led the team to theorize that the Eva population were long-term residents of the area, having moved into the area prior to 8,000 years ago (Lewis and Lewis, 1961). Further, males exhibited the dental peculiarities twice as often as females, which is perhaps indicative of male philopatry and patrilocal organization.

Indian Knoll teeth are larger and less complex than Woodland period samples from the Ohio Valley (Sciulli, 1979) and Mesolithic and Australoid groups (Perzigian, 1976; Ward, 2005). The biological distance analysis presented here for dental metrics was performed on size-standardized data.

Biological Distance Based on Post-Cranial Indices

Coefficients of variation for brachial, crural, and intermembral indices for both sexes showed that in general, females were more variable for these computed measures than males were. Only in southern Illinois were males more variable than females for crural and intermembral indices (both of which contributed less to the pattern of variation than the brachial index). If these indices are indeed established early in the ontological process of long bone growth and development, these results indicate that males share more biological affinity than females.

The biological distance matrices between groups based on their post-cranial indices of long bone lengths is the least reliable of the three data sets included in the present analysis. Let us briefly review the pattern of variation seen in these data for sexes within each sub-region, and then between sexes in each sub-region.

Comparing sexes within each sub-region showed males and females were the most different (highest D score) for post-cranial indices in central Tennessee. The sample from southern Illinois was the closest (lowest D score) between males and females for these measures. Comparing sexes between each sub-region, the greatest distance between males was found between central Tennessee and western Kentucky. The closest groups amongst the females, though, were these same two – central Tennessee and western Kentucky. For females the greatest distance was found between southern Illinois and central Tennessee. The closest relationship (least biological distance score) for males was found between southern Illinois and western Kentucky. So, while males in western Kentucky and southern Illinois had greater biological affinity, females were closer between western Kentucky and central Tennessee.

Clyde Snow noted that Indian Knoll individuals (the western Kentucky sample used here) had long arms compared to modern Europeans and that their forearms and lower legs in particular were longer (1948). He did not compare them in any formal way, so this was an anecdotal observation. If the distal elements in their arms and legs really were rather long, the western Kentucky sample should have the highest indices in the pooled sample. Their indices fall right in line with the other samples used in the present study.

Evaluating Hypotheses

With an idea of the pattern of biological relatedness outlined above, we now return to the two hypotheses defined in Chapter 1.

- → Hypothesis 1: Biological distance and archaeological patterns of cultural exchange are congruent.

Relying more heavily on the cranial and dental data sets presented above, it appears that groups in western Kentucky, here represented by individual skeletons from Indian Knoll, were somewhat different from other groups in the mid-South. Both the dental and cranial data support greater biological affinity (lower biological distance) between southern Illinois and central Tennessee groups, though the lowest D scores of all came from a comparison between southern Illinois males and western Kentucky male dentitions.

The groups along the Green River (here represented by Indian Knoll) were definitely exchanging goods with other areas. Their burials included copper artifacts and fragments from the Great Lakes region as well as marine shell sourced from Florida and the Carolinas (Marquardt and Watson, 1983; Brown, 2004). The pattern of archaeological exchange presented in Chapter 2 above would suggest that groups along the Green River were trading bone pins (Jefferies, 2004), fishhooks (Moore, 2010b), and lithic materials (Jefferies and Butler, 1982; Johnson and Brookes, 1989) across the region but preferentially south. Winters postulated that the Green River region was a little too far removed from the mainstream of exchange routes along the Mississippi River (in Marquardt and Watson, 1983: 334). Marquardt and Watson (1983) agree that significant engagement by the Green River peoples in overland or river trade routes remains to be demonstrated, despite the presence of non-local grave goods. Cultural connections via exchange suggests that groups in central Tennessee and western Kentucky would perhaps be closest for measures of biological distance if the two were also trading mates. That does not seem to be the case. The Indian Knoll peoples represented in the western Kentucky sample were perhaps keeping to themselves more so than other groups.

Another possibility exists to explain the relative place of the western Kentucky sample compared to the other two regions. Of the southeastern United States specifically, Sassaman (2010: 26) asks: "What if the various societies of the Eastern Archaic descended from more than one founding population?" He hypothesizes two ancestral lines in the Southeast. "The most unorthodox feature of this model is its assertion of at least two separate ancestral roots, one traceable to the Paleoindian populations of eastern North America (what I've termed Ancestry I), the other to the later influxes of populations whose affinity to Paleoindians is uncertain: Ancestry II" (Sassaman, 2010: 38). He goes on to specify that Ancestry II "…immigrated into eastern North America long after the Clovis era, begetting what is arguable the definitive cultural milieu of the Archaic era, the so-called Shell Mound Archaic" (Sassaman, 2010: 32). These are the very people that went into the western Kentucky sample, here. Their cranial morphology suggests they are the most different from the other two groups analyzed here. Dentally though, western Kentucky males were extremely close to southern Illinois males. The results of the present analysis do support Sassaman's hypothesis that the Green River groups (the Shell Mound Archaic peoples) were somewhat different – either due to cultural isolation (they were not isolated completely, but perhaps participated less in networks of exchange) and/or a different biological history in the period Paleoindian and Early Archaic periods that immediately proceeded the era of the samples used here.

Sassaman's question is an intriguing one for anthropologists working in the American Southeast. The accompanying material record is for archaeologists to debate. The present study, though, was designed to speak to biological variation in Middle and Late Archaic groups in three sub-regions of the mid-South. The data here suggest that the Green River peoples in western Kentucky may indeed be a different lineage. Alternatively, they were not exchanging males or females as readily across the region.

→ Hypothesis 2: Females will show higher levels of biological variation reflective of patrilocality.

The three sets of morphological data used here also support a pattern of much similarity between groups and between sexes, but the pattern of similarities and differences is not the same between sub-regions. Females were more biologically variable than males for the majority of variables used, and there is some suggestion that the western Kentucky groups kept to themselves. The general pattern of post-marital residence evidenced in these data would be patrilocality, though adherence to such a system may not have been consistent.

Future Directions

Small sample sizes are an ever-present problem in any research that utilizes ancient human remains. The samples are often small to begin with and likely to be rather fragmentary. In the future, it would be useful to obtain larger sample sizes of the groups used here; though, the author’s review of the available skeletal material was quite thorough and it is unlikely that more individuals would be found to add to the present sample using standard metric analyses. More importantly, these groups need a larger context in which to evaluate their biological relatedness. This work purposefully focused on biological variation at the regional scale. An outlier group (or groups) would aid in understanding how the pattern of biological variation seen here relates to patterns seen across the Southeast United States and the rest of the Americas. Lastly, DNA analyses would also be useful towards understanding the relationships of Archaic groups.

Summary and Conclusions

Inter-disciplinary research that marries archaeological, ecological, biological, and genetic data is changing our perceptions of group composition in the Southeast during the Archaic period. Multiple examples of patterned exchange habits and shifting lifeways over the long Archaic period in the Southeast (reviewed above but also see Jefferies, 1996 for additional review) highlights the importance of the present study in better defining the biological component to these exchange patterns.

Challenges to the traditional, macroevolutionary view of the peopling of the New World and subsequently the Southeast are mounting (Sassaman, 2010, 2011). At the time of the Last Glacial Maximum (approximately 18,000 kya) Asian migrants that had been living in Beringia for quite some time began moving south to populate the rest of the Americas (Fagundes et al., 2008b). From a single genetic source they carried considerable morphological and haplogroup variation. The processes of gene flow and genetic drift affected these small groups as they moved across North America towards the Southeast region. Groups in the Southeast further differentiated as they populated the region, though they maintained a considerable amount of genetic diversity via gene flow.

As the present analysis consists of Archaic period individuals from watersheds in western Kentucky, central Tennessee, and southern Illinois, the individuals used in this study had biological antecedents that migrated to the New World from parts of Asia. As discussed above, while certain parts of the process of the peopling of the New World are generally agreed upon within the anthropological community, others remain quite contentious (see Auerbach, 2010 for recent bioarchaeological and biocultural perspectives on the peopling of the New World). Regardless of observed homogeneity at the genetic level and heterogeneity in the phenotype, regardless of the number of waves, and regardless of whether variation is explained by replacement or genetic drift, the conclusions end up the same (Powell and Neves, 1999): macroscopically, peoples of the New World appear as a cohesive group while smaller-scale analyses reveal considerable genetic and morphological variation. Part of this variation is due to cultural mores regarding who is “us” versus “them.” Constructing that “otherness” is “among the qualities of humanness that bridge the ‘prehistoric’ with the historic and, with it, the theories of modernity with the study of ancient people.” (Sassaman, 2010: xvi). Historical relationships matter; cross-cultural comparisons and interpretation of social and cultural variation are mere conjecture without historical context (Sassaman, 2010).

In speaking of this resurgence and reformulation of long-held notions about Archaic peoples, Sassaman (2008: 8) suggests that “…the time is ripe for a paradigmatic shift.” Researchers of the Archaic mid-South are pushing into a middle-range area by asking how people relate to the environment and how they relate to each other (Kidder, 2010). The challenge facing future scientists interested in these problems is to put people back into their interpretations and to see variation in interactions between individuals and groups (Kidder, 2010). With a clearer picture of the variation that existed during the long Archaic period, new questions emerge regarding specific levels of interaction, the contexts and manner of interactions, how group membership and identity was formed and maintained, the role of ritual in reflecting group identity, what choices were available and employed as distant groups began to come into repeated contact, and how group interactions effected the pace, course, structure, and rhythm of life (Sassaman, 2010). These are areas where archaeologists and biological anthropologists will find fruitful collaboration.

In asking and seeking answers to these questions we are able to insert humanity into modern conceptions of past archaeological populations making Archaic groups of the Southeast into more than trait lists, point styles, ratomorphic automatons (Robarchek, 1989), and evolutionary stations on a progressive trajectory. Anthropology has traditionally placed itself as a bridge between the 'other' and 'self,' between 'us' and 'them,' between the past and present. “Anthropologists and archaeologists have come to realize that the functions of culture are (1) to relate man to his environment – his terrestrial habitat and the circumambient cosmos – on one hand, and (2) to relate man to man, on the other” (White, 1959: 8 in Paulsen, 1981). An alternative to the old determinism is to: “take people seriously, not only as biological beings in ecological contexts, but also as human beings in sociocultural contexts, deriving their humanity from the systems of meanings, of values and beliefs, of symbols and significations, that many anthropologists call ‘culture’” (Robarchek, 1989: 903).

Archaeologists and bioarchaeologists working in the Southeast have long grappled with many aspects of Archaic lifeways – diet and subsistence, settlement patterns, mobility, ritual and mortuary practices, and ecogeographic settings. Much work, however, still remains to be done towards an understanding of ancient Native American dispersal and subsequent movement across the North American continent as a backdrop to understand human cultural interactions in the Archaic and subsequent periods. As comprehensive datasets emerged in the 1960s the picture of the Archaic period as a long North American “Dark Ages” began to dissolve. It was replaced, and is still being replaced in the minds of some, with notions of local and regional distinctiveness based on cultural or ethnic distinctions embodied in place-making through the construction of burial mounds and settlements. Rather than hopeless wanderers barely subsisting without pottery and agriculture Archaic peoples are now understood to be more adept and socially complex than previously thought.

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APPENDICES

APPENDIX I: IMPUTATION

Amelia II uses a process called multiple imputation (Honaker et al, 2013; also: http://gking.harvard.edu/amelia). The name is fitting as it harkens back to the famed aeronautical pioneer and long-lost pilot Amelia Earhart. The imputation process involves a bootstrap-based algorithm that can handle many variables and works quite efficiently (i.e. quickly) compared to older methods. Users can input trends and priors into the imputation algorithm, as well as receive diagnostic reports regarding the fit of the multiple imputation models. The imputation process avoids biases in variance and co-variance data matrices that can result from means-based imputations and certainly retains more observed data points than a list-wise deletion procedure. Amelia II assumes the data set is multivariate normal and that the missing data points are missing at random. For each missing observation, Amelia II imputes *m* values reflective of the uncertainty of the missing data points. The resulting data set includes the observed values (left untouched) and the imputed data points. The default number of *m* values that Amelia calculates for each missing element is five. Five imputations (five "passes" over the data) are sufficient unless the data set has unusually high rates of missing values. Any one of the five imputed data set files could be used for further statistical analyses. The program can run either as a stand-alone interface and program, AmeliaView, or can also be utilized from within R via various packages (http://gking.harvard.edu/amelia).

Each subset of raw data were saved as a CSV (comma-separated value) file, necessary for Amelia II's imputation process. Once in Amelia II, each CSV file was opened and prepared for imputation. The variables GEOG and SEX were labeled (“transformed”) as identifiers so they would not be used in the imputation process. An example of how the imputation process transformed the current data set is provided below using female long bones.

Following the linear regression methods described in Chapter 3: Methods, I needed to decide whether to use linear regression to estimate all missing long bone lengths, or to use an Imputation procedure. To evaluate how each method performed, I took the left female long bones used to make the linear regression formulae and ran them through the imputation process in Amelia. I averaged the five imputations that Amelia calculated. I then had a data set that consisted of observed, regressed, and imputed measures for all females (from all sites) for the maximum length of the humerus, radius, femur, and tibia (Table 51). The coding for these is given in Table 50 (for all four bones, even though only humerus is listed).

Table 50. Codes for dealing with missing data

HXLL	Humerus Maximum Length Left Side (observed)
HXLL REG	Humerus Maximum Length Left Side (regressed)
HXLL AM AVG	Humerus Maximum Length Left Side (average of 5 Amelia imputations)
RXLL	Radius Maximum Length Left Side (observed)
RXLL REG	Radius Maximum Length Left Side (regressed)
RXLL AM AVG	Radius Maximum Length Left Side (average of 5 Amelia imputations)
FXLL	Femur Maximum Length Left Side (observed)
FXLL REG	Femur Maximum Length Left Side (regressed)
FXLL AM AVG	Femur Maximum Length Left Side (average of 5 Amelia imputations)
TXLL	Tibia Maximum Length Left Side (observed)
TXLL REG	Tibia Maximum Length Left Side (regressed)
TXLL AM AVG	Tibia Maximum Length Left Side (average of 5 Amelia imputations)

Table 51. Observed, regressed, and imputed data for female left long bones

Individual	HXLL	HXLL REG	HXLL AM AVG	RXLL	RXLL REG	RXLL AM AVG	FXLL	FXLL REG	FXLL AM AVG	TXLL	TXLL REG	TXLL AM AVG
IKF117	265.000	277.597	297.562	211.000	201.343	230.833	384.000	380.222	420.096	317.000	307.207	344.087
IKF291	269.000	271.302	307.000	198.000	206.180	245.000	384.000	385.573	433.000	307.000	313.584	360.950
CMF83A	269.000	279.105	301.000	210.000	210.977	219.961	390.000	397.095	406.000	320.000	314.712	341.000
IKF328	270.000	273.811	309.901	204.000	203.988	242.000	386.000	382.919	432.288	316.000	318.916	363.252
IKF545	272.000	280.672	296.592	207.000	208.938	224.978	392.000	393.528	416.000	312.000	321.545	340.233
IKF107	278.000	290.185	281.913	223.000	217.937	210.201	405.000	406.256	393.863	340.000	321.285	327.477
IKF470	282.000	282.830	301.914	215.000	213.249	231.248	390.000	398.222	421.815	320.000	312.519	348.153
IKF191	283.000	284.972	280.347	207.000	207.457	208.000	403.000	385.976	398.000	317.000	321.523	328.000
EVF182	283.000	276.575	299.000	214.000	205.283	228.000	383.000	380.926	407.000	325.000	320.485	336.535
IKF518	283.000	285.986	324.991	214.000	212.039	248.791	404.000	394.662	460.000	331.000	320.083	373.000
IKF570	283.000	289.446	314.745	221.000	215.662	243.919	407.000	397.192	449.459	341.000	317.911	378.000
EVF158	283.500	292.824	272.000	223.000	216.205	201.000	403.000	401.620	387.183	329.000	328.621	314.219
EVF153	284.000	283.157	271.869	217.000	214.825	204.991	386.000	401.704	380.616	317.000	330.055	306.000
IKF411	285.000	282.024	311.000	212.000	211.812	248.000	392.000	392.553	439.605	319.000	322.690	374.472
IKF13	286.000	286.291	303.920	224.000	213.402	225.850	394.000	397.040	430.000	336.000	319.677	350.000
CHF61	288.000	281.189	298.359	216.000	213.919	228.666	385.000	395.269	411.000	319.000	319.452	343.000
IKF608	288.000	287.603	300.000	217.000	219.646	227.000	401.000	406.230	417.000	328.000	327.341	340.168
IKF440	289.000	281.510	318.795	209.000	211.398	245.000	402.000	390.957	451.832	330.000	321.984	375.681
IKF590	289.000	290.951	288.000	214.000	216.671	216.000	410.000	401.591	385.000	326.000	328.550	319.000
CMF188A	289.000	285.163	300.772	216.000	220.706	232.000	401.000	410.218	409.307	333.000	338.793	341.308
CMF145	289.000	293.929	290.504	227.000	220.729	224.178	412.000	411.040	405.059	349.000	336.657	338.616
IKF140	290.000	280.890	300.000	205.000	221.110	230.054	397.000	406.760	427.487	315.000	336.717	347.748
CMF190	290.000	290.114	319.000	227.000	220.644	242.000	405.000	409.771	435.000	349.000	337.784	360.000
EVF92	291.000	295.513	289.099	219.000	225.685	221.845	419.000	417.049	408.660	338.000	341.814	340.753
IKF588	292.000	294.660	293.936	226.000	219.157	227.099	406.000	402.237	414.124	335.000	338.928	340.097
EVF164	294.000	296.126	274.819	222.000	215.442	213.690	421.000	397.579	393.278	346.000	336.418	320.000

Table 51. Observed, regressed, and imputed data for female left long bones (continued)

Individual	HXLL	HXLL REG	HXLL AM AVG	RXLL	RXLL REG	RXLL AM AVG	FXLL	FXLL REG	FXLL AM AVG	TXLL	TXLL REG	TXLL AM AVG
IKF72	294.000	291.276	279.000	225.000	220.968	223.497	408.000	409.542	381.000	346.000	337.317	332.500
IKF261	294.000	290.393	288.024	227.000	223.868	214.946	408.000	417.006	402.095	353.000	342.831	328.569
CMF185	294.000	302.584	305.594	230.000	221.100	228.500	430.000	403.997	416.000	359.000	332.088	336.000
IKF205	295.000	279.304	290.000	209.000	230.329	217.002	388.000	423.571	415.000	314.000	344.168	337.317
IKF17	295.000	285.070	290.000	215.000	227.310	220.672	391.000	416.089	399.532	315.000	337.998	332.799
IKF183	295.000	301.891	291.000	226.000	226.975	227.000	423.000	417.431	401.924	341.000	337.360	336.000
IKF464	296.000	296.724	312.182	221.000	221.082	237.509	416.000	406.393	435.535	334.000	338.458	356.192
CMF99	296.000	295.994	299.000	224.000	223.130	224.594	423.000	412.708	414.675	354.000	346.315	336.018
IKF220	297.000	296.324	300.732	219.000	226.731	225.533	418.000	417.413	423.000	334.000	337.214	352.331
IKF90	299.000	297.257	320.000	223.000	226.719	261.000	413.000	414.518	453.000	332.000	343.269	388.915
IKF366	300.000	302.946	297.529	234.000	227.929	229.668	414.000	415.147	416.063	341.000	339.428	342.260
IKF75	300.000	300.998	287.500	234.000	231.006	218.460	421.000	420.615	404.000	358.000	339.874	325.000
CMF20B	301.000	298.344	290.000	230.000	233.815	223.480	416.000	428.479	409.722	349.000	347.710	342.652
IKF52	302.000	294.606	284.000	225.000	230.232	217.000	411.000	424.680	386.000	341.000	350.499	317.000
CMF201	304.000	300.131	287.929	229.000	230.221	213.934	425.000	424.462	400.832	356.000	348.427	330.300
IKF586	304.000	311.377	283.500	240.000	231.424	223.000	425.000	424.083	403.000	347.000	353.908	329.000
LFF10	305.000	303.192	290.000	223.000	230.239	211.447	427.000	421.106	405.637	337.000	344.871	323.914
IKF168	305.000	305.435	263.793	229.000	234.519	196.000	431.000	432.108	360.000	350.000	348.071	302.920
IKF233	306.000	296.368	294.000	226.000	225.930	222.000	411.000	413.293	421.000	338.000	347.874	346.000
CMF27	307.000	304.478	278.000	229.000	234.031	213.250	428.000	425.839	395.009	348.000	351.444	327.750
IKF520	307.000	308.223	290.777	235.000	237.141	223.412	436.000	433.612	409.118	363.000	358.135	335.699
IKF391	308.000	314.192	270.566	235.000	228.903	199.000	437.000	422.433	384.536	347.000	358.374	310.159
IKF634	319.000	306.719	283.000	231.000	229.063	210.879	430.000	418.317	401.000	349.000	358.028	328.703
CHF71	319.000	313.910	285.009	242.000	239.702	213.568	435.000	436.706	383.000	360.000	360.939	319.000
IKF638	319.000	318.102	283.000	250.000	247.427	214.000	433.000	452.488	383.000	362.000	371.439	325.000
IKF269	323.000	322.743	298.716	254.000	241.008	226.663	446.000	435.622	418.557	378.000	367.423	343.868

Table 51. Observed, regressed, and imputed data for female left long bones (continued)

Individual	HXLL	HXLL REG	HXLL AM AVG	RXLL	RXLL REG	RXLL AM AVG	FXLL	FXLL REG	FXLL AM AVG	TXLL	TXLL REG	TXLL AM AVG
CMF86	327.000	322.105	300.000	243.000	249.171	220.789	458.000	448.666	411.339	375.000	376.721	333.000

Having these three sets of data I ran some ANOVAs. The three data sets were not statistically significantly different from one another for the left female humerii, F (2, df error) = 0.007726, MSE (mean-square error) = 173.223, p = 0.9923. For the left female radii the results were the same: F (2, df error) = 0.2714, MSE = 139.453, p = 0.7627. Left femora showed the same non-significant results: F (2, df error) = 0.0004707, MSE = 334.509, p = 0.9995. The three data sets were likewise not statistically significantly different for left tibiae: F (2, df error) = 0.1652, MSE = 286.44, p = 0.7892.

Since the methods are statistically the same (as in not statistically different from the known and observed variables) (Table 52) I needed to decide which method for dealing with missing data would best represent the observed sample. From a cursory glance at the imputed and regressed data it appeared that Amelia’s imputation was consistently overestimating long bone length (despite again, this not being statistically different from what the regression analysis gave me). I wanted to see how big the effect was. I subtracted the observed value from each estimated value and summed that column. Values approaching zero are closest to the observed values (Table 53).

Table 52. One-way ANOVA for differences between means for observed, regressed, and imputed long bone lengths for left females

	F (df effect, df error)	F-value	MSE (mean-square error) w/in groups	p(same)
Humerus	2, df error	0.007726	173.223	0.9923
	Levene’s test for homogeneity of variance, based on means: p(same) = 0.8371			
	Welch F test in the case of unequal variances: F = 0.00755, df = 103.7, p = 0.9925			
Radius	2, df error	0.2714	139.453	0.7627
	Levene’s test for homogeneity of variance, based on means: p(same) = 0.7124			
	Welch F test in the case of unequal variances: F = 0.2455, df = 103.3, p = 0.7828			
Femur	2, df error	0.0004707	334.509	0.9995
	Levene’s test for homogeneity of variance, based on means: p(same) = 0.5059			
	Welch F test in the case of unequal variances: F = 0.0004766, df = 103.2, p = 0.9995			
Tibia	2, df error	0.1652	286.44	0.8479
	Levene’s test for homogeneity of variance, based on means: p(same) = 0.7892			
	Welch F test in the case of unequal variances: F = 0.1555, df = 103.7, p = 0.8562			

Table 53. Differences between observed, regressed, and imputed/averaged datasets

Individual	HXLL REG-HXLL	HXLL AM AVG-HXLL	RXLL REG-RXLL	RXLL AM AVG-RXLL	FXLL REG-FXLL	FXLL AM AVG-FXLL	TXLL REG-TXLL	TXLL AM AVG-TXLL
IKF117	12.597	32.562	-9.657	19.833	-3.778	36.096	-9.793	27.087
IKF291	2.302	38.000	8.180	47.000	1.573	49.000	6.584	53.950
CMF83A	10.105	32.000	0.977	9.961	7.095	16.000	-5.288	21.000
IKF328	3.811	39.901	-0.012	38.000	-3.081	46.288	2.916	47.252
IKF545	8.672	24.592	1.938	17.978	1.528	24.000	9.545	28.233
IKF107	12.185	3.913	-5.063	-12.799	1.256	-11.137	-18.715	-12.523
IKF470	0.830	19.914	-1.751	16.248	8.222	31.815	-7.481	28.153
IKF191	1.972	-2.653	0.457	1.000	-17.024	-5.000	4.523	11.000
EVF182	-6.425	16.000	-8.717	14.000	-2.074	24.000	-4.515	11.535
IKF518	2.986	41.991	-1.961	34.791	-9.338	56.000	-10.917	42.000
IKF570	6.446	31.745	-5.338	22.919	-9.808	42.459	-23.089	37.000
EVF158	9.324	-11.500	-6.795	-22.000	-1.380	-15.817	-0.379	-14.781
EVF153	-0.843	-12.131	-2.175	-12.009	15.704	-5.384	13.055	-11.000
IKF411	-2.976	26.000	-0.188	36.000	0.553	47.605	3.690	55.472
IKF13	0.291	17.920	-10.598	1.850	3.040	36.000	-16.323	14.000
CHF61	-6.811	10.359	-2.081	12.666	10.269	26.000	0.452	24.000
IKF608	-0.397	12.000	2.646	10.000	5.230	16.000	-0.659	12.168
IKF440	-7.490	29.795	2.398	36.000	-11.043	49.832	-8.016	45.681
IKF590	1.951	-1.000	2.671	2.000	-8.409	-25.000	2.550	-7.000
CMF188A	-3.837	11.772	4.706	16.000	9.218	8.307	5.793	8.308
CMF145	4.929	1.504	-6.271	-2.822	-0.960	-6.941	-12.343	-10.384
IKF140	-9.110	10.000	16.110	25.054	9.760	30.487	21.717	32.748
CMF190	0.114	29.000	-6.356	15.000	4.771	30.000	-11.216	11.000
EVF92	4.513	-1.901	6.685	2.845	-1.951	-10.340	3.814	2.753
IKF588	2.660	1.936	-6.843	1.099	-3.763	8.124	3.928	5.097
EVF164	2.126	-19.181	-6.558	-8.310	-23.422	-27.722	-9.582	-26.000
IKF72	-2.724	-15.000	-4.032	-1.503	1.542	-27.000	-8.683	-13.500

Table 53. Differences between observed, regressed, and imputed/averaged datasets (continued)

Individual	HXLL REG-HXLL	HXLL AM AVG-HXLL	RXLL REG-RXLL	RXLL AM AVG-RXLL	FXLL REG-FXLL	FXLL AM AVG-FXLL	TXLL REG-TXLL	TXLL AM AVG-TXLL
IKF261	-3.607	-5.976	-3.132	-12.054	9.006	-5.905	-10.169	-24.431
CMF185	8.584	11.594	-8.900	-1.500	-26.003	-14.000	-26.912	-23.000
IKF205	-15.696	-5.000	21.329	8.002	35.571	27.000	30.168	23.317
IKF17	-9.930	-5.000	12.310	5.672	25.089	8.532	22.998	17.799
IKF183	6.891	-4.000	0.975	1.000	-5.569	-21.076	-3.640	-5.000
IKF464	0.724	16.182	0.082	16.509	-9.607	19.535	4.458	22.192
CMF99	-0.006	3.000	-0.870	0.594	-10.292	-8.325	-7.685	-17.982
IKF220	-0.676	3.732	7.731	6.533	-0.587	5.000	3.214	18.331
IKF90	-1.743	21.000	3.719	38.000	1.518	40.000	11.269	56.915
IKF366	2.946	-2.471	-6.071	-4.332	1.147	2.063	-1.572	1.260
IKF75	0.998	-12.500	-2.994	-15.540	-0.385	-17.000	-18.126	-33.000
CMF20B	-2.656	-11.000	3.815	-6.520	12.479	-6.278	-1.290	-6.348
IKF52	-7.394	-18.000	5.232	-8.000	13.680	-25.000	9.499	-24.000
CMF201	-3.869	-16.071	1.221	-15.066	-0.538	-24.168	-7.573	-25.700
IKF586	7.377	-20.500	-8.576	-17.000	-0.917	-22.000	6.908	-18.000
LFF10	-1.808	-15.000	7.239	-11.553	-5.894	-21.363	7.871	-13.086
IKF168	0.435	-41.207	5.519	-33.000	1.108	-71.000	-1.929	-47.080
IKF233	-9.632	-12.000	-0.070	-4.000	2.293	10.000	9.874	8.000
CMF27	-2.522	-29.000	5.031	-15.750	-2.161	-32.991	3.444	-20.250
IKF520	1.223	-16.223	2.141	-11.588	-2.388	-26.882	-4.865	-27.301
IKF391	6.192	-37.434	-6.097	-36.000	-14.567	-52.464	11.374	-36.841
IKF634	-12.281	-36.000	-1.937	-20.121	-11.683	-29.000	9.028	-20.297
CHF71	-5.090	-33.991	-2.298	-28.432	1.706	-52.000	0.939	-41.000
IKF638	-0.898	-36.000	-2.573	-36.000	19.488	-50.000	9.439	-37.000
IKF269	-0.257	-24.284	-12.992	-27.337	-10.378	-27.443	-10.577	-34.132
CMF86	-4.895	-27.000	6.171	-22.211	-9.334	-46.661	1.721	-42.000
Sum diff.	-0.389	14.39	-11.623	71.106	-3.488	2.249	-20.567	74.617

The estimated values from the regression analysis are closer to the observed. The difference is greatest in the tibia and radius (which is not surprising given that distal elements are slightly more variable than the proximal elements).

However, since indices will be calculated from this data, one further step away from the original data anyway, I ran similar analyses above with calculated brachial, crural, and intermembral indices to see how the apparent systematic bias of the imputation process to overestimate length (again, to a non-significantly different degree, but it is there nonetheless) may affect missing data points (Table 54).

Table 54. Computed measures (brachial, crural, and intermembral indices) for observed, regressed, and imputed data from all females with all four long bones present (left)

Indiv.	BR OBSV	BR REG	BR AM AVG	BR REG-BR OBSV	BR AM AVG-BR OBSV	CR OBSV	CR REG	CR AM AVG	CR REG-CR OBSV	CR AM AVG-CR OBSV	IM OBSV	IM REG	IM AM AVG	IM REG-IM OBSV	IM AM AVG-IM OBSV
IKF117	79.623	72.531	77.575	-7.092	-2.048	82.552	80.797	81.907	-1.755	-0.645	67.903	69.671	69.145	1.768	1.242
IKF291	73.606	75.996	79.805	2.391	6.199	79.948	81.329	83.360	1.381	3.412	67.583	68.294	69.526	0.711	1.943
CMF83A	78.067	75.591	73.077	-2.476	-4.990	82.051	79.254	83.990	-2.798	1.939	67.465	68.850	69.740	1.386	2.276
IKF328	75.556	74.500	78.089	-1.056	2.534	81.865	83.285	84.030	1.420	2.165	67.521	68.079	69.374	0.557	1.853
IKF545	76.103	74.442	75.854	-1.661	-0.249	79.592	81.708	81.787	2.116	2.195	68.040	68.470	68.970	0.430	0.930
IKF107	80.216	75.103	74.562	-5.113	-5.654	83.951	79.084	83.145	-4.866	-0.806	67.248	69.841	68.222	2.593	0.974
IKF470	76.241	75.398	76.594	-0.843	0.353	82.051	78.479	82.537	-3.573	0.486	70.000	69.797	69.245	-0.203	-0.755
IKF191	73.145	72.799	74.194	-0.346	1.049	78.660	83.301	82.412	4.641	3.752	68.056	69.601	67.265	1.546	-0.790
EVF182	75.618	74.223	76.254	-1.395	0.636	84.856	84.133	82.687	-0.723	-2.170	70.198	68.698	70.878	-1.499	0.680
IKF518	75.618	74.143	76.553	-1.475	0.935	81.931	81.103	81.087	-0.828	-0.844	67.619	69.679	68.881	2.060	1.262
IKF570	78.092	74.509	77.497	-3.583	-0.594	83.784	80.040	84.101	-3.744	0.317	67.380	70.634	67.516	3.255	0.136
EVF158	78.660	73.834	73.897	-4.825	-4.763	81.638	81.824	81.155	0.186	-0.483	69.194	69.707	67.436	0.513	-1.758
EVF153	76.408	75.868	75.401	-0.541	-1.008	82.124	82.164	80.396	0.039	-1.728	71.266	68.053	69.451	-3.213	-1.815
IKF411	74.386	75.104	79.743	0.718	5.357	81.378	82.203	85.184	0.825	3.806	69.902	69.045	68.667	-0.857	-1.235
IKF13	78.322	74.540	74.312	-3.781	-4.009	85.279	80.515	81.395	-4.764	-3.884	69.863	69.720	67.919	-0.143	-1.944
CHF61	75.000	76.077	76.641	1.077	1.641	82.857	80.819	83.455	-2.038	0.598	71.591	69.273	69.897	-2.318	-1.694
IKF608	75.347	76.371	75.667	1.024	0.319	81.796	80.580	81.575	-1.215	-0.221	69.273	69.148	69.601	-0.125	0.329
IKF440	72.318	75.094	76.852	2.776	4.534	82.090	82.358	83.146	0.268	1.057	68.033	69.137	68.131	1.104	0.098
IKF590	74.048	74.470	75.000	0.421	0.952	79.512	81.812	82.857	2.300	3.345	68.342	69.524	71.591	1.181	3.249
CMF188A	74.740	77.396	77.135	2.656	2.394	83.042	82.589	83.387	-0.454	0.344	68.801	67.538	70.978	-1.263	2.177
CMF145	78.547	75.096	77.169	-3.451	-1.378	84.709	81.904	83.597	-2.805	-1.112	67.806	68.832	69.208	1.027	1.402
IKF140	70.690	78.718	76.685	8.028	5.995	79.345	82.780	81.347	3.435	2.002	69.522	67.521	68.373	-2.002	-1.149
CMF190	78.276	76.054	75.862	-2.222	-2.414	86.173	82.432	82.759	-3.740	-3.414	68.568	68.324	70.566	-0.244	1.998
EVF92	75.258	76.371	76.737	1.113	1.479	80.668	81.960	83.383	1.292	2.715	67.371	68.681	68.179	1.310	0.808

Table 54. Computed measures (brachial, crural, and intermembral indices) for observed, regressed, and imputed data from all females who had all four long bones present (left) (continued)

Indiv.	BR OBSV	BR REG	BR AM AVG	BR REG-BR OBSV	BR AM AVG-BR OBSV	CR OBSV	CR REG	CR AM AVG	CR REG-CR OBSV	CR AM AVG-CR OBSV	IM OBSV	IM REG	IM AM AVG	IM REG-IM OBSV	IM AM AVG-IM OBSV
IKF588	77.397	74.376	77.261	-3.021	-0.136	82.512	84.261	82.125	1.748	-0.388	69.906	69.326	69.083	-0.580	-0.823
EVF164	75.510	72.753	77.756	-2.757	2.246	82.185	84.617	81.367	2.431	-0.818	67.275	69.696	68.488	2.421	1.213
IKF72	76.531	75.862	80.107	-0.669	3.576	84.804	82.364	87.270	-2.439	2.466	68.833	68.586	70.427	-0.246	1.594
IKF261	77.211	77.091	74.628	-0.119	-2.583	86.520	82.212	81.714	-4.307	-4.805	68.463	67.680	68.837	-0.782	0.375
CMF185	78.231	73.071	74.772	-5.161	-3.459	83.488	82.201	80.769	-1.288	-2.719	66.413	71.145	71.023	4.731	4.610
IKF205	70.847	82.465	74.828	11.618	3.981	80.928	81.254	81.281	0.326	0.353	71.795	66.381	67.392	-5.414	-4.403
IKF17	72.881	79.738	76.094	6.857	3.212	80.563	81.232	83.297	0.669	2.734	72.238	67.947	69.732	-4.291	-2.506
IKF183	76.610	75.184	78.007	-1.426	1.397	80.615	80.818	83.598	0.203	2.983	68.194	70.068	70.197	1.874	2.003
IKF464	74.662	74.508	76.081	-0.155	1.418	80.288	83.283	81.783	2.995	1.494	68.933	69.518	69.429	0.585	0.496
CMF99	75.676	75.383	75.115	-0.292	-0.561	83.688	83.913	81.032	0.225	-2.656	66.924	68.394	69.748	1.470	2.824
IKF220	73.737	76.515	74.995	2.777	1.257	79.904	80.787	83.293	0.882	3.389	68.617	69.313	67.876	0.696	-0.741
IKF90	74.582	76.270	81.563	1.688	6.981	80.387	82.812	85.853	2.424	5.466	70.067	69.146	69.009	-0.922	-1.058
IKF366	78.000	75.238	77.192	-2.762	-0.808	82.367	81.761	82.262	-0.606	-0.105	70.728	70.354	69.521	-0.374	-1.207
IKF75	78.000	76.747	75.986	-1.253	-2.014	85.036	80.804	80.446	-4.232	-4.590	68.549	69.956	69.405	1.406	0.855
CMF20B	76.412	78.371	77.062	1.959	0.650	83.894	81.150	83.630	-2.744	-0.264	69.412	68.560	68.248	-0.851	-1.164
IKF52	74.503	78.149	76.408	3.646	1.905	82.968	82.532	82.124	-0.436	-0.844	70.080	67.705	71.266	-2.374	1.186
CMF201	75.329	76.707	74.301	1.378	-1.028	83.765	82.087	82.404	-1.678	-1.361	68.246	68.619	68.642	0.374	0.396
IKF586	78.947	74.323	78.660	-4.625	-0.288	81.647	83.453	81.638	1.805	-0.009	70.466	69.770	69.194	-0.697	-1.272
LFF10	73.115	75.938	72.913	2.824	-0.202	78.923	81.896	79.853	2.974	0.930	69.110	69.641	68.734	0.531	-0.376
IKF168	75.082	76.782	74.301	1.700	-0.781	81.206	80.552	84.144	-0.655	2.938	68.374	69.209	69.359	0.835	0.985
IKF233	73.856	76.233	75.510	2.377	1.654	82.238	84.171	82.185	1.933	-0.053	71.028	68.618	67.275	-2.410	-3.753
CMF27	74.593	76.863	76.709	2.270	2.116	81.308	82.530	82.973	1.221	1.664	69.072	69.281	67.969	0.209	-1.103
IKF520	76.547	76.938	76.833	0.391	0.285	83.257	82.593	82.054	-0.663	-1.203	67.835	68.881	69.036	1.046	1.201
IKF391	76.299	72.854	73.549	-3.444	-2.749	79.405	84.836	80.658	5.431	1.253	69.260	69.556	67.593	0.295	-1.667

Table 54. Computed measures (brachial, crural, and intermembral indices) for observed, regressed, and imputed data from all females who had all four long bones present (left) (continued)

Indiv.	BR OBSV	BR REG	BR AM AVG	BR REG-BR OBSV	BR AM AVG-BR OBSV	CR OBSV	CR REG	CR AM AVG	CR REG-CR OBSV	CR AM AVG-CR OBSV	IM OBSV	IM REG	IM AM AVG	IM REG-IM OBSV	IM AM AVG-IM OBSV
IKF634	72.414	74.682	74.516	2.268	2.102	81.163	85.588	81.971	4.425	0.808	70.603	69.013	67.682	-1.590	-2.921
CHF71	75.862	76.360	74.934	0.498	-0.928	82.759	82.650	83.290	-0.108	0.531	70.566	69.406	71.022	-1.160	0.456
IKF638	78.370	77.782	75.618	-0.588	-2.752	83.603	82.088	84.856	-1.515	1.254	71.572	68.638	70.198	-2.934	-1.375
IKF269	78.638	74.675	75.879	-3.963	-2.759	84.753	84.344	82.156	-0.409	-2.598	70.024	70.202	68.909	0.177	-1.115
CMF86	74.312	77.357	73.596	3.045	-0.716	81.878	83.965	80.955	2.087	-0.923	68.427	69.213	69.967	0.786	1.539
Summed differences				-4.595	18.287				-4.698	17.755				0.384	4.466

The absolute difference between observed, regressed, and imputed data sets for calculated values like indices are again consistently higher in the imputed data set (following the pattern seen in total limb bone length, since those data went into the indices).

I ran some ANOVAs on the indices to see if the three data sets are different from one another. Those are given in Tables 55-57. Again, while there were not any statistically significantly different ANOVAs for calculated indices, I used the regression values as they are somewhat closer to the observed.

Table 55. Anova for brachial indices (observed, regressed, and imputed data sets)						
Groups	Count	Sum	Average	Variance		
BR OBSV	53	4018.0398	75.812071	4.7445205		
BR REG	53	4013.4446	75.725369	3.3123599		
BR AM AVG	53	4036.3264	76.157102	3.2564975		
Source of Variation	SS	df	MS	F	P-value	F crit
Between Groups	5.5288994	2	2.7644497	0.7330568	0.48208560	3.05400417
Within Groups	588.29565	156	3.771126			
Total	593.82455	158				

Table 56. Anova for crural indices (observed, regressed, and imputed data sets)						
Groups	Count	Sum	Average	Variance		
CR OBSV	53	4357.9049	82.224621	3.5211527		
CR REG	53	4353.2073	82.135987	2.1912326		
CR AM AVG	53	4375.6601	82.559626	2.0544077		
Source of Variation	SS	df	MS	F	P-value	F crit
Between Groups	5.2921213	2	2.6460606	1.0220668	0.36224716	3.05400417
Within Groups	403.87324	156	2.5889310			
Total	409.16536	158				

Table 57. Anova for intermembral indices (observed, regressed, and imputed data sets)						
Groups	Count	Sum	Average	Variance		
IM OBSV	53	3659.5553	69.048214	1.9327544		
IM REG	53	3659.9392	69.055456	0.7536485		
IM AM AVG	53	3664.0213	69.132478	1.2157794		
Source of Variation	SS	df	MS	F	P-value	F crit
Between Groups	0.2311762	2	0.1155881	0.0888642	0.91501609	3.05400417
Within Groups	202.91348	156	1.3007274			
Total	203.14466	158				

APPENDIX II: POST-CRANIAL BI-VARIATE ANALYSES

To visualize interactions between post-cranial variables, or changes in one long bone relative to another, I graphed the linear regression models developed from individuals with all four long bones observed, along with their slopes.

Below are the models for Maximum Length of the Radius on the Humerus given by sex and by group (Table 58). Among females, the southern Illinois sample has the highest slope line (meaning greater growth in the humerus relative to the radius). Central Tennessee and western Kentucky samples are closely aligned for these variables. Among the males it is the central Tennessee sample that has a slight deviation of slope but not much. In the pooled sex sample the central Tennessee sample has the lowest slope.

The models for Maximum Length of the Tibia on the Femur, again given by sex and by group (Table 59). The slopes that stand out among these figures are the central Tennessee females and the southern Illinois males. Each group deviates from the other two in their respective slopes. The pooled sexes samples have nearly the same slope.

The models for Femur Maximum Length on Humerus Maximum Length (as both are proximal elements within their respective limbs) (Table 60). The southern Illinois females have a steeper slope line than the other groups of females. Among the males it is the western Kentucky line that stands out with a flatter slope line. Pooled sexes shows the central Tennessee and western Kentucky sample nearly aligned while the southern Illinois sample has a higher line of slope but a lower intercept.

The models for Radius Maximum Length on Tibia Maximum Length (as both are proximal elements within their respective limbs) are given in Table 61. The slope line for central Tennessee females rises more steeply than in the other samples. The pattern is the same among central Tennessee males with the other two groups being rather aligned for both males and females. The slope lines are nearly the same between all three groups in the pooled sexes sample.

The models for Crural Index on Brachial Index are given in Table 62. These computed indices compare the length of the radius to humerus within the arm, and the length of the tibia relative to the femur in the leg. Plotting them against one another is not all that informative (see R-square values in the table below) but the results are presented here for thoroughness. In the sample of female indices the three samples are rather similar. The males, however, have very different slope lines given that the southern Illinois males have a negative slope. The situation is then similar for the pooled sexes sample.

Table 58. Linear Regression Model for HXL ~ RXL

	Grouping	Subgroup	Linear Model	R-square
By sex	Females	SOILF	HXL = 58.108 + RXL (1.058)	0.74
		CTNF	HXL = 86.741 + RXL (0.929)	0.83
		WKYF	HXL = 86.774 + RXL (0.932)	0.69
	Males	SOILM	HXL = 50.611 + RXL (1.089)	0.74
		CTNM	HXL = 59.243 + RXL (1.046)	0.81
		WKYM	HXL = 46.740 + RXL (1.102)	0.69
	Pooled sexes	SOILPOOL	HXL = 54.324 + RXL (1.074)	0.85
		CTNPOOL	HXL = 75.524 + RXL (0.980)	0.90
		WKYPOOL	HXL = 69.467 + RXL (1.010)	0.82
By group	SoIL	SOILF	HXL = 58.108 + RXL (1.058)	0.74
		SOILM	HXL = 50.611 + RXL (1.089)	0.74
	CTN	CTNF	HXL = 86.741 + RXL (0.929)	0.83
		CTNM	HXL = 59.243 + RXL (1.046)	0.81
	WKY	WKYF	HXL = 86.774 + RXL (0.932)	0.69
		WKYM	HXL = 46.740 + RXL (1.102)	0.69

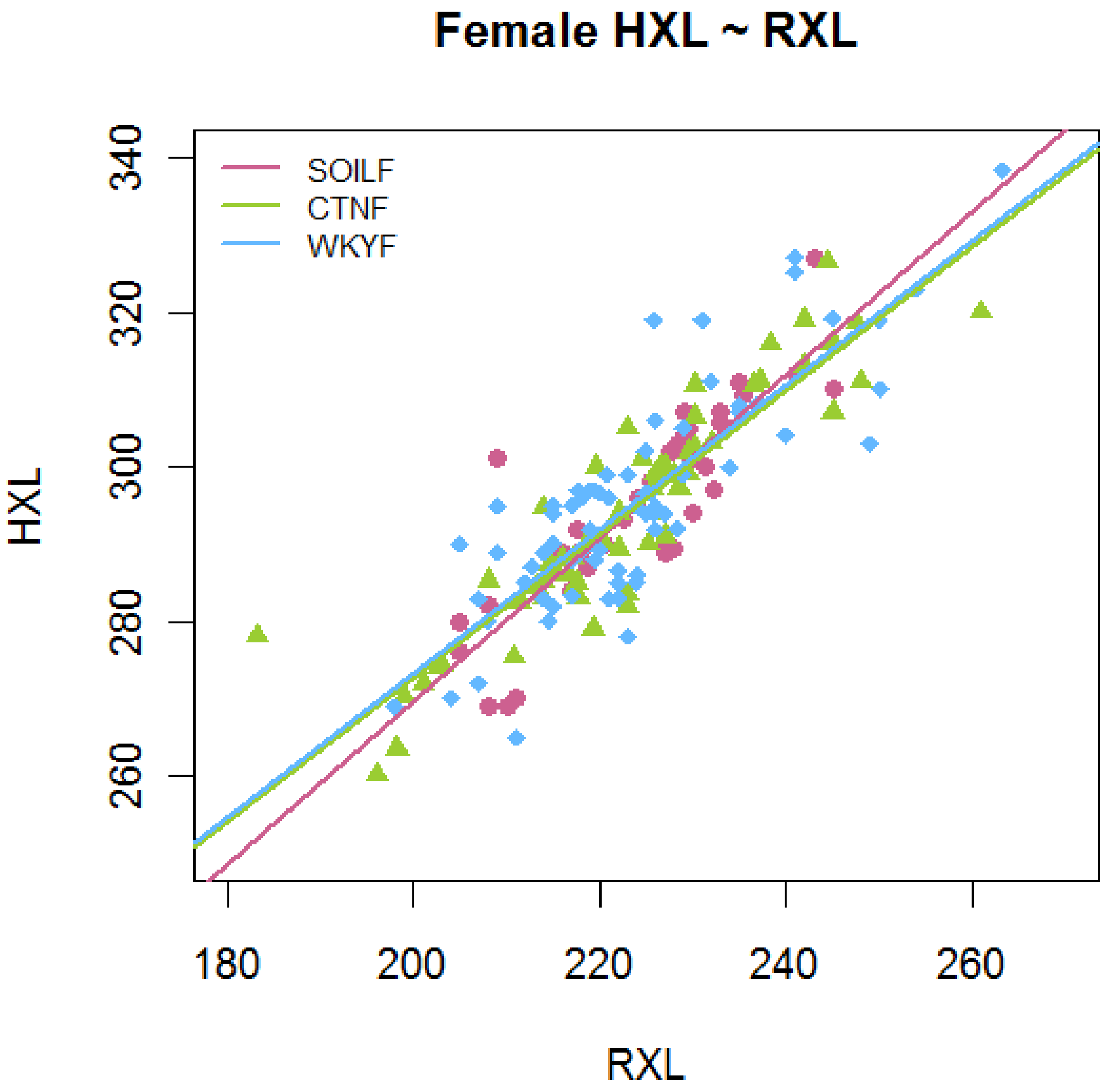

Figure 35. Linear regression for females HXL ~ RXL

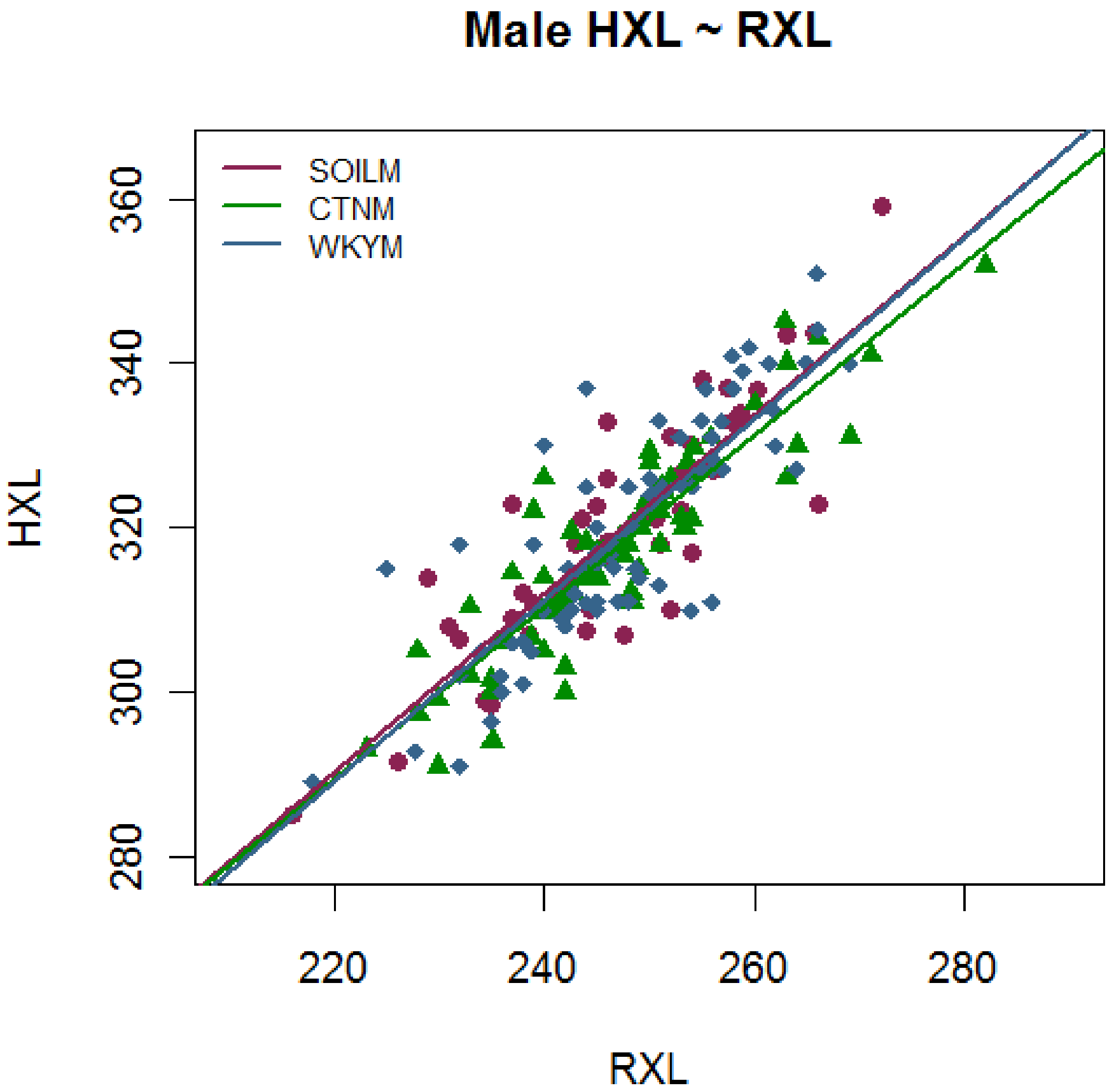

Figure 36. Linear regression for males HXL ~ RXL

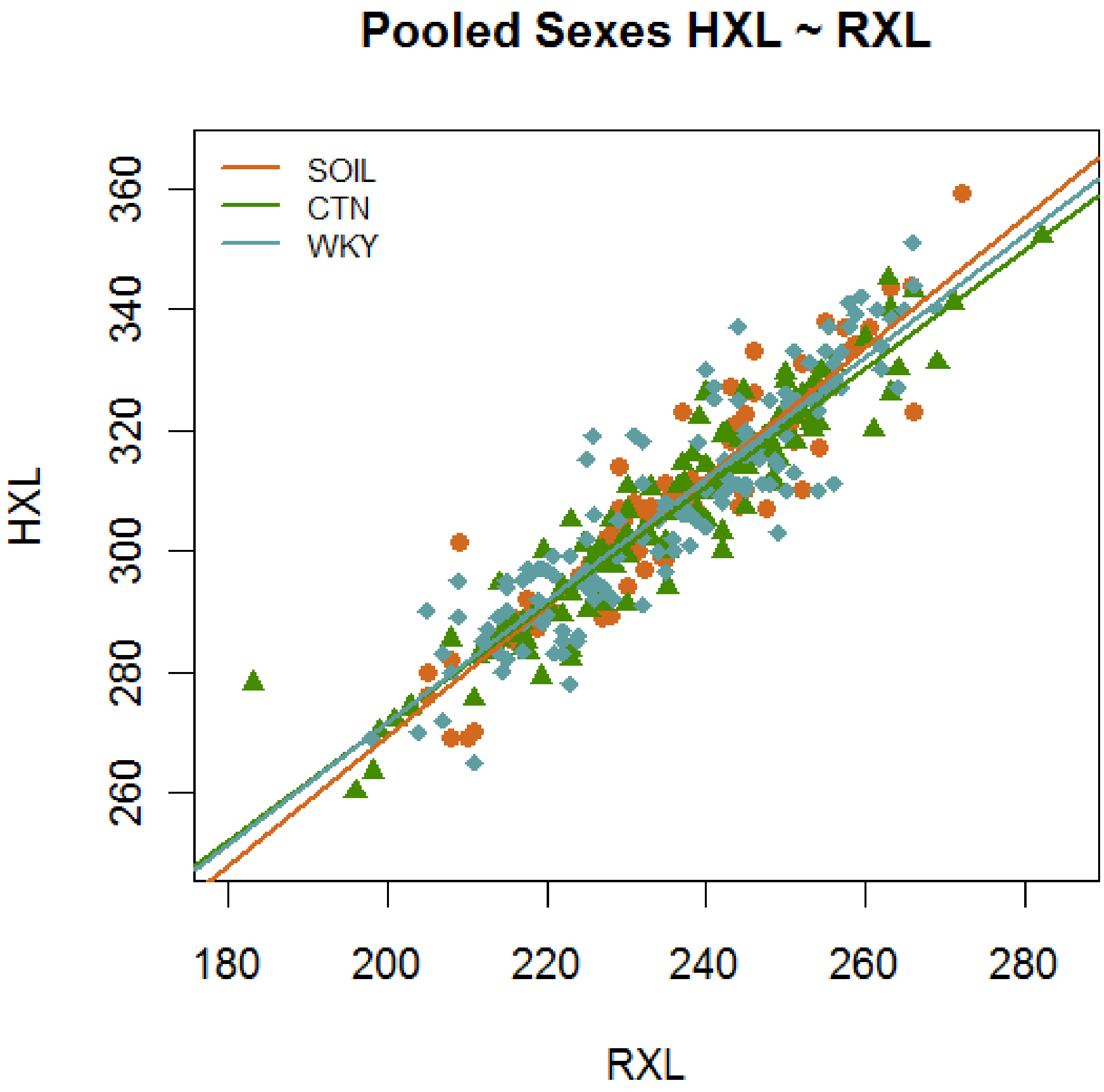

Figure 37. Linear regression for pooled sexes HXL ~RXL

Table 59. Linear Regression Model for FXL ~ TXL

	Grouping	Subgroup	Linear Model	R-square
By sex	Females	SOILF	FXL = 97.417 + TXL (0.930)	0.81
		CTNF	FXL = 66.066 + TXL (1.018)	0.86
		WKYF	FXL = 96.193 + TXL (0.934)	0.78
	Males	SOILM	FXL = 74.455 + TXL (1.002)	0.81
		CTNM	FXL = 86.733 + TXL (0.970)	0.81
		WKYM	FXL = 28.100 + TXL (1.128)	0.81
	Pooled sexes	SOILPOOL	FXL = 69.162 + TXL (1.015)	0.89
		CTNPOOL	FXL = 56.957 + TXL (1.049)	0.90
		WKYPOOL	FXL = 61.397 + TXL (1.037)	0.87
By group	SoIL	SOILF	FXL = 97.417 + TXL (0.930)	0.81
		SOILM	FXL = 74.455 + TXL (1.002)	0.81
	CTN	CTNF	FXL = 66.066 + TXL (1.018)	0.86
		CTNM	FXL = 86.733 + TXL (0.970)	0.81
	WKY	WKYF	FXL = 96.193 + TXL (0.934)	0.78
		WKYM	FXL = 28.100 + TXL (1.128)	0.81

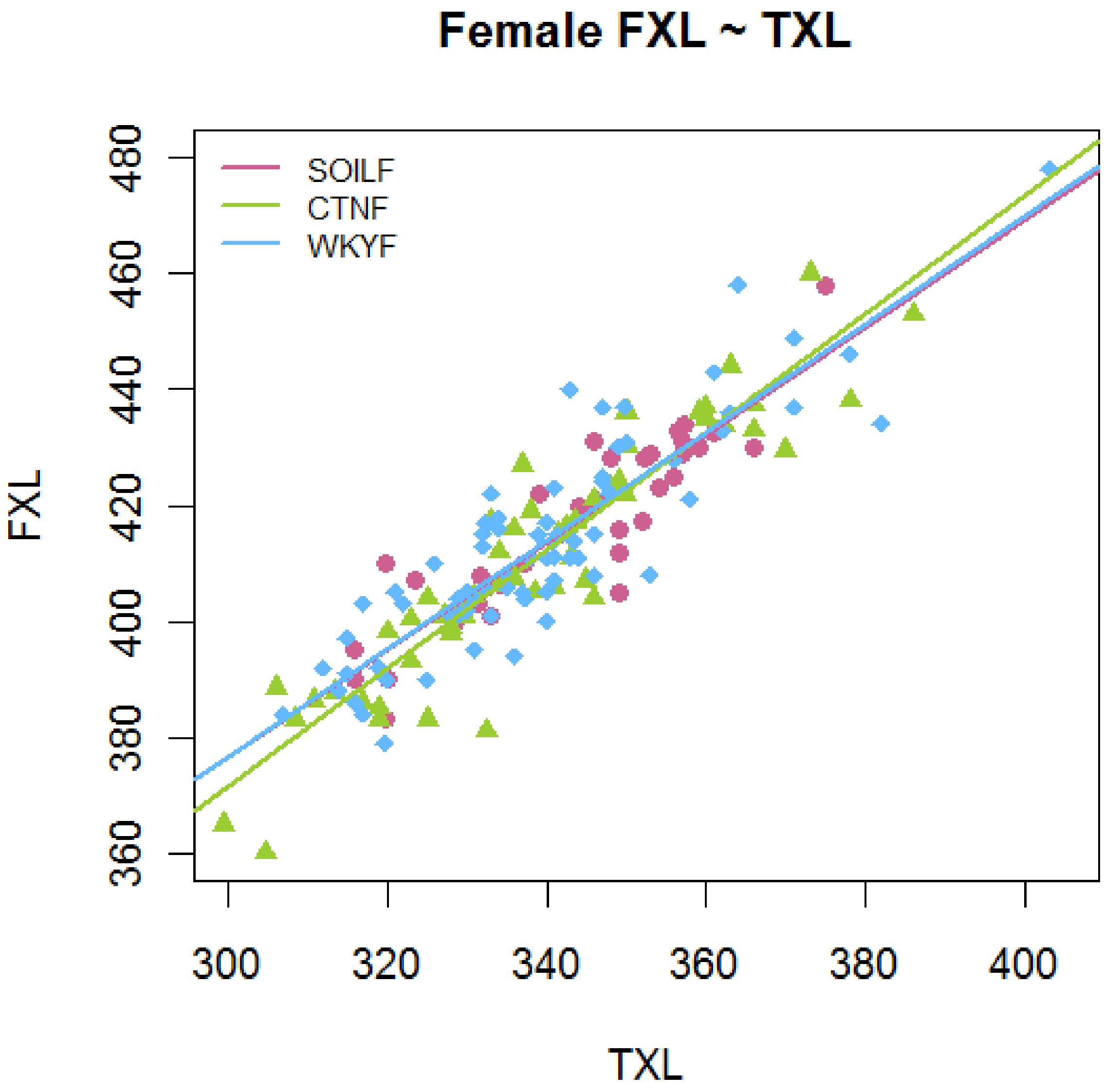

Figure 38. Linear regression for females FXL ~ TXL

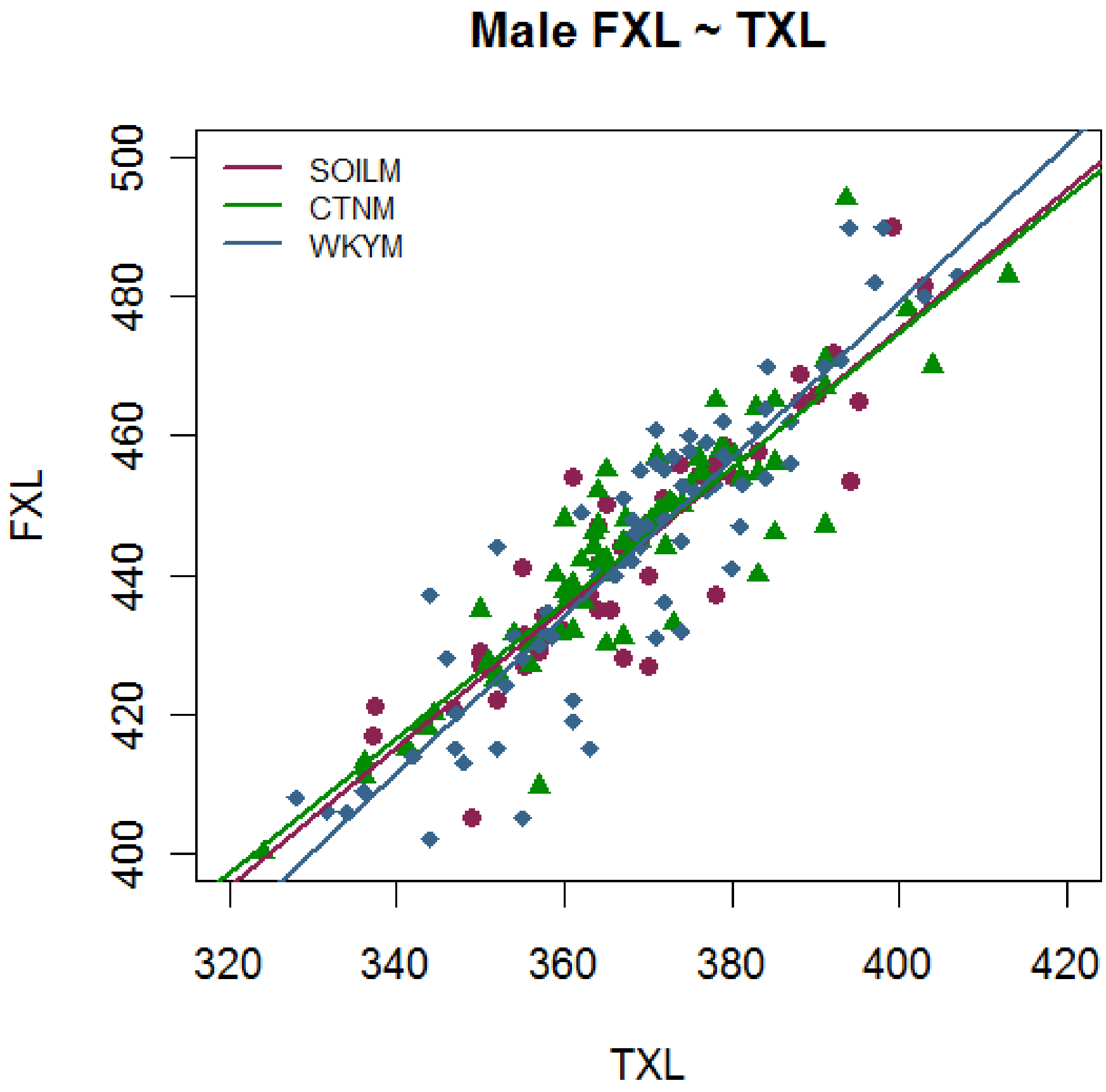

Figure 39. Linear regression for males FXL ~ TXL

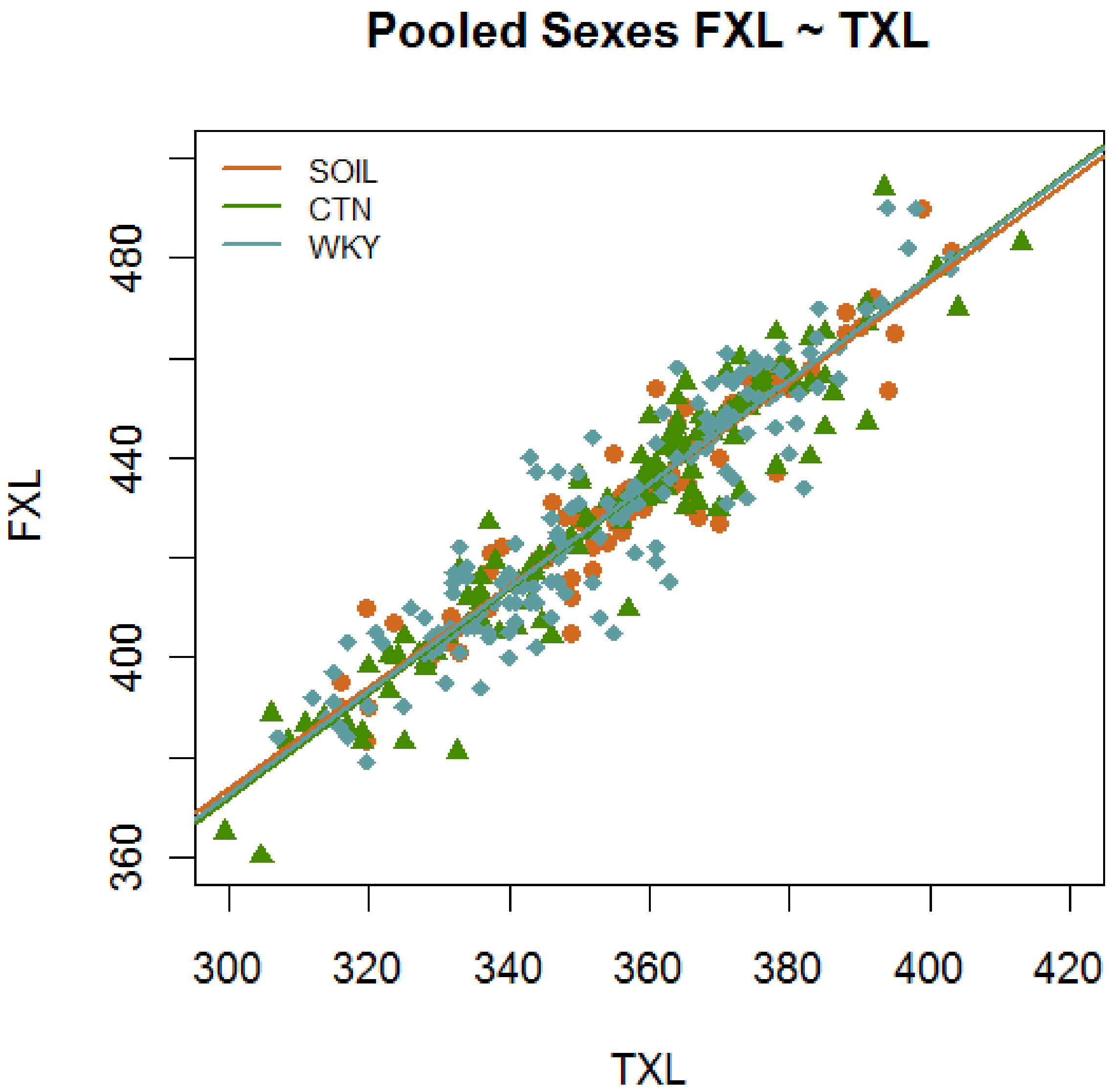

Figure 40. Linear regression for pooled sexes FXL ~ TXL

Table 60. Linear Regression Model for HXL ~ FXL

	Grouping	Subgroup	Linear Model	R-square
By sex	Females	SOILF	HXL = -31.125 + FXL (0.786)	0.84
		CTNF	HXL = 12.240 + FXL (0.686)	0.92
		WKYF	HXL = 16.025 + FXL (0.676)	0.81
	Males	SOILM	HXL = 16.420 + FXL (0.683)	0.74
		CTNM	HXL = 22.679 + FXL (0.665)	0.89
		WKYM	HXL = 66.409 + FXL (0.571)	0.77
	Pooled sexes	SOILPOOL	HXL = -26.425 + FXL (0.777)	0.87
		CTNPOOL	HXL = 7.673 + FXL (0.698)	0.94
		WKYPOOL	HXL = 14.150 + FXL (0.685)	0.87
By group	SoIL	SOILF	HXL = -31.125 + FXL (0.786)	0.84
		SOILM	HXL = 16.420 + FXL (0.683)	0.74
	CTN	CTNF	HXL = 12.240 + FXL (0.686)	0.92
		CTNM	HXL = 22.679 + FXL (0.665)	0.89
	WKY	WKYF	HXL = 16.025 + FXL (0.676)	0.81
		WKYM	HXL = 66.409 + FXL (0.571)	0.77

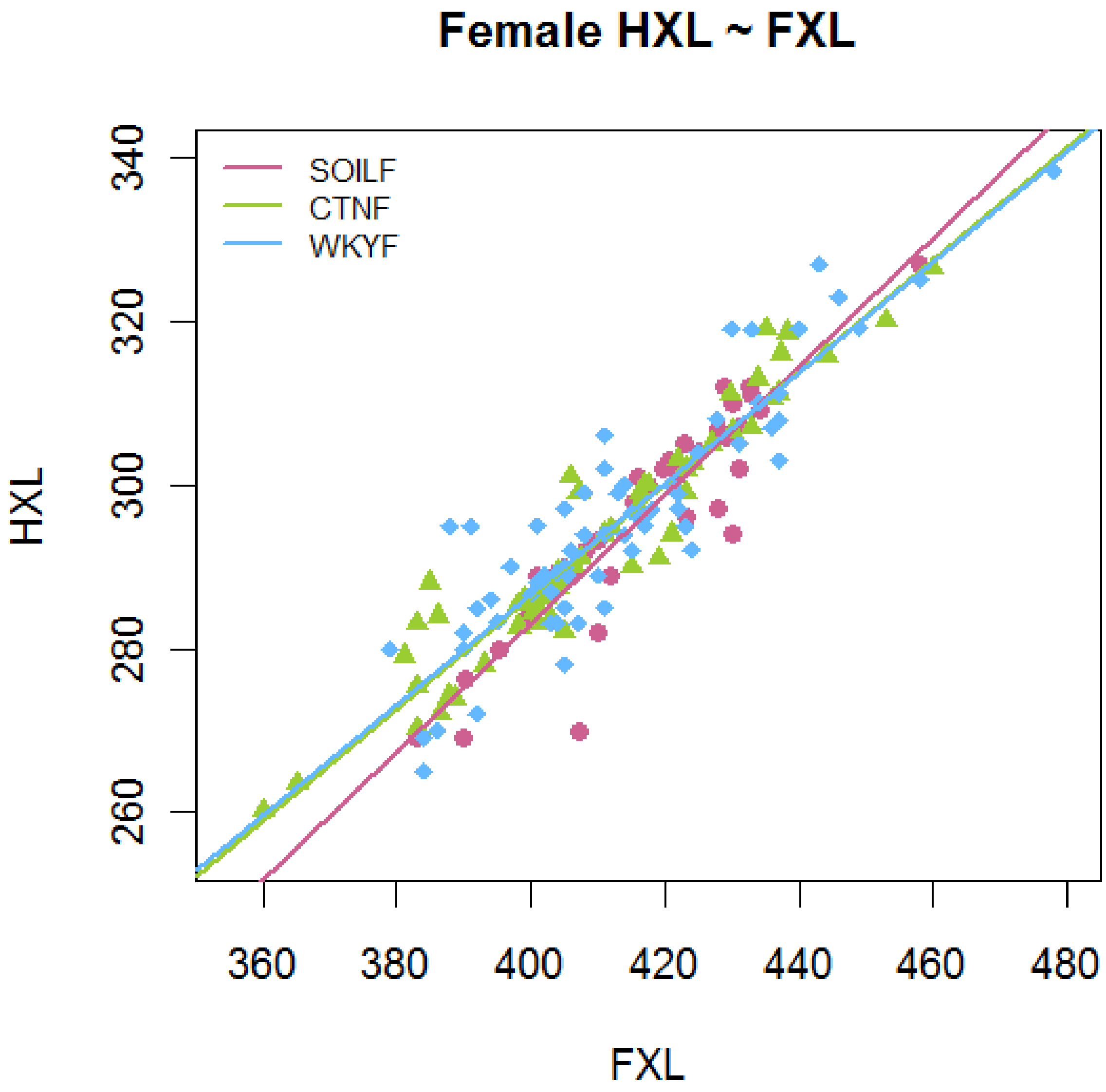

Figure 41. Linear regression for females HXL ~ FXL

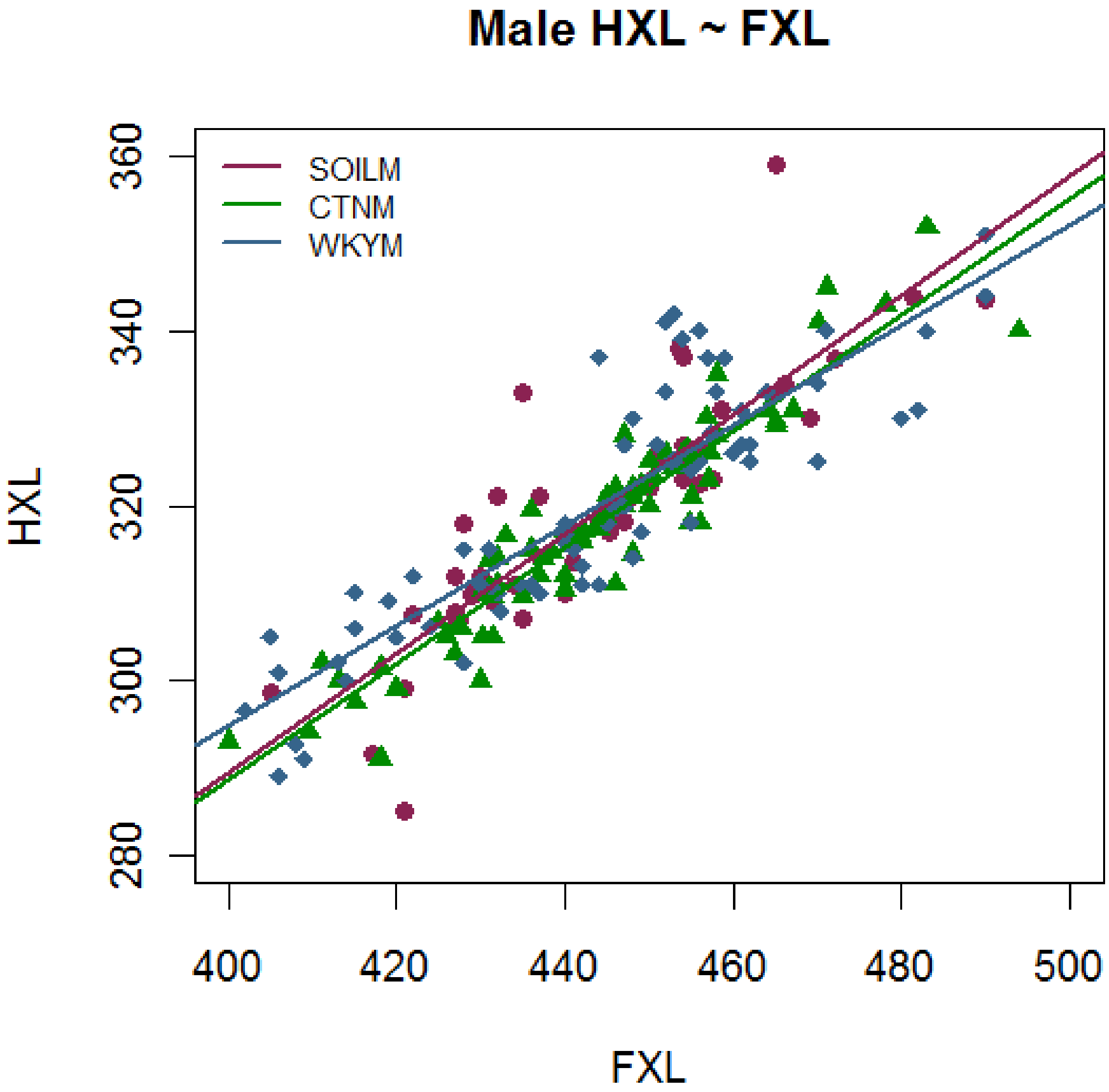

Figure 42. Linear regression for males HXL ~ FXL

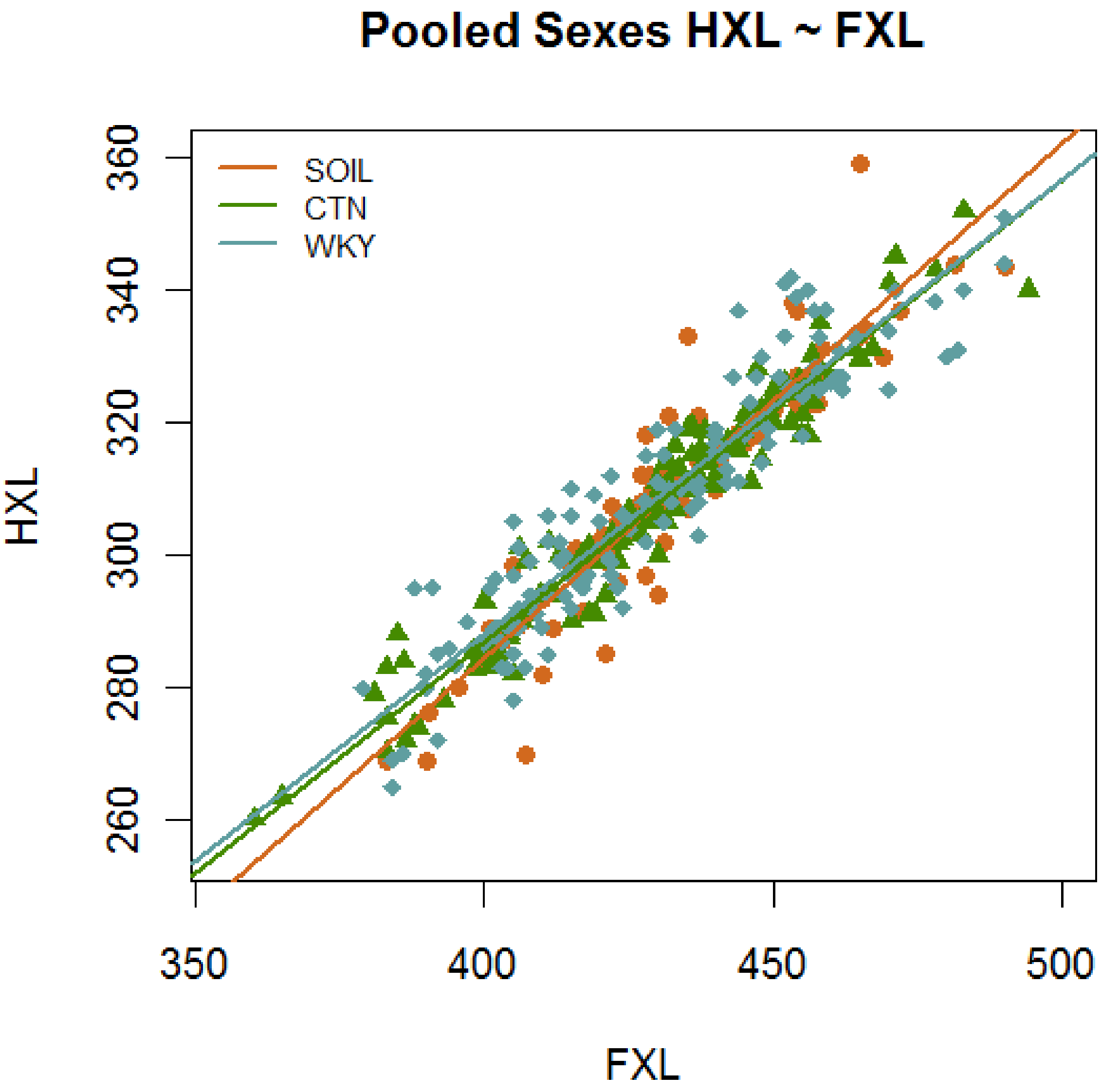

Figure 43. Linear regression for pooled sexes HXL ~ FXL

Table 61. Linear Regression Model for RXL ~ TXL

	Grouping	Subgroup	Linear Model	R-square
By sex	Females	SOILF	RXL = -4.987 + 0.670 (TXL)	0.86
		CTNF	RXL = -22.144 + 0.724 (TXL)	0.89
		WKYF	RXL = -4.118 + 0.672 (TXL)	0.91
	Males	SOILM	RXL = 38.457 + 0.565 (TXL)	0.65
		CTNM	RXL = 30.390 + 0.589 (TXL)	0.81
		WKYM	RXL = 56.174 + 0.520 (TXL)	0.72
	Pooled sexes	SOILPOOL	RXL = -17.182 + 0.712 (TXL)	0.84
		CTNPOOL	RXL = -22.734 + 0.730 (TXL)	0.91
		WKYPOOL	RXL = -9.680 + 0.694 (TXL)	0.89
By group	SoIL	SOILF	RXL = -4.987 + 0.670 (TXL)	0.86
		SOILM	RXL = 38.457 + 0.565 (TXL)	0.65
	CTN	CTNF	RXL = -22.144 + 0.724 (TXL)	0.89
		CTNM	RXL = 30.390 + 0.589 (TXL)	0.81
	WKY	WKYF	RXL = -4.118 + 0.672 (TXL)	0.91
		WKYM	RXL = 56.174 + 0.520 (TXL)	0.72

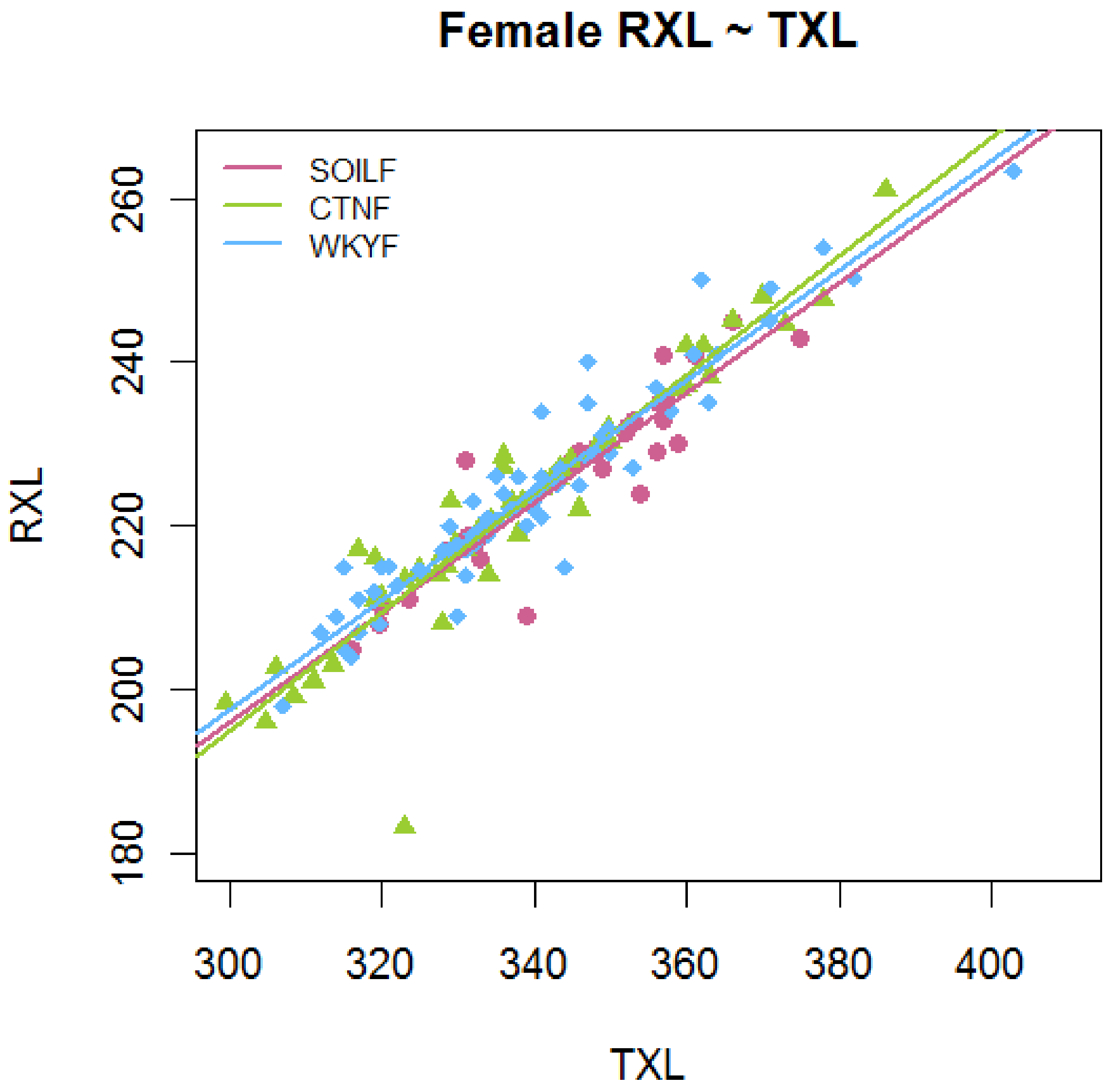

Figure 44. Linear regression for females RXL ~ TXL

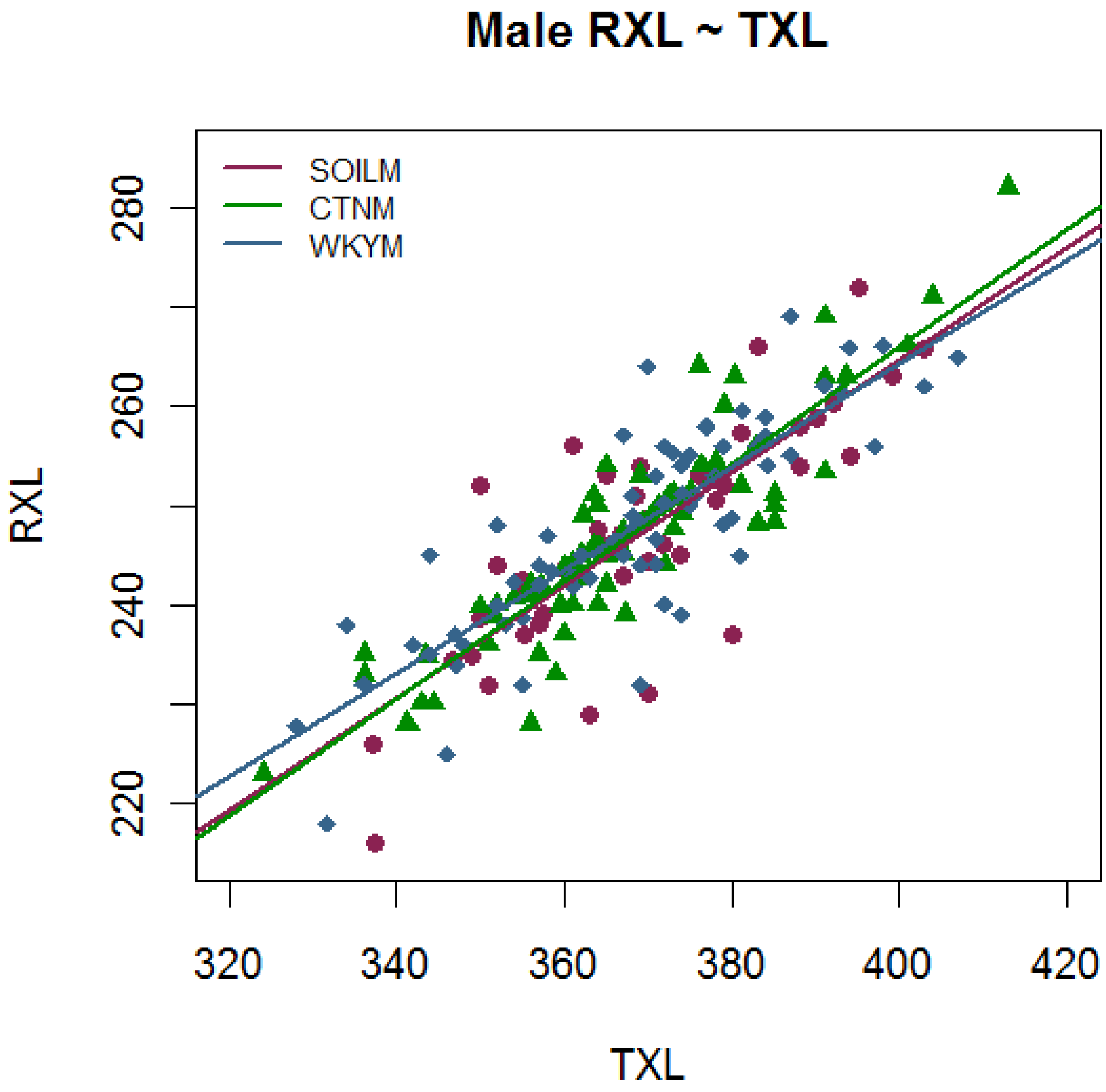

Figure 45. Linear regression for males RXL ~ TXL

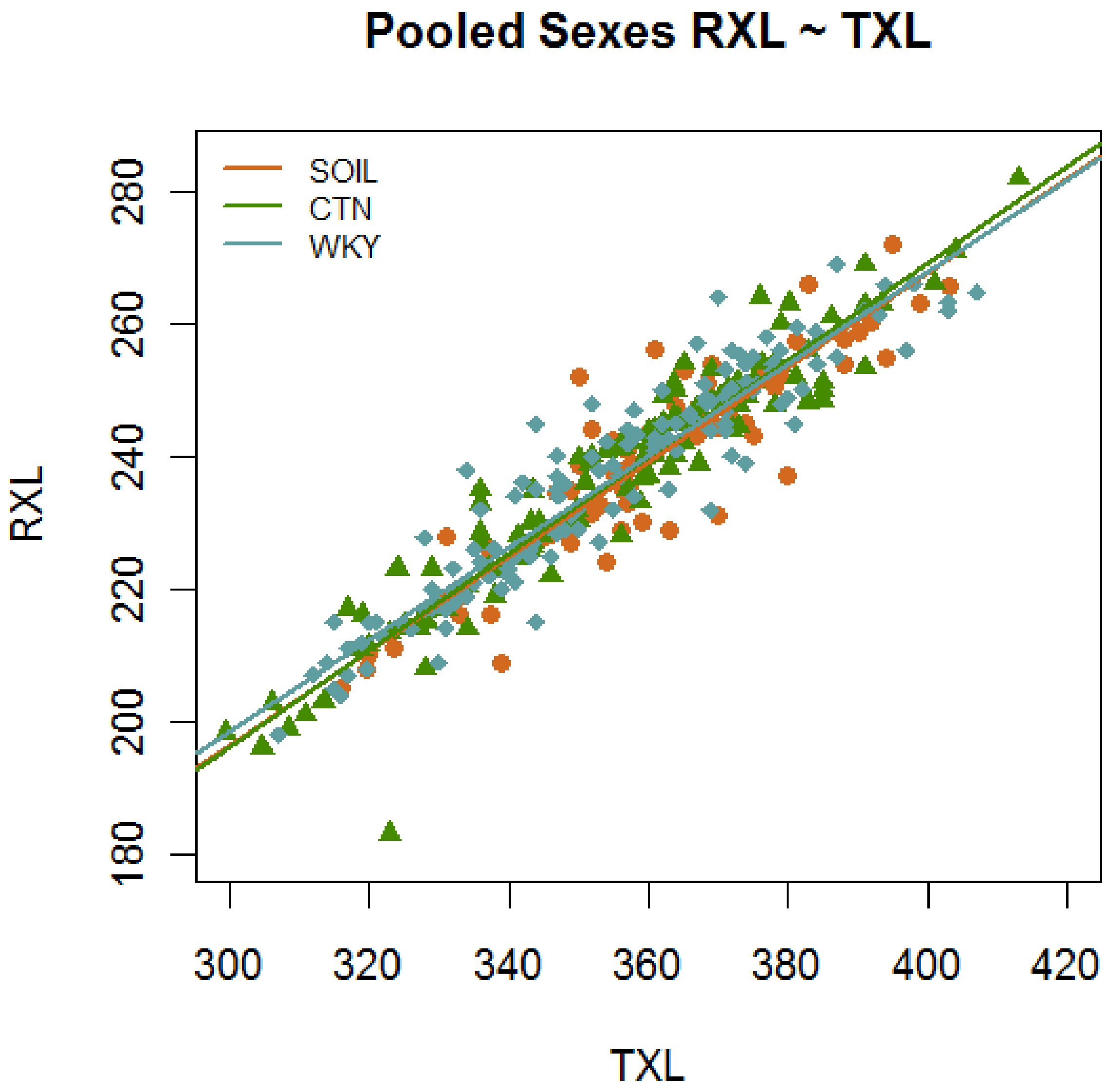

Figure 46. Linear regression for pooled sexes RXL ~ TXL

Table 62. Linear Regression Model for Brachial Index ~ Crural Index (BR ~ CR)				
	Grouping	Subgroup	Linear Model	R-square
By sex	Females	SOILF	BR = 21.593 + 0.661 (CR)	0.31
		CTNF	BR = 17.984 + 0.702 (CR)	0.31
		WKYF	BR = 10.148 + 0.799 (CR)	0.46
	Males	SOILM	BR = 89.657 – 0.149 (CR)	0.02
		CTNM	BR = 38.072 + 0.479 (CR)	0.28
		WKYM	BR = 52.621 + 0.300 (CR)	0.08
	Pooled sexes	SOILPOOL	BR = 53.582 + 0.280 (CR)	0.05
		CTNPOOL	BR = 22.159 + 0.662 (CR)	0.29
		WKYPOOL	BR = 22.641 + 0.654 (CR)	0.30
By group	SoIL	SOILF	BR = 21.593 + 0.661 (CR)	0.31
		SOILM	BR = 89.657 – 0.149 (CR)	0.02
	CTN	CTNF	BR = 17.984 + 0.702 (CR)	0.31
		CTNM	BR = 38.072 + 0.479 (CR)	0.28
	WKY	WKYF	BR = 10.148 + 0.799 (CR)	0.46
		WKYM	BR = 52.621 + 0.300 (CR)	0.08

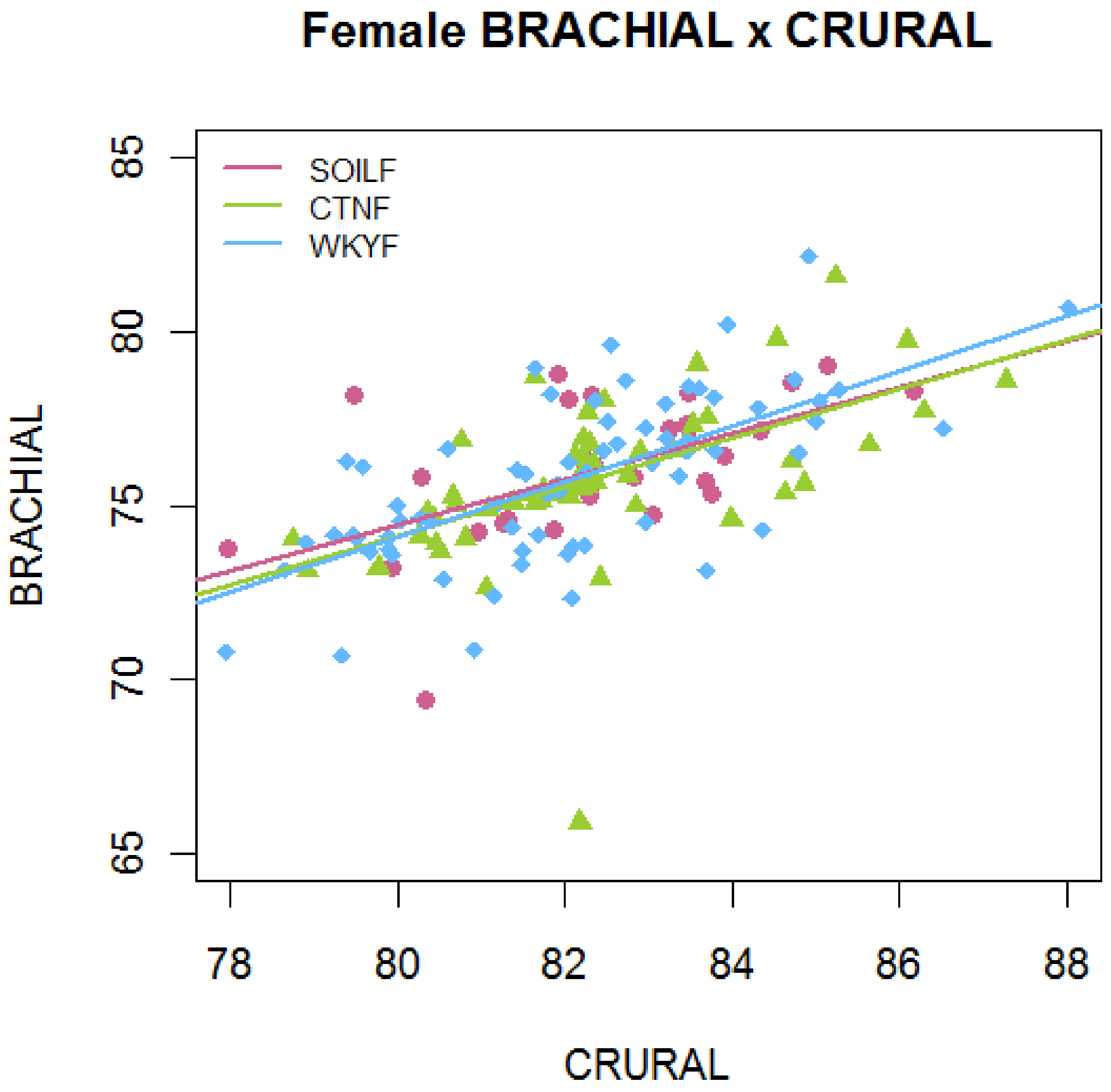

Figure 47. Linear regression for females Brachial ~ Crural Indices

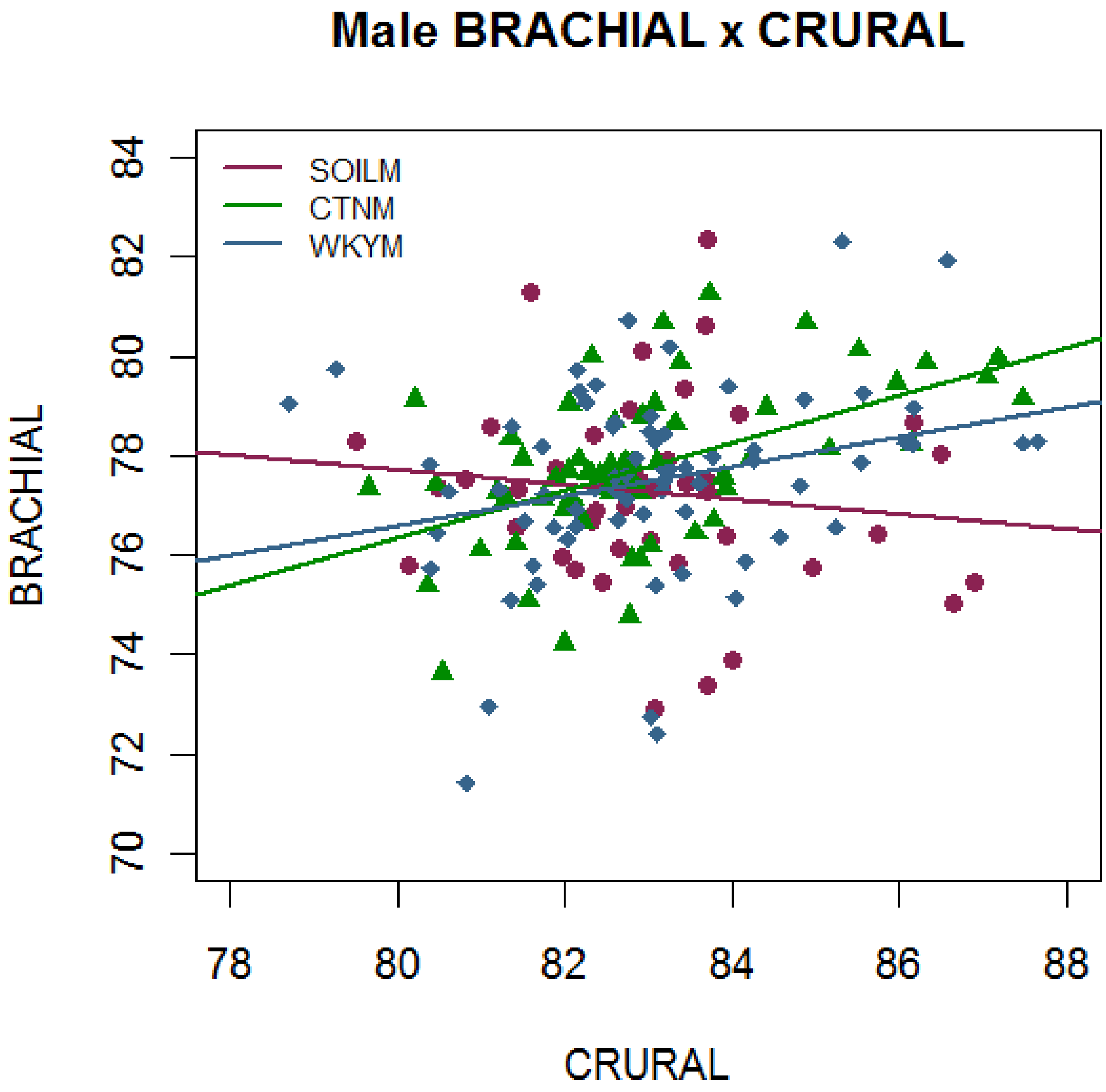

Figure 48. Linear regression for males Brachial ~ Crural Indices

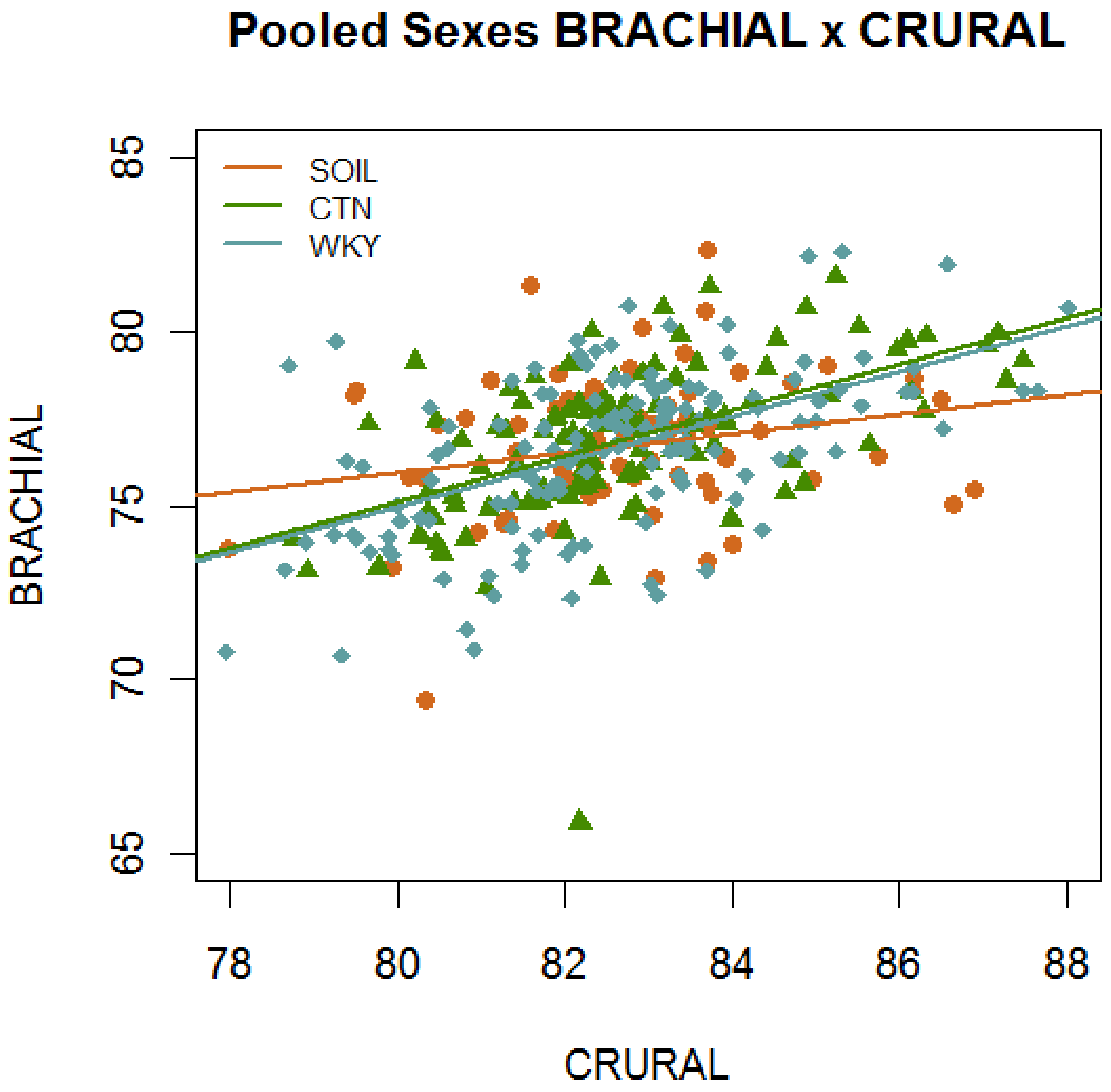

Figure 49. Linear regression for pooled sexes Brachial ~ Crural Indices

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