COMMUNITY IDENTITY AND THE ARCHAEOLOGICAL COMPLEX OF TÚCUME, PERÚ: A SYTHESIS OF CRANIAL AND DENTAL NONMETRIC VARIATION

by

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ABSTRACT

The archaeological complex of Túcume was once a regional center of political and religious importance on the north coast of Perú (ca. AD 1000-1532). Previous research into the identity of the individuals interred at the site has yielded conflicting results. Within this intrasite biodistance analysis, community identity as reflected in the cranial and dental nonmetric variation and burial patterns is examined. This research also addresses methodological issues in nonmetric biodistance studies by examining the utility of combining cranial and dental nonmetric datasets. The sample examined (*n*=161) includes male and female crania from five distinct burial locations within Túcume. Gower's coefficient was applied to the cranial and dental nonmetric data separately, then in tandem, and the results were compared using a tanglegram, often employed when comparing phylogenetic dendrograms. There were no major statistically significant differences between males and females, nor were there any clustering patterns associated with sex or burial location. In light of the previous research conducted at Túcume, the high degree of biological homogeneity within the site is perhaps a reflection of the broader Lambayeque region. The politico-religious importance of Túcume may have had a homogenizing effect on the population, drawing people from throughout the region to participate in both the quotidian and the ritual. This research highlights how large urban spaces of social importance may serve to expand and homogenize the notion of community identity. Furthermore, the comparative analysis of the cranial and dental nonmetric data suggests that there is perhaps no biologically justifiable reason to consider cranial and dental nonmetric data in an exclusive manner.

To my wife, Aphrodite Kocięda, and my entire family.

I would not be where I am today without you.

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CHAPTER 1: INTRODUCTION

In this thesis, skeletal cranial and dental nonmetric traits are used to investigate the genetic composition of the local population, or deme (a group of interbreeding individuals in a given locality) (Mayr 1963; Perez 2007) at the archaeological complex at Túcume, Perú. Túcume was once an urban center of political and religious importance within the north coast region of the Perúvian Andes (ca. AD 1000-1532) (Narváez Vargas 1995b). There have been several decades of research conducted at Túcume, but much of the history of the site is still not well understood. Recent research has provided different interpretations concerning the social identity of the sacrificed individuals from the Temple of the Sacred Stone location within the site (Toyne 2008; 2011; Hewitt 2013). Using biological distance (biodistance) analysis, the goal of this research is to examine the biological variation within the site, focusing primarily on burial location and sex differences. By investigating the biological variation in relation to the archaeological evidence, it becomes possible to make inferences about the the community identity at the site.

Biodistance analysis is the reconstruction of population structure and/or history through phenotypic or genotypic features (traits) (Knudson and Stojanowski 2008). This biodistance research uses nonmetric traits, which are discrete morphological features found throughout the skeleton and dentition that are observed, rather than metrically defined. Biodistance studies are inherently bioarchaeological as they generate hypotheses for the investigation of archaeological populations, operating within the wider anthropological framework (Buikstra 1977; Larsen 1997; Wright and Yoder 2003). Bioarchaeological investigations of group/community identities often incorporate multiple lines of evidence such as mortuary practices and/or features, genetic relatedness, and artifact distributions, to name a few. Burial placement is an aspect of mortuary practices that embody the relationship between the deceased and those who participated in the internment (Hendon 2000; Pearson 2003). Community identity is an aspect of social identity that is difficult, if not impossible, to fully understand because bioarchaeologists are only able to examine proxies for identity (Nystrom 2006). For the purposes of this research, community identity can be succinctly defined as a social construct were groups of people share social practices and interests, biological kinship, as wells as spatial and temporal propinquity. Understanding the patterns of biological relatedness, as well as potential sex differences, in relation to the burial patterns at Túcume makes it possible to infer how community membership was articulated in ancient Túcume. How is community membership defined, and what does it mean to be a member of a community? These questions are the overarching anthropological focuses of this research; the specific research questions are designed to elucidate these broader areas of interest.

The investigation of sex and burial location differences as they relate to patterns in the biodistance data serves to potentially identify kin-based systems of hierarchy and/or sex-based patterns of migration. If, for example, the adult females are more closely related to each other than to the males, this might suggest that groups of males are migrating to Túcume from outside the region, possibly as a result of the shifts in political administration at the site. If groups of related individuals are found to be buried in the same locations, it would suggest that biological ancestry plays an important in role in organizing mortuary activities, but also social power structures within the site. There is also a unique burial context within Túcume, the Temple of the Sacred Stone, where a large number of individuals were deliberately put to death as part of a sacrificial ritual (Toyne 2011). Several individuals interred within Huaca Larga, the largest platform mound on the site, are also thought to have been sacrificed or part of a ritual inclusion accompanying an elite burial. Understanding the network of kinship relations within Túcume through biodistance analysis will aid in the identification of the potential relationships among local, non-local, elite, non-elite, sacrificed, and non-sacrificed individuals. Quantifying the degree of variability within and between these groups is crucial to understanding how community identity was articulated in ancient Túcume.

The intrasite approach adopted for this study offers a glimpse into how community identity and social processes played a role in structuring biological affinities at a single site. Sites of social significance, like Túcume, likely attracted people from the surrounding region to participate in various activities at the site. This interaction could have had a homogenizing effect, both socially and biologically, and perpetuated an extension of community identity well beyond the boundaries of the site. By investigating how politico-religious interactions, and spaces of social significance, correspond and influence biological variation, this research incorporates both social and evolutionary theory. A more clear understanding of how social and evolutionary processes intermingled at Túcume provides more information for the ongoing research at the site.

Cranial and dental nonmetric data are often considered in an exclusive manner within biodistance studies. This research offers a novel methodological approach as it compares cranial and dental nonmetric datasets with a “tanglegram”; cranial and dental nonmetric data are also considered in tandem within this research. A “tanglegram”, is a method of visually and statistically comparing phylogenetic dendrograms (Venkatachalam et al. 2010). I argue that combining cranial and dental nonmetric traits is more phenotypically comprehensive, and may therefore be a more informative method when reconstructing biological and social processes, and the intermingling of the two.

Sample Background, Methods, and Research Objectives

Sample Background

The skeletal collection at Túcume serves as an excellent sample to investigate the above research questions because it is large and well preserved, and the skeletons have all been tentatively dated to within several hundred years of each other. Of the 414 burials currently in the collection, 161 individuals were examined for this study, each coming from one of five locations within the site. Most of the individuals were adults; however, 17 subadults were included. By examining a sample that includes individuals found throughout the site, it is more likely that the sample examined is representative of the overall population including a range of mortuary variation that might reflect social status.

Túcume was initially constructed by the Lambayeque (or Middle Sicán) culture (ca. AD 1000-1350) but was later integrated into the Chimú (ca. AD 1350-1470) and the Inca Empires (ca. AD 1350-1532). The Lambayeque and the Chimú shared similar cultural origins (Heyerdahl et al. 1995; Moore and Mackey 2008). However, the Inca originated from the distance southern highlands, and later expanded their territory to include the north coast (Shimada et al. 2004; Moore and Mackey 2008; Covey 2008). The degree to which these cultural occupations effected the biological variation at Túcume has not been previously investigated, but it might be expected that new genetic information would have likely been introduced. If there is a high degree of heterogeneity at the site this might suggest an influx of migrants from other distant areas. The archaeological evidence suggests that the burials from the Temple of the Sacred Stone may have been members of the local community (Toyne 2008; 2011; 2015a; 2015b). If these individuals are more closely related to each other than to the rest of the sample, a reevaluation of their origin and role in the community may be called for. Using isotopic analysis, Hewitt (2013) found that at least some of the individuals interred at the Temple of the Scared Stone did not originate from the site, and likely came from the surrounding Lambayeque valley region. The conclusions of Hewitt (2013) should, however, be considered tentative due to the conflicting results within that study. This research, in part, is aimed at expanding upon the previous research conducted at the site.

Methods

Biodistance analysis has been an essential tool within bioarchaeology (Buikstra et al. 1990; Larsen 1997; 2002). The majority of biodistance studies have utilized phenotypic (observable) features to determine the degree of similarity between groups (Stojanowksi and Schillaci 2006), but more recent studies have also incorporated mitochondrial, nuclear, and Y chromosome DNA (e.g., Herrera et al. 2014; Hubbard et al. 2015) in concert with metric and/or nonmetric data. This research focuses on cranial and dental nonmetric traits because they are argued to reflect patterns of genetic relatedness (e.g., Herrera et al. 2014), and recording nonmetric traits has become a standard approach within bioarchaeology (Turner et al. 1991; Buikstra and Ubelaker 1994). Nonmetric traits are morphological variants found throughout the skeleton. The different forms that these traits can assume have been well documented (e.g., Hauser and DeStefano 1989; Turner et al. 1991), and thus it is possible to record the various states in which they occur in an accurate manner. However, within biodistance studies cranial and dental nonmetric traits are not typically considered in a simultaneous manner. Even when these traits are included within a single study, they are statistically treated in an exclusionary manner, with few exceptions (e.g., Ricaut et al. 2010). Moreover, in populations that exhibit cranial modification (i.e. Túcume), using a wide variety of traits may offset the obscuring impact these cultural/environmental factors may have on biodistance measures (Del Papa and Perez 2007). By comparing, and then combining these data sets, it becomes possible to evaluate the utility of an "exclusive" approach to nonmetric data. This research calls into question the trend of exclusionary treatment within nonmetric biodistance studies and echoes the call for a more inclusive approach (Herrera et al. 2014). Both univariate and multivariate statistics are employed to investigate the nonmetric data collected for this research. Several dendrograms are used to demonstrate the degree of statistical distance between the individuals examined. Dendrograms are visual representations of the statistical distance between the individuals being examined (Saraf and Patil 2014). Lastly, several tanglegrams are employed to compare the cranial and dental nonmetric dendrograms. Tanglegrams are used to compare phylogenetic dendrograms, and are widely used in evolutionary biology (Scornavacca et al. 2011)

Research Objectives

The primary objective of this research is to determine how the examined biological variation reflects social dynamics, community identity, and population history at ancient Túcume. As a large urban center of social significance, people likely gravitated to the site which perhaps had an influence on the deme. Understanding how the deme was influenced by the potenital burgeoning demographic complexity may provide key insights about, the site, the region, and perhaps spaces of social aggregation in general (e.g., Stojanowksi 2004).

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The archaeological complex of Túcume is an important archaeology site in the Andes, with the largest collection of monumental platform mounds in Perú. However, the site is perhaps not given the acknowledgement that it deserves within the literature and wider public. Túcume experienced several cultural occupations, and it might be expected that these socio-political events introduced new genetic information into the deme which may have been previously isolated. Thus it follows that the genetic variability would have likely been altered (i.e. increased) and perhaps the social boundaries of the community were altered as well. This research project is the most comprehensive examination of the biological variation at Túcume to date, and as such allows for several lines of inquiry to be addressed.

Specific Research Questions, Expectations, and Hypotheses

Archaeological Questions and Expectations

There are several specific questions about the ancient society at Túcume this research aims to address. What does the biological variation examined in this study tell us about social variation at the site? Are there differences between the males and females that suggest an influx of outside genetic information (migration) based on sex? Are the biological patterns consistent with the available chronological and burial location information, and what does this tell us about the history of Túcume? Is the biological variation within the site consistent with inferences about social status?

Based on the archaeological evidence, I expect that individuals examined in this study will not all be from the same deme since Túcume potentially experienced an influx of outside genetic information when the Chimú and Inca took control of the site. Based on this I would expect that there would be significant differences in trait frequencies between burial locations and between males and females throughout the site. I also expect that the patterns found in the cluster analysis and dendrograms will generally correspond to burial location. Unlike the majority of the other burials excavated thus far at Túcume, the individuals buried at the Temple of the Sacred Stone were deliberately put to death in a ritualistic fashion (Toyne 2008; 2011; 2015a; 2015b) and several individuals from Huaca Larga are likely sacrificed individuals as well. This sacrificed group represents a unique comparative sample within the site. The archaeological evidence suggests that these individuals were part of the local community, but the isotopic evidence tentatively suggests they come from the surrounding Lambayeque valley region. Based on the archaeological evidence, I expect that the individuals buried in the sacrificial group will exhibit a similar degree of variation found throughout the site.

Methodological Questions and Expectations

As previously mentioned, this research also investigates methodological questions within biodistance studies. When used together, cranial and dental nonmetric traits have produced concordant biological distance predictions (e.g., Prowse and Lovell 1996; Ricuat 2010; Herrera et al. 2014). However, within the Andes these two types of nonmetric data have not been considered in tandem within a single study. Will the cranial traits produce similar clustering patterns when compared to the data from dental traits? How will combining cranial and dental nonmetric data affect the clustering patterns?

Based on the results of the cluster analysis and the incorporation of tanglegrams, I expect to find a statistically significant concordance between the cranial and dental traits when considered separately. I also expect that when both cranial and dental traits are considered in unison, similar grouping patterns will emerge.

Hypotheses

From these archaeological and methodological expectations I have generated the following testable hypotheses:

1. All individuals from Túcume will exhibit dissimilar levels of variation indicating there is heterogeneity at the site; the levels of variation between males and females will be dissimilar.

    Alternative 1: All individuals will exhibit similar levels of variation indicating that the burial groups are from the same deme; the levels of variation between males and females will be similar.

2. The nonmetric variants will group individuals based on the defined temporal contexts and burial locations; higher levels of variation will be found between the documented contexts than within them.

    Alternative 2: The nonmetric variants being examined will not group individuals based on the defined temporal contexts and burial locations; higher levels of variation will be found within the documented contexts than between them.

3. The cranial and dental nonmetric traits will exhibit similar statistical results when considered separately and when combined, thus demonstrating they reflect similar or complementary information about the population.

> *Alternative 3*: The dental and cranial nonmetric traits will exhibit dissimilar statistical results when considered separately and when combined indicating that the traits are not genetically controlled in the same ways.

Thesis Organization

The remainder of this thesis is organized as follows. Chapter Two will provide background information on anthropological studies of biodistance as it relates to bioarchaeology; the social theory of identity; and, the intrasite approach and Andean biodistance studies. Chapter Two also includes a brief history of nonmetric traits and background information about the archaeological complex at Túcume, as well as the importance of conducting a biodistance study at the site. Chapter Three includes a detailed description of the skeletal sample examined and the methodological approach adopted for this study, including nonmetric trait recording procedures and the statistical methods. Chapter Four provides the results of the univariate and multivariate statistical analyses. Chapter Five presents the discussion of the statistical results of the nonmetric analysis, the basis for rejecting or failing to reject the hypotheses, and the interpretation and implications of these results. Chapter Six provides a summary of the information presented, some concluding remarks, and potential future directions.

CHAPTER 2: BACKGROUND

Introduction

This research incorporates both social and biological theory to support the methodological approach adopted. This chapter will begin with an overview of biodistance analysis as applied within the discipline of bioarchaeology. Using biodistance analysis to understand social processes and aspects of identity has been important in anthropology. The social theory of identity as well as a brief history of the utilization of nonmetric traits within biodistance studies will be discussed. A discussion of the intrasite approach and Andean biodistance studies will be provided. Lastly, this chapter includes an overview of the archaeological research at Túcume with a brief description of the site, a brief summary of the available skeletal material, and the importance of incorporating biodistance analysis at the site.

Biodistance Analysis as Bioarchaeology

Bioarchaeology serves as a figurative bridge between social and evolutionary theory (Knudson and Stojanowski 2008) as it considers cultural, environmental, and biological contexts when interpreting archaeological skeletal remains (Larsen 2002; Wright and Yoder 2003; Buikstra and Beck 2006). Biodistance studies operate within a bioarchaeological framework (Stojanowski and Schillaci 2006), and such studies are essentially investigating evolutionary processes by attempting to quantify the degree of genetic relatedness in and between populations (Buikstra et al. 1990; Larsen 1997; Perez et al. 2007).

Biodistance studies operate under the assumption that populations with many shared features or attributes are more closely related than populations expressing many differences

(Perez et al. 2007). Biodistance analysis primarily incorporates phenotypic information by using either metric or nonmetric data obtained from measurable/observable skeletal features, but can also be conducted using DNA or even blood group data (e.g., Goicoechea et al. 2001). Phenotypic features are physical characteristics that are a product of genes, and the environment in which those genes are expressed (Falconer 1960). Both metric and nonmetric data are used within biodistance studies because the environmental influences are assumed to have a minimal or randomly distributed effect on the populations being studied (Stojanowksi and Schillaci 2006). Cranial and dental nonmetric traits have been widely used in biodistance studies because they are assumed to reflect patterns of genetic relatedness (e.g., Herrera et al. 2014), they are easy to observe, and the method is nondestructive and inexpensive (Greenberg et al. 1986; Stojanowski and Schillaci 2006).

The goal of biodistance studies is to reconstruct the history and structure of populations. Within the context of microevolutionary theory, the reconstruction of population history focuses on the degree of similarity between groups as a result of common ancestry and/or gene flow (Harpending and Jenkins 1973; Relethford 1996; Knudson and Stojanowski 2008). Reconstructions of population structure focus on the investigation of how evolutionary forces influence genetic homogeneity and/or increase heterogeneity within a population and, moreover, how these forces impact the distribution, size, and composition of a population (Harpending and Jenkins 1973; Relethford 1996). Studies of population history tend to operate at the continental level, and studies of population structure examine the regional level (Knudson and Stojanowksi 2008). However, biodistance analysis can also be conducted at the intrasite and even intracemetery level (Stojanowski and Schillaci 2006). Generally speaking, there are three steps in the biodistance analysis following data acquisition. The first and most obvious would be the acquisition of the distance measures; within this study this is done through statistical methods. Second, a graphic representation of these statistical distances is often used to display the information, typically with a dendrogram or principle coordinate plot. The third, and perhaps most difficult aspect, is the process of interpreting the results (Relethford 1996).

Within bioarchaeology, biodistance has played a key role (Buikstra et al. 1990; Konigsberg 2006) in part because it can illuminate patterns of gene flow and mate exchange that are assumed to be imbued with social significance (Stojanowksi 2013). Sex based exogamous or endogamous marriage practices, for example, influence human populations in non-random ways (Hamilton et al. 2005). In a system where females marry outside of their social group, this will result in males within a site being more closely related, and the females will be more heterogeneous (e.g., Spence 1974). Thus, marriage and mate exchange practices have the potential to produce discernible patterns in biological data that reflect social parameters and constructs, such as with whom it is acceptable to produce offspring (Klaus 2013). However, discerning social processes from biological data is a difficult task that must be supported with several lines of evidence, such as ethno-historic documents, burial inclusions, and burial location. When multiple lines of evidence are incorporated into biodistance analyses, researchers then have a greater ability to address questions regarding social organization and identity in past societies (Stojanowski and Schillaci 2006; Stojanowksi 2013).

Social Theory of Identity

Bio-cultural concepts such as ethnicity and community identity have been investigated through biodistance analysis (Nystrom 2009; Knudson and Stojanowski 2008; 2009; Stojanowski

2013), operating under the assumption that biological affinities are a foundational aspect of human social identity (Fix 2012). Identifying biological kinship (i.e., family groups) within archaeological sites has played an important role within biodistance studies (Spence 1974; Stojanowski and Schillaci 2006) and can be used to address broader bio-cultural concepts. Bio-cultural groups, or ethnic groups, can be operationally defined as “groups that demonstrate ethnic affiliation as indicated by culturally based behavior, genetic relatedness, and shared economic activities and interests” (Sutter 2005: 184). Social identity can be described as a multilayered personal and communal process wherein people continuously attempt to articulate multiple roles and levels of status to form a self and group “image” (Epstein 1978; Knudson and Stojanowksi 2008). Identity is, therefore, culturally constructed and is continually informed by conceptions of justice or morality, for example; but identity is also based on observable biological characteristics (sex, age, skin color, etc.).

Community and social identity research has long been of interest to anthropologists (e.g., Murdock 1949), and archaeological research into community identity has experienced multiple waves of theoretical adjustment (see Canuto and Yager 2000). Community identity can be thought of as a continually emergent social institution, generated by people living together in particular places within particular temporal and historical contexts (Yaeger and Canuto 2000). Communities past and present are composed of diverse actors (Potter and Yoder 2008), and as such, it is important to avoid essentialist definitions of “the community” (Isbell 2000) that may obscure the more nuanced aspects of human social systems (Schachner 2008). Contemporarily, the term *community* has often been used to refer to minority groups in a discursively pejorative manner (Sweeney 2011).This highlights an important aspect of how community membership is defined: it is not just about group solidarity, but is also reified through the distrust of difference (Sweeney 2011). As an intrasite level study, this thesis research is positioned to make comments at the community level, “the somewhat neglected medium scale between the household and the region” (Sweeney 2011: 28). With this in mind, this thesis research prudently examines certain aspects of identity that are assumed to be core factors in the configuration of the community at Túcume: gender, biological relatedness, spatial and temporal propinquity.

Gender, for example, is an aspect of social identity that has been an important area of research within bioarchaeology (Holliman 2011). Anthropological interpretations of gender potentially harbor androcentric, heteronormative anachronisms (Geller 2008). Extrapolating social practices from a strict “male/female” dichotomy potentially obscures social variability and difference in the past (Geller 2008). In the ancient Moche culture of northern Perú, for example, gender did not necessarily determine one’s political position in society, which has complicated archaeological interpretations of Moche social organization (Alcalde 2004). However, the observable osteological differences between males and females are not an “irrelevant mirage” (Sofaer 2006: 96), and the ability to identify the biological sex of a skeleton is of pivotal importance to all disciplines that involve human osteology. Sex identification can therefore be considered a “first step” in understanding more nuanced and complicated notions like gender. When estimations of sex are combined with other information (e.g., biodistance data, archaeological data), patterns begin to emerge that may reveal deeper information about social organization and identity in the past.

The ritualized treatment of mortuary remains often reflects aspects of individual and communal identity (e.g., gender, status, religion). Within the context of this research a ritual can be defined as a communally significant act meant to simultaneously communicate with supernatural forces and to reinforce social hierarchies (Hastorf 2001). Death can be viewed as a challenge the ontological security of individuals and communities (Reimers 1999) because it highlights the ephemeral nature of human existence. Funerary rituals act as a means of collectively diminishing the threat of erasure posed by death by reinforcing the importance and the memory of individual(s) within familial groups and the wider community. When a person dies, this initiates a physical dissolution of the corpse yet the social networks, perhaps in most cases, persist and continue to inscribe the deceased into the social memory (Munn 1986; Byrd 1995; Joyce 2001; Gillespie 2001). Therefore, material remains found within interments can be thought of as the residues of past cultural and ideological beliefs about death, identity, and community membership (Rowe 1995; Barrett 1994). Using a biodistance that incorporates both biological and cultural "variables" offers a way to at least partially reconstruct how social identities were articulated in the past.

At Túcume, and throughout the Andes, socially sanctioned death in the form of human sacrifice played an important role in the reification of religious and political authority (Toyne 2011; 2015a; 2015b). The archaeological evidence suggests that ritualized human sacrifices at Túcume involved individuals from the local community, and was performed to maintain social stability, an act that was both religious and political (Toyne 2008; 2011; 2015a; 2015b). Human sacrifice can be seen as an act that allows communities to engage in communication/exchange with the supernatural (e.g., Duncan and Schwartz 2014), therefore, the social identity of the sacrificed individuals may be subsumed by the ritual act itself (Fowler 2008). The complexities of symbolically motivated activities associated with funerary rituals, including acts of human sacrifice, may not be fully represented archaeologically (Buikstra and Nystrom 2003). However, incorporating biodistance analysis into ongoing archaeological investigations may illuminate patterns that would not otherwise be apparent.

The underlying assumption is that biodistance analysis is, therefore, more than just a complicated pedigree precisely because it can be used to understand how microevolutionary patterns (e.g., migration, genetic drift) affect populations, while simultaneously incorporating a social perspective that avoids reducing "identity" to a purely taxonomic description (Knudson and Stojanowski 2008). Thus, within this current research, the concept of social identity as interpreted through nonmetric skeletal features and burial contexts, "may reflect only the crudest and most overarching portions that may affect macrolevel decisions and interactions" (Stojanowksi 2005: 418). The act of interpreting the past is a process of cognitive articulation with material residues, and this imposes layers of meaning upon the remains, not unlike the past actors who produced the archaeological deposits (Barrett 1994). Thus, with careful and reflexive consideration it is possible to make inferences about past societies from a suite of skeletal features, but this is only tenable provided there is a solid biological understanding of such features.

Nonmetric Traits

Brief History

Throughout the literature, nonmetric traits have had many different aliases over the years. The terms *quasi-continuous, epigenetic, discrete, dichotomous, minor skeletal variant, nonmetrical,* and *nonmetric* have all been used in a practically interchangeable manner. The reasoning behind the selection for each term reflects methodological and theoretical differences in how these skeletal features may be defined (Saunders and Rainey 2008). The term *nonmetric* is used within this research because it is the most widely used, and it is the most general term for referring to a large group of traits (Saunders and Rainey 2008).

Nonmetric traits are morphological variants of the skeleton that are not measured by means of calipers or a “measuring implement” of some kind (Hauser and DeStefano 1989; Yavormitzky 2002). Nonmetric traits can be recorded on an ordinal scale based on the degree of expression, and the number of degrees of expression may vary between traits (Hauser and DeStefano 1989; Scott and Turner 1991). Nonmetric traits can also be recorded dichotomously as either “present” or “absent” (e.g., Hauser and DeStefano). An individual skull may have, for example, one or more infraorbital foramina (Figure 2.1); a researcher may simply observe, count, and record the number of foramina that occur. Figure 2.1 displays examples of many of the cranial nonmetric traits, and Figure 2.2 displays an example of several of the dental nonmetric traits examined in this study.

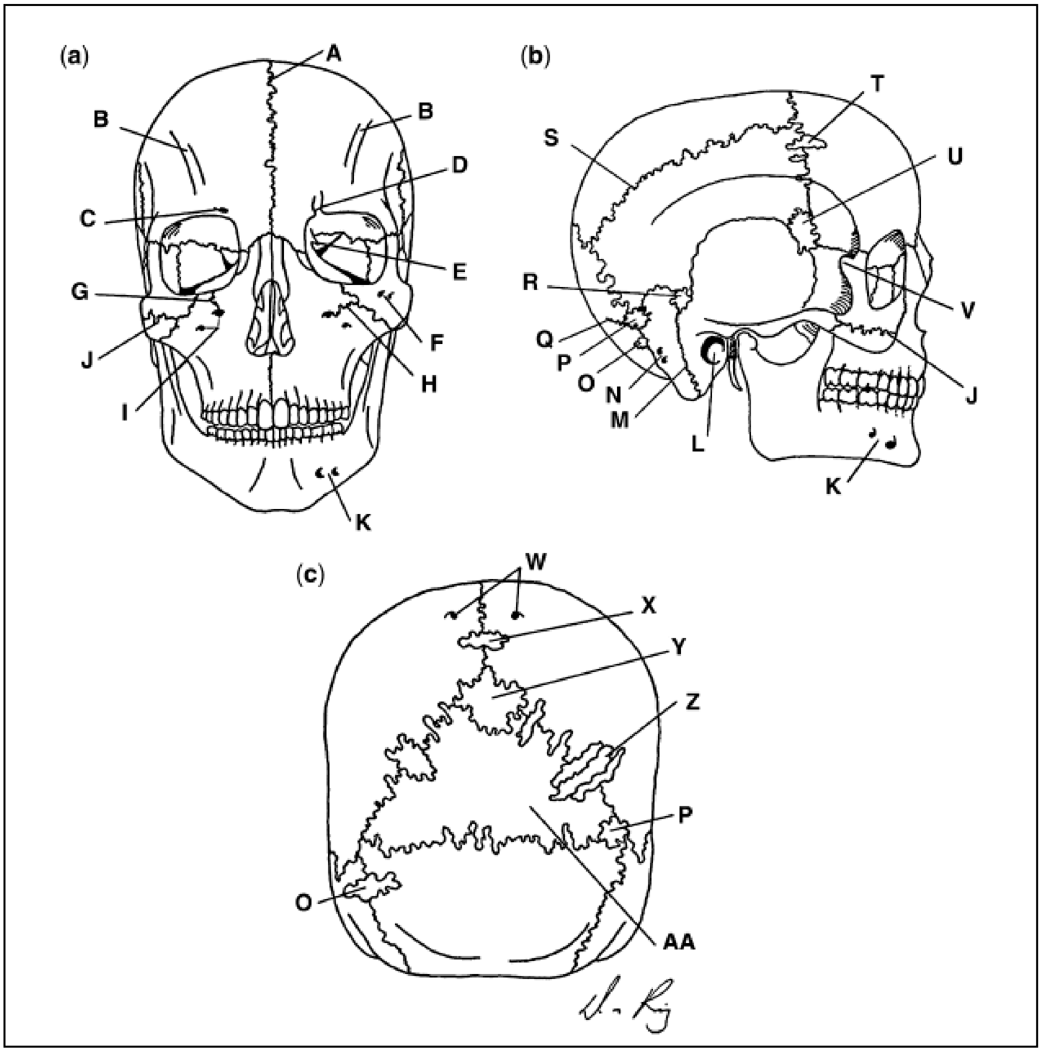

Figure 2.1: Cranial Nonmetric Examples:

a) Anterior view of skull: A. metopism, B. frontal grooves (bilateral), C. supraorbital foramen, D. supraorbital notch, E. trochlear spur, F. zygomatico-facial foramina, G. infraorbital suture medial from infraorbital rim, H. infraorbital suture fromzygomaxillary suture, I. infraorbital foramina, J. Os japonicum (bipartite zygomatic bone) and K. mental foramina (b) Lateral view of skull: J. Os japonicum (bipartite zygomatic bone), K. mental foramina, L. auditory exostosis, M. Squamomastoid suture, N. mastoid foramina, O. occipitomastoid ossicle, P. ossicle at asterion, Q. sutura mendosa, R. parietal notch bone, S. bipartite parietal bone, T. coronal ossicle, U. epipteric bone and V. marginal tubercle **(c)** Posterior view of skull: O. occipitomastoid ossicle, P. ossicle at asterion, W. parietal foramina, X. sagittal ossicle, Y. ossicle at lambda, Z. lambdoid ossicles (wormian bones) and AA. Os inca. (Saunders and Rainey 2008: 534). (Saunders and Rainey 2008: 534).

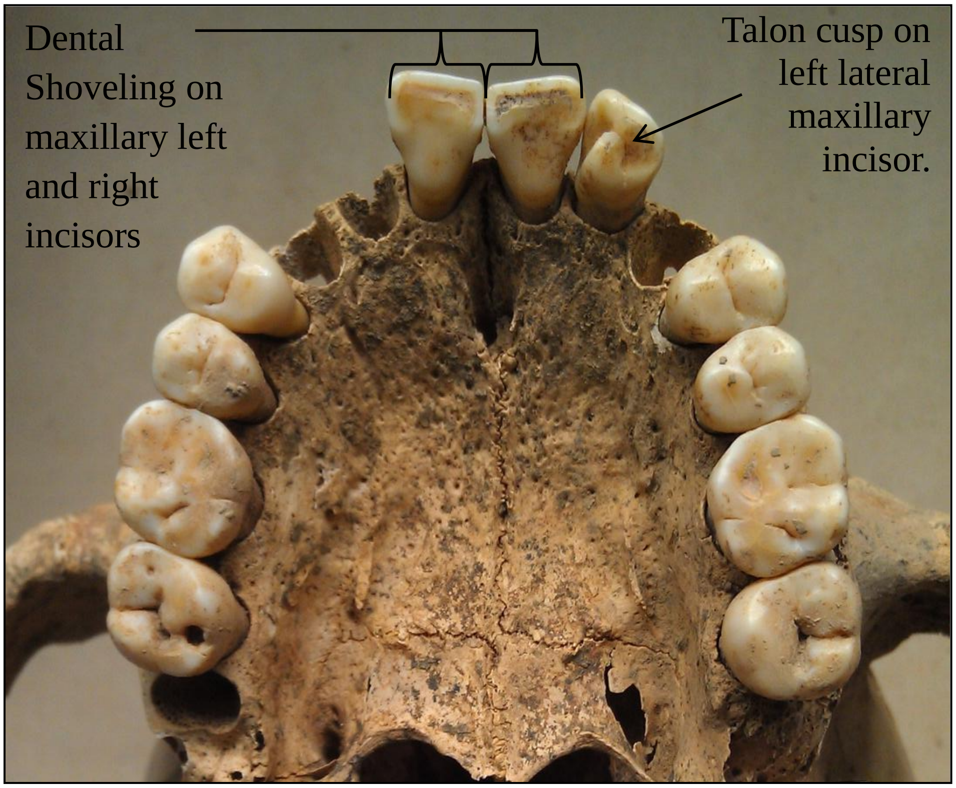

Figure 2.2: Dental Nonmetric Examples:
Maxillary dentition from burial T-TPS F66 Ent 81. Dental shoveling can be seen on the central incisors though there is dental attrition. A large talon cusp can be seen the left lateral incisor.

Contemporary biological distance studies using skeletal nonmetric traits stem from a long history of research using non-human animal data (Grüneberg 1943, 1952; Wright 1934; Cheverud and Buikstra 1981a; 1981b; 1982), studies of disease (e.g., Grüneberg 1963), and population studies of human subjects (e.g., Berry and Berry 1967). Nonmetric traits have also been used to determine ethnic and “racial” affinity (e.g., Rhine 1990; Tyrrell 2000), although not without justifiable contention (Tallbear 2000), sex and age (e.g., Perizonius 1979), and kinship analysis (e.g., Alt and Vach 1995). For centuries nonmetric traits were observed (Kerckring 1670; Le Double 1903; Testut 1889; Blumenbach 1776) but their significance was not fully understood. Some of the earliest non-human animal studies of nonmetric traits used inbred guinea pigs (Wright 1934) and mice (Grüneberg 1943; 1952) to better understand the mechanisms of inheritance of these traits. These studies demonstrated that the phenotypic expression of cranial traits was the result of a confluence of multiple genes rather than simple Mendelian inheritance. The ABO blood group system, for example, follows simple Mendelian principles and is controlled by a single gene with two co-dominant alleles, A and B, and the recessive O allele (Franchini and Liumbruno 2013).

Cheverud and Buikstra (1981a; 1981b; 1982) studied large cranial samples of rhesus macaques with known matrilineal membership to obtain direct estimates of the heritability of several nonmetric cranial traits. Non-human animal studies of nonmetric traits are considered "indirect" evidence when comparisons are then drawn to humans (Prowse and Lovell 1995), more direct evidence has been demonstrated in studies that considered both human DNA and phenotypic skeletal data (e.g., Herrera et al. 2014). Perhaps most influential in the effort to develop a standardized recording scheme for human cranial nonmetric traits was put forward by Berry and Berry (1967). This was followed by an increase in the use of nonmetric traits within physical anthropology (e.g., Ossenberg 1969; Pietrusewsky 1971; Dodo 1974; Gualdi-Russo et al. 1999). Later, Hauser and DeStefano (1989) provided a more comprehensive standardization scheme of cranial nonmetrics, and today recording nonmetric traits is one of the standard procedures within physical anthropology (Buikstra and Ubelaker 1994).

As would be expected, dental nonmetric analysis may also be used as proxies for inferring genetic relationships as teeth demonstrate similar morphological variants within humans (Hughes and Townsend 2013). Some of the pioneering studies into human dental nonmetric analysis investigated the genetic aspects of these traits by building pedigrees of living families (Kraus 1951). Among the first researchers to suggest that dental traits were non-Mendelian in nature was Sofaer (1970), and he was also among the first to examine these traits in non-human animals (Sofaer 1969). Biodistance studies using dental nonmetric traits have been applied in concert with linguistic and genetic evidence (Greenberg et al. 1986) to reconstruct large migration events, like the peopling of the Americas (Turner 1969; 1971; 1983a; 1983b; 1984; 1985). The first attempt to standardize dental scoring procedures was undertaken by Dahlberg (1956), and this initial effort was later expanded upon by Turner et al. (1991), which culminated in the development of the Arizona State University (ASU) Dental Anthropology System. The ASU dental system has become the primary scoring method for dental nonmetrics in Anthropology (Turner 2013).

Expression and Inheritance

It has long been known that there are many genes involved in the expression of both cranial and dental nonmetric traits, (Grüneberg 1963; Sjøvold 1973), yet no specific genes have been identified (Saunders and Rainey 2008). There are internal (genetic) and external (environmental) factors involved in nonmetric trait expression (Falconer 1960; Fraser 1976; Hauser and DeStefano 1989). This section describes the theoretical model developed in quantitative genetics (Falconer 1960; 1967) used to understand how nonmetric traits are inherited and expressed.

Nonmetric traits are polygenic discontinuous phenotypic variants, where the physical expression or observable trait is governed by many genes, and the inheritance patterns are, as previously mentioned, non-Mendelian in nature (Sofaer 1970). Some nonmetric traits are considered discontinuous, or “quasi-continuous”, because they are expressed in “set” categories (Grüneberg 1952), analogous to blood groups. Though not governed by simple Mendelian rules of inheritance, all nonmetric skeletal traits are assumed to have an underlying genetic component (Pietrusewsky and Douglas 1992).

Evidence for significant genetic control over nonmetric traits has been found in heritability estimation (Self and Leamy 1978; Sjøvold 1977; 1984), and most traits exhibit a relatively low level of heritability. The term “heritability” is perhaps counterintuitive, and should be explained. A trait with low heritability is difficult to alter, regardless of the phenotype manifested in the parents of the individual processing the trait. Conversely, traits with high heritabilities are more susceptible to environmental influence and manipulation (Scott and Turner 1997). Examples of environmental factors include maternal age and parity, both of which may play a role in trait expression (Pietrusewsky and Douglas 1992).

Other studies have demonstrated that groups of related individuals will exhibit a high instance of certain traits (e.g., Suzuki and Sakai 1960; Berry 1963; Berry and Berry 1967; Molto 1983; Ricuat et al. 2010). Moreover, there have been numerous studies of prehistoric/precolonial populations, contemporary populations, and studies of twins using morphological data that have produced similar results when compared to DNA evidence or known genealogical information (e.g., Potter et al. 1976; Scott 1972; Hanihara et al. 1974; Zoubov and Nikityuk 1978; Kaul et al. 1985; Corruccini et al. 1986; Scott and Turner 1997; Ricaut et al. 2010; Hughes and Townsend 2013; Herrera et al. 2014). These studies corroborate the concordance between phenotypic and genotypic data.

Wright (1934) and Grüneberg (1943; 1952) proposed that the heritability patterns of nonmetric traits are analogous to the threshold model of multifactorial disease liability within a population; this notion was later echoed by Falconer (1960). Multifactorial refers to the phenotypic expression being governed by many genes and perhaps several environmental factors. Falconer (1965) defines liability as a measurement of variation that is normally distributed, "this gives a unit for the expression of the degree of liability, the unit being the standard deviation" (Falconer 1965: 52-53). The term "threshold" is thus defined as, "the point on the scale of liability above which all individuals are affected and below which none are affected" (Falconer 1965: 53). Figure 2.3 is an illustration of the liability-threshold model; in population A, five percent of individuals are expressing the trait(s); in population B, 20 percent of the individuals are exhibiting the trait(s). Two important features of this model are illustrated in Figure 2.3. First, the threshold for trait expression can vary between populations based on a confluence of environmental and genetic factors (Falconer 1960; Fraser 1976). Second, the liability for trait expression is normally distributed within populations (Falconer 1965). Though the precise genetics behind nonmetric traits remains unknown, the application of the threshold-liability model has provided a theoretical basis from which all nonmetric biodistance studies operate. While both cranial and dental nonmetric traits are understood through the liability-threshold model, there are important differences between these morphological variants regarding their biology, and their treatment within the literature.

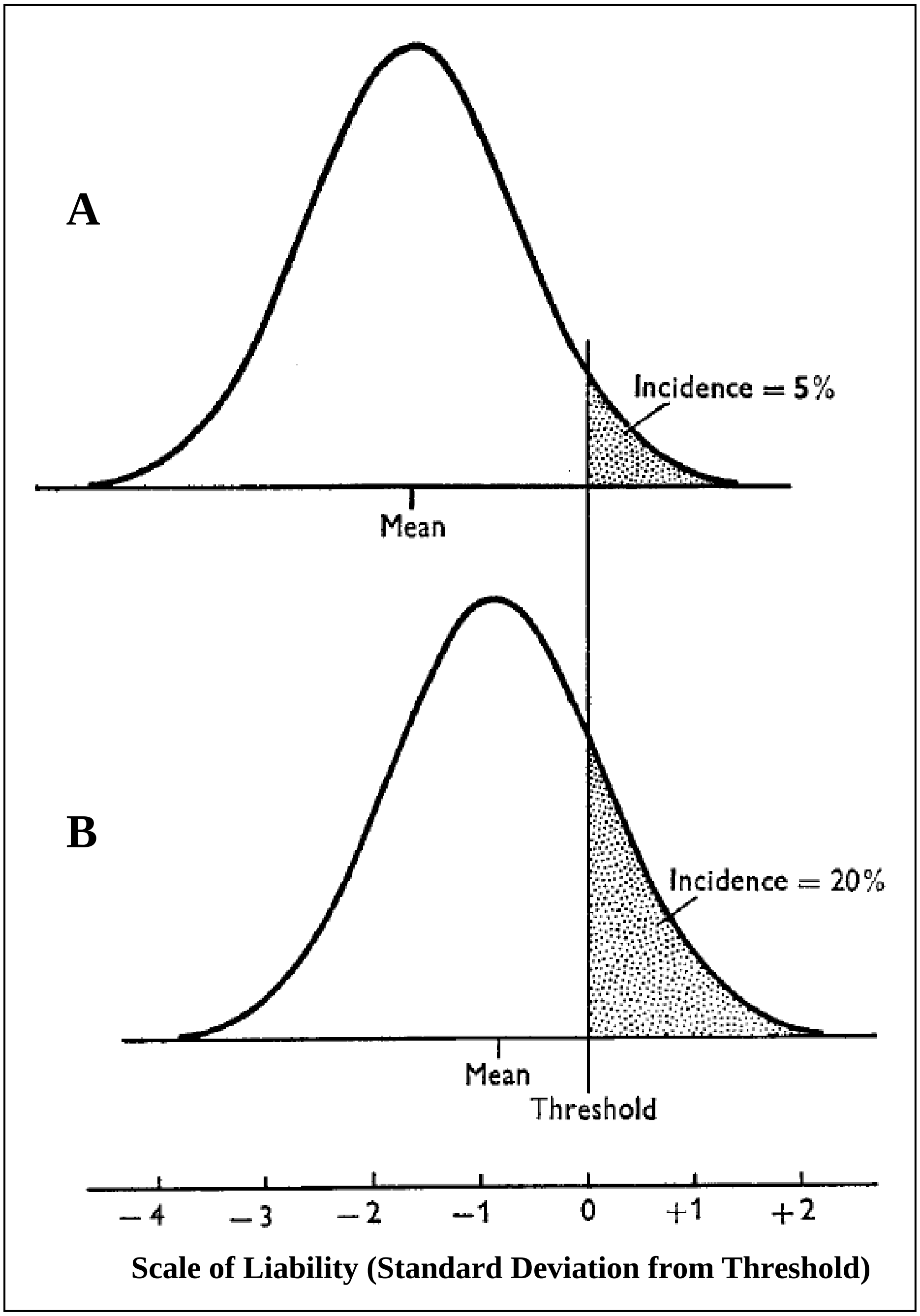

Figure 2.3: Liability-Threshold Model:
A and B represent two separate populations in which the threshold for the expression of a hypothetical trait is different. The shaded area to the right of the threshold represents the incidence of expression (adapted from Falconer 1965: 53).

Cranial vs. Dental Trait Observation

Researchers have used metric data (e.g., Pietrusewsky 2008), nonmetric data (e.g., Scott 1972), molecular data (e.g., Bowcock et al. 1991), or some combination of these (e.g., Ricaut et al. 2010; Herrera et al. 2014) to ascertain the degree biological relatedness in and between human populations. In nonmetric trait studies, researchers will often exclusively use cranial nonmetrics (e.g., Hanihara and Ishida 2001a; 2001b; 2001c; 2001d; Sutter and Mertz 2004; Jahnke 2009) or dental nonmetrics (e.g., Sutter 1997; Corruccini and Shimada 2002; Sutter and Verano 2007; Aubry 2009; Cook and Aubry 2014). Both cranial and dental traits are thought to be largely independent of natural selection and are not dramatically influenced by sex or age, and intertrait correlations are generally low (Turner et al. 1991; Saunders and Rainey 2008). Yet, cranial traits are thought to be more susceptible to environmental/cultural influences, such as cranial modification (Saunders and Rainey 2008; Del Papa and Perez 2007). It is generally accepted that dental traits more reliably reflect genetic relationships than cranial traits because they are believed to be under stronger genetic control (Tryell 2000; Khudaverdyan 2014). Moormann et al. (2013), however, found that molar cusp traits, such as Carabelli's trait and hypocone, develop in an interrelated manner, challenging the assumed independence of these traits. This revelation makes testing for intertrait correlations necessary within biodistance studies.

Cranial modification, or deformation, was a common practice at ancient Túcume, considering almost all individuals examined exhibited some degree of vault modification. Researchers have found that cranial modification has some influence on the frequency of expression of certain cranial nonmetric traits, specifically wormian or extra-sutural bones

(Ossenberg 1970; Konigsberg et al. 1993; O'Loughlin, 2004; Rhode and Arriaza 2006; Del Papa and Perez 2007). As described by Konigsberg et al. (1993: 45), the degree of influence that cranial modification may have on the expression of nonmetric traits is primarily based on two factors. First, traits that are established prenatally cannot be altered postnatally by cranial modification (e.g., accessory infra orbital foramen, divided hypocanal, postcondylar canal, accessor lesser palatine foramen). Second, the degree to which cranial modification affects nonmetric trait frequencies appears to be related to the proximity of the trait to the area of altered growth. Konigsberg et al. (1993) concludes that while cranial modification affects the frequency of particular nonmetric traits, cranial metrics are more drastically altered by this process. O'Loughlin (2004:154) argues that "the data show that posteriorly placed wormian bones appear in greater numbers in deformed crania. The data cannot answer whether cranial deformation affects the initial presence or absence of these ossicles". The degree to which cranial modification actually influences the expression of cranial nonmetric traits is not fully understood because it is difficult to find appropriate samples to investigate these relationships (Wilczak and Ousley 2009; Van Arsdale and Clark 2012).

For the purposes of this biodistance study, it is assumed that using cranial nonmetric traits is relatively unproblematic even though most of the individuals examined in this study exhibited cranial modification. Most of the nonmetric traits found by other researchers to be influenced by cranial modification (e.g., Verano 1987; Konigsberg et al. 1993; O'Loughlin 2004; Perez 2007) were excluded for other reasons (e.g., intertrait correlations, missing values because traits were unobservable). Additionally, using cranial and dental nonmetric traits within this study may aid in mitigating the influence that cranial modification may have on the biodistance measure. Dental morphology is not directly altered by cranial modification, and using a large number of nonmetric traits has been found to decrease the impact cranial modification has on skewing biodistance measures (Del Papa and Perez 2007).

Skeletal material from archaeological contexts is often deteriorated or damaged, making it impossible to record certain skeletal features. Incorporating both dental and cranial nonmetric traits in a single study will increase the number of traits, potentially offering a more comprehensive sample of the variation being studied. Prowse and Lovell (1996) demonstrated that there is concordance between cranial and dental nonmetric traits when predicting biological affinity. Ricaut et al. (2010) demonstrated that an approach that incorporates cranial, mandibular, dental, and infracranial traits can be used as a means of discerning genetic kinship within a single site. Using morphological variables from one restricted part of the body, such as dental nonmetrics, may perhaps not reveal overall trends in a particular deme (a group interbreeding individuals in a given locality) (Mayr 1963; Perez 2007), but may reflect specific selective pressures on a single body system (Sofaer et al. 1986). Herrera et al. (2014:334) argue that while skeletal data may never display a perfect correlation with DNA due to environmental influences, “combining data types leads to a richer knowledge of biological affinity”, primarily because such data sets have been demonstrated to be complementary.

The Intrasite Approach

The level of analysis (e.g., intrasite, intraregional) within biodistance research is selected by nature of the questions and goals of a particular study. As such, the level of analysis imposed on a sample population will undoubtedly influence the reconstruction and interpretation of social identity and organization in the past (Nystrom 2009). In the past few decades there has been a shift in trends within biodistance studies from an interregional or continental focus to an intrasite and intracemetery approach (e.g., Pietrusewsky and Douglas 1992; Alt and Vach 1995; Howell and Kintigh 1996; Spence 1996; Stojanowski and Schillaci 2006; Ricaut et al. 2010; Piloud and Larsen 2011). In general, the intrasite approach has four broad foci or interest: postmarital residence, kinship analysis, temporal microchronology, and analyses of statistical variation (Stojanowski 2003). One assumption these four categories all rely on is that the skeletal assemblages being examined are representative of the past population (Stojanowksi 2003). Differences in nonmetric trait frequencies and biodistance measures between males and females have been used to reconstruct postmarital residence practices within archaeological sites (e.g., Lane and Sublett 1972; Spence 1974; Birkby 1982; Tomczak and Powell 2003). Other researchers at the intrasite level have made inferences about other aspects of social organization, such as political status (Howell and Kintigh 1996), from biodistance data.

Examining kinship as the basis of social organization in the past has also been a topic of interest (e.g., Piloud and Larsen 2011). By incorporating burial locations, and often incorporating traits that occur at a low frequency (between 0-5%) (e.g., Corruccini and Shimada 2002; Ricaut 2010; Paul et al. 2011; Piloud and Larsen 2011) researchers may be able to interpret the role of biological kinship in structuring social organization and/or social status. The location of burials and their proximity to each other is typically a deliberate, highly symbolic act, which reflects the underlying systems of values of the society in question (Hodder 1982; Pearson 1999; Hendon 2000). The combination of both burial location and biological kinship data is highly relevant in the endeavor to understand membership in ceremonial groups, postmarital residence practices, and other aspects of social organization (McClenad 2003; Goldstein 2006).

Importantly, the intrasite and intracemetery approach does not fall prey to recent critiques of biodistance analysis (e.g., Armelagos and Van Gerven 2003) as a fundamentally typological enterprise (Stojanowski and Schillaci 2006; Knudson and Stojanowksi 2008). The intrasite focus is not aimed at reducing overall variation into small a number of essential features, but emphasizes the central tendencies within the variation observed (Knudson and Stojanowksi 2008). There are multiple factors, however, that may affect the level of intrasite variability such as the number of biological/family lineages, variation in group size, overall population size, and migration patterns (Raemsch 1995; Stojanowkis 2003) which may include kin and clan structured migration (Fix 1999; 2004; 2012; Williams-Blangero 1987; 1989a; 1989b). The regional context of any site being investigated must also be taken into consideration partly because geography influences patterns in human variation, by creating physical barriers and funneling people into specific areas (Sutter 2005; O'Rourke and Enk 2012).

Andean Biodistance

Archaeological evidence demonstrates a long history of occupation within the Andean region, dating to around 10,000-15,000 years ago (Lynch 1990; Moseley 2001; Bryan and Gruhn 2003; Dillehay 2008; Pearsall 2008). Biodistance analysis has suggested that initial peopling of South America occurred in several waves (Sutter 2005), and from this, later civilizations achieved state level complexity including large urban cities (Moseley 1975). Throughout the Andean region, researchers have investigated topics such as migration, colonization, ethnicity, ethnogenesis, and ritual practices as reflected by biological variation (e.g., Dricot 1977; Rothhammer et al. 1984; Verano 1987; Guillen 1992; Kato et al. 1995; Blom et al. 1998; Lozada and Buikstra 2005; Blom 2005; Sutter and Verano 2007; Sutter 2005; Kurin and Choque 2012).

Sutter and Mertz (2004), for example, investigated social interaction between groups located in Peruvian coastal valleys and neighboring groups in highland areas. They concluded that overtime gene flow between these geographically separated groups increased. Similarly, Lozada and Buikstra (2005) used biodistance analysis as one line of evidence to examine ethnic identity based on different labor activities (farming and fishing) within the Osmore Valley. The regional topography of the Peruvian coast includes many valleys and highland areas, which may have acted as ecological boundaries for past peoples, and this most certainly played a role in how neighboring groups defined themselves and each other (Mantha 2009). The social and biological variation exhibited in the Andean region, however, is not simply the product of geographic happenstance. Yet, the distribution of resources across the landscape (e.g., fertile river valleys) had a tangible effect on the patterns seen in the archaeological record.

At the Moche site of Huaca de la Luna, located in northern Peru, Sutter and Verano (2007) used biological distance analysis to determine if sacrificed individuals were local or non-local warriors. They concluded that the sacrificed warriors were of non-local origin, suggesting that the Moche captured warriors from neighboring groups in the process of expanding their territory. However, isotopic evidence (Toyne et al. 2014) indicates that the sacrificed burials did not consist entirely of nonlocal individuals, highlighting perhaps some of the limitations inherent within biodistance studies. Isotopic research has also been conducted at Túcume and has yielded similar results regarding the disparate origins of the individuals interred within the site (discussed below)

At the intracemetery level, Corruccini and Shimada (2002) conducted a biodistance study using dental nonmetrics at the site of Huaca Loro (~AD 1000). They found that biological kinship played a key role in the spatial distribution of burials within and between tombs. They conclude that biological kinship was an important factor in structuring social status at the site. All of these Andean examples illustrate several different levels of analysis that have been explored with biodistance research. Conducting biodistance research at Túcume contributes to the ongoing effort to understand the Andean past by providing an analysis of the intrasite variation at this significant regional center. This research provides not only an analysis of the overall biological variation, but also offers a glimpse of the past social processes operating at the site.

The Archaeological Complex at Túcume: History and Context

The North Coast

There were several cultural periods in the north coast region well before Túcume became a heavily developed, regional center. The Lambayeque (or Middle Sicán) (ca AD 1000-1350) culture initially constructed Túcume, and the Chimú culture (ca. AD 1350 - 1470) later had influence over the site (Sandweiss 1995; Shimada et al. 2004; Dulanto 2008). The center, or quasi-capital, of the Lambayeque culture was first Batán Grande (Shimada 1990), and then later Túcume (Sandweiss 1995), both of which are located in the La Leche-Lambayeque river valleys (Figure 2.4). The Chimú (Keatinge and Conrad 1983; Tschauner 2001) (and later the Inca) (Bonavia 2000; Shimada 1990; Covey 2008; 2014) would move new administrators into conquered areas, building new architectural features and modifying existing ones (Sandweiss 1995; Bawden 1996), while simultaneously retaining local elites as part of a system of "shared control" (Moore and Mackey 2008: 796). The Inca established control over the north coast around AD 1470, after a fierce military campaign against the Chimú (Netherly 1988; Rostoworowski de Diez Canseco 1990). Once the Inca gained control over much of the north coast they made Túcume an important regional center within their empire (Sandweiss 1995). These regime changes potentially increased the level of heterogeneity in the deme through an influx of people from outside the region.

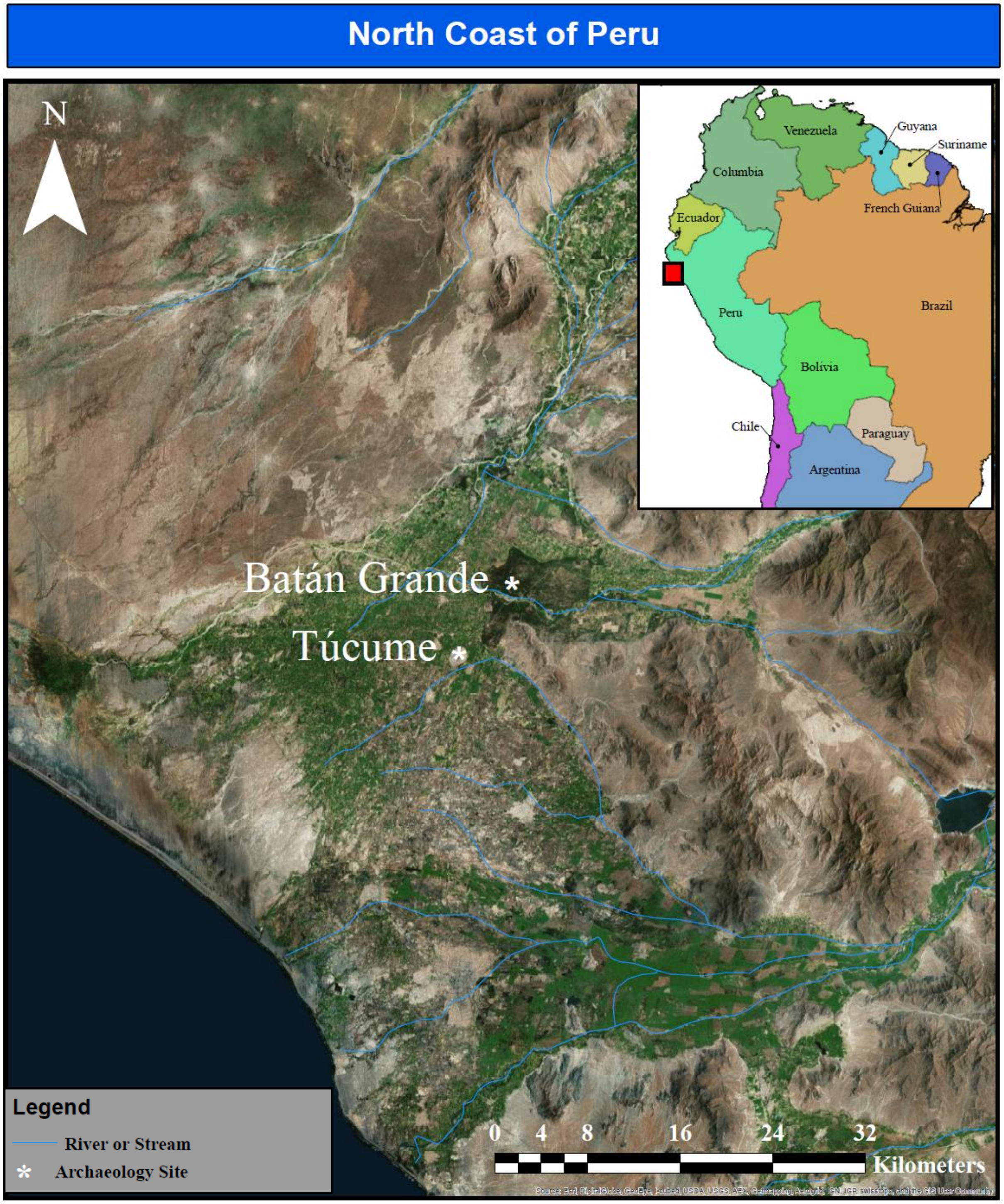

Figure 2.4: Map of Peruvian North Coast:
Image created from information in Shimada (1981) and Bing® satellite imagery; data provided in ArcGIS® software by Esri.

The Site

The archaeological complex of Túcume, also known as El Purgatorio (Purgatory), is located approximately 30 kilometers from the Pacific Ocean on the north coast of Perú (Heyerdahl et al. 1995). Túcume contains the largest concentration of platform mounds in Perú, most of which are constructed on the north and northwest base of a large rock outcropping, known as Cerro la Raya (Mountain of the Ray Fish) (Sandweiss 1995). The largest of these, Huaca Larga, is approximately 700 meters long (north to south) and up to 280 meters at its widest (Figure 2.5). The monumental structures at Túcume were built and continuously modified over a 500 year period (Narváez Vargas 1995b). Túcume was first described by European colonizers in the 16th century by Cieza de Leon, (1984 [1553]). At this time the site was largely abandoned and in ruins. Another historical account comes from Francisco de Xérez, the secretary to the conquistador Don Francisco Pizarro. While Xérez does not specifically mention Túcume, traveling some 40 kilometers north of Túcume, he describes the practice of human sacrifice which apparently involved willing participants from the local community (Xérez 1872 [1534]). The archaeological and ethnohistoric evidence suggests that the sacrificed individuals found at Túcume were from the local community (Toyne 2008; 2011; 2015a; 2015b). Using oxygen isotope composition and strontium isotope ratios, Hewitt (2013) examined three of the burial locations within Túcume: The Temple of the Sacred Stone, Huaca Larga, and South Cemetery. The isotopic evidence combined with the archaeological data indicated that these three burial locations represented three distinct social groups, based primarily on the level of mobility within the region. Hewitt (2013) concluded that the sacrificed individuals from the Temple of the Sacred Stone may have contained highly mobile foreigners. The Huaca Larga sample included elites and their entourage, many of which are thought to have been sacrificed as well (Toyne 2002), exhibited a low to mid-level mobility. These results add to previous interpretations concerning community identity within Túcume (Hewitt 2013), specifically in regard to the sacrificed individuals from the Temple of the Sacred Stone (Toyne 2008; 2011; 2015a; 2015b). The biodistance data offers yet another line of evidence from which interpretations about the identity of the individuals interred at Túcume can be made.

It is thought that periods of climatic change in the region often coincided with an increase in ritual offerings, including human sacrifice, which perhaps culminated in site burning and abandonment (Shimada et al. 1991). Archaeological excavations at the Túcume suggest that at the time of its occupation, administrative power was held by a small minority that held both religious and political authority within the community (Narváez Vargas 1995b). Using biodistance analysis may reveal biological patterns that reflect how these power structures were maintained within the community and provides new information about the history of ancient Túcume in terms of the conflicting interpretations regarding the identity of the sacrificed people within the community. In general, there is a high degree of variability in the burial practices at the site, with a variety of burial positions and grave inclusions. Burials have been found in residential areas, in simple burial pits within designated cemeteries, elaborate shaft tombs for elites, and sacrificed burials (Narváez Vargas 1995a). Due to the arid environment found on the northern coast of Peru, the skeletal remains are generally well preserved, making biodistance analysis a viable research tool to investigate the pre-history of Túcume.

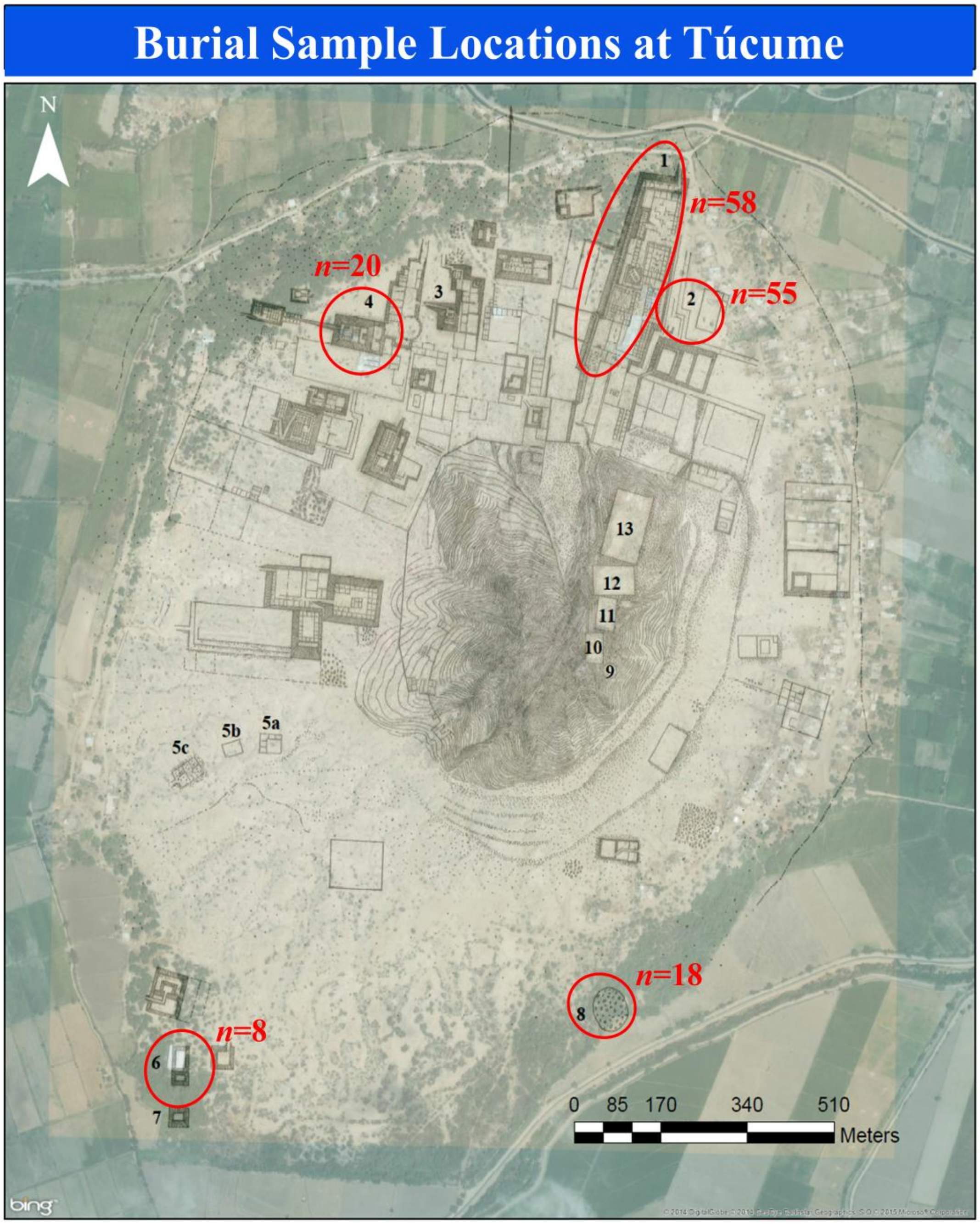

Figure 2.5: Map of the Archaeological Complex at Túcume and Burial Sample Locations: 1. Huaca Larga; 2. Temple of the Sacred Stone; 3. Huaca Las Estacas; 4. Huaca I; 5a. Sector V Rectangular Compound; 5b. Sector V West Mound; 5c. Sector V Funerary Platform; 6. Huaca Las Balsas; 7. Huaca Facho; 8. South Cemetery; 9.White Cave; 10. East Spur Subsector I; 11. East Spur Subsector II; 12. East Spur Subsector III; 13. East Spur Subsector IV. Adapted from Sandweiss (1995: 78) and Bing® satellite imagery provided in ArchGIS® software.

Biodistance at Túcume

Examining the nonmetric variation at the site offers a nuanced glimpse of how patterns of mate exchange reflect overarching social practices at the site. Túcume contains a variety of burial practices and it was an urban center of power which likely had people who came from different cultural traditions within the region. Understanding how the confluence of regional cultures within an urban environment has influenced the biological variation at the site is an important endeavor in the illumination of social structure in the Andean past.

Evolutionarily speaking, the relatively narrow time frame being examined in this study (approximately 500 years) ensures that any drastic divergence in the biological variation observed is the result of a migratory event rather than an *in situ* genetic change (Wright 1943; Konigsberg 1990; Fix 1999; 2004). Ancient population centers would be expected to have very little genetic variation if all occupants are locally born and buried (Konigsberg 1990). However, as urban centers like Túcume began to grow, migration and social upheaval would have likely increased gene flow. The Chimú likely introduced new genetic variation, but perhaps not so dissimilar from the existing deme, as the Lambayeque/Sicán and the Chimú shared similar cultural origins and were in close geographic proximity to Túcume (Shimada et al. 2004; Moore and Mackey 2008). The Inca conquest, however, often involved the movement of large communities to distant areas as a means of establishing control over the conquered (Covey 2008). Many of the elite individuals at Túcume were likely local lords, due the system of shared control often employed by the Inca. However, a group of Incan female elites have been identified at the site (Toyne 2002), and thus it might be expected that these women will exhibit different levels of variability compared to the other individuals at the site. The archaeological evidence clearly indicates that the cultural atmosphere at Túcume was impacted by these conquest events, in the form of architectural modifications and burial inclusions (Narváez Vargas 1995b; Narváez Vargas and Delgado Elias 2013).

Summary

This chapter has provided background information on several key concepts. Biodistance is a bioarchaeological endeavor in that it uses skeletal remains to reconstruct social processes in the past. Extrapolating human social identity from a suite of nonmetric skeletal features and archaeological information requires knowledge of the social theory of identity. Moreover, both cranial and dental nonmetric traits have been used in biodistance studies, and an overview of the underlying biology of these features was provided in this chapter. Biodistance analysis has been applied in a variety of contexts within the Andean region. Archaeological research at Túcume has demonstrated that the site was an important center of interaction within the north coast region. An intrasite biodistance analysis of the skeletal collection at Túcume provides a window into past social organization as reflected in the biological variation.

CHAPTER 3: MATERIALS AND METHODS

Introduction

This chapter provides an overview of the archaeological sample examined and the methodological approach adopted for this study. This chapter describes the sample including sex and age estimates, the laboratory methods, nonmetric trait scoring procedures and the dichotomization scheme; lastly, the statistical approach is described in detail.

Sample

At Túcume, several decades of research and excavation have recovered at least 414 human burials, of which 161 crania of which were examined for this research. Every adult with a complete or mostly complete skull was examined, and 17 subadults were also examined, for a total of 85 males, 58 females, and 18 of indeterminate sex (Table 3.1). Incorperating subadults who are at least 10 years of age is not problematic because cranial nonmetric traits are stable within this age range (e.g., Ossenberg 1969; Wood 2012), and dental nonmetric traits are fully developed at this age. The burials examined come from five different locations within the site: Huaca Las Balsas and the Southwest Burials, Huaca Larga, Huaca I, the South Cemetery, and the Temple of the Sacred Stone (Figure 2.5). The burials from Huaca Las Balsas, Huaca Larga, and Huaca I seem to contain individuals that are part of the elite social structure. Huaca Larga, for example, 19 females (possibley sacrificed), and 3 males with elaborate offerings. The 19 females were found with artifacts such as spindles, spindle whorls, needles, and balls of thread that suggesting that they were *acllas*, or elite Inca weaving women (Narváez Vargas 1995b; Toyne 2002; Hewitt et al. 2008). In the South Cemetery, however, the majority of the individuals interred there do not appear to be part of the sites' upper elite (Narváez Vargas 1995a); 18 of these individuals were examined in this research. The sacrificed burials from the Temple of the Sacred Stone represent a unique context within this study. Almost all of the 116 individuals from the Temple of the Sacred Stone are adult males, and because it is clear they were deliberately put to death in a ritualistic fashion these individuals are distinct from the other burials at the site (Toyne 2011; 2015a; 2015b). Within this thesis research individuals within the Temple of the Sacred Stone were examined and compared to the other individuals within the sample. Table 3.1 provides the general location of the burials within the site and includes the sample sizes from each location. The burials being considered in this study are from three distinct cultural occupations or periods, the Lambayeque Period (or Middle Sicán) (ca. AD 1000-1350), the Chimú Phase (ca. AD 1350-1470), and the Inca Phase (ca. AD 1470-1532) (Narváez Vargas 1995b). However, the chronological information for the burials at the site is not fully understood. Individuals that have been assigned to a particular chronological period are listed in Appendix A, along with the age, sex, and burial location information for the total sample examined found in Table 3.1.

Table 3.1: Sample Summary of Sex and Age by Location.

Location	Sex			Total	Age			Total
	Females	*Males*	*Indeterminate*		*Adults*	*Subadults*	*Indeterminate*	
Huaca Las Balsas & South West Burials	4	3	1	8	8	0	0	8
Huaca Larga	32	14	12	58	46	10	2	58
Huaca I	11	6	3	20	15	4	1	20
South Cemetery	9	9	0	18	17	0	1	18
Temple of the Sacred Stone	0	53	2	55	52	3	0	55
Context Unknown	2	0	0	2	2	0	0	2
Total	58	85	18	**161**	140	17	4	**161**

In this study, only the cranial elements and teeth were examined, as time did not permit a full examination of all skeleton elements present for each individual. Sex and age estimates were based on the standardized parameters found in Buikstra and Ubelaker (1994), focusing only on the features of the skull. All individuals examined in this study had been previously been documented by Dr. J. M. Toyne, including the estimation of sex and age. Throughout the data recording process, when ambiguities in sex and age estimates were encountered, the previously documented sex and age estimates were referenced. Age was estimated into five broad categories based on the ranges from Buikstra and Ubelaker (1994): old adult (>50 years), middle aged adult (35-50 years), young adult (20-34 yeas), juvenile or adolescent (<20 years), and indeterminate age. Sex estimation followed a similar scheme: male, possible male, female, possible female, and indeterminate sex. In the final analysis, all “possible males” individuals were included in the “male”, and all “possible females” individuals were consolidated into the “female” category for statistical purposes.

Laboratory Methods

The skeletal collection is housed in the Museo de Sito Túcume, adjacent to the site itself (Figure 3.1). Using original data recording sheets (Appendices A and B), burial identification codes, sex and age estimates, and nonmetric traits were recorded. With traits that occur bilaterally, both the left and right sides were recorded. The recording sheets also contain sections for comments on the state of the bone/tooth being examined. In Figure 2.2, for example, several of the teeth exhibit dental attrition. If cranial elements or teeth were damaged or not present this was documented. When examining the dentition, the degree of dental attrition and the presence/absence of dental caries were also documented.

Several resources were consistently referenced throughout the data recording process. Buikstra and Ubelaker (1994) were referenced for sex and age estimation; Berry and Berry (1967), Ossenberg (1969), and Hauser and DeStefano (1989) for cranial nonmetric traits; and Turner et al. (1991) and the associated plaques for dental nonmetric traits. Several tools were used in the process of recording traits including a small flash light, tooth brush, various paint brushes, and small wooden dowels. The brushes and wooden dowels were used to remove small amounts of dirt when traits were obscured. The flashlight was used to illuminate features that were difficult to see, such as osseous bridges inside foramen, otherwise the natural light was sufficient (Figures 3.1, 3.2).

Figure 3.1: Photograph From Inside the Museum of Túcume Collection Area: Boxes contain artifacts and skeletal remains; photo demonstrates natrual light in the museum.

Figure 3.2: Workstation Illuminated Natural and Artificial Light: Cranium and mandible of an individual examined in this study; notebooks, reference books, and dental plaques aslo visible.

Nonmetric Trait Selection and Recording Procedures

By examining the trait lists used by other researchers (e.g., Rothammer et al. 1984; Verano 1987; Sutter 1997; Corrucini and Shimada 2002; Sutter and Cortez 2005; Sutter and Mertz 2004; Sutter and Verano 2007; Toyne 2008; Jahnke 2009; Bollini et al. 2009), I developed a extensive list of traits and recorded them, consistently referencing standardized recording schemes (Berry and Berry 1967; Ossenberg 1969; Hauser and DeStefano 1989; Turner et al. 1991; Buikstra and Ubelaker 1994).

A total of 123 traits (41 cranial and 82 dental) were examined in this study (Appendix C). Six of the cranial traits (metopic suture, bregmatic bone, os incae, ossicle at lambda, sagittal ossicle, precondylar tubercle) occurred in midline and the other 35 cranial traits occurred bilaterally. Of the dental traits observed in this study, seven were root traits, and the other 75 dental traits are found in the enamel and crown morphology. In several cases teeth were glued into their sockets or could not be removed from the sockets making root traits, such as mandibular molar root number, unobservable.

In both cranial and dental nonmetric biodistance studies the standard approach is to record as many traits as possible, and then exclude traits that are not useful in discriminating between the groups being studied (Irish 2010). For example, if a trait is observed in every individual it will not be useful in discriminating between groups of individuals; it would be analogous to using the presence of orbital sockets to discriminate between groups. Similarly, if a trait is not observed in any of the individuals, it will also not be useful in biodistance analysis. Using a large number of traits also mitigates potential bias that may be introduced by selecting a small number of traits (Harris and Sjøvold 2004).

Figure 3.3 provides an example of several cranial nonmetric traits examined in this study, and Figure 3.4 provides examples of dental nonmetric traits. Many of the cranial traits examined in this study were wormian bones, or extra sutural ossicles. When lambdoid ossicles were observed, for example, the side on which it occurred was also recorded. Figure 3.3 depicts an individual with lambdoid ossicles on the right side, and this bilateral asymmetry would have been documented in this study. However, following the “individual count” method (discussed below), the lambdoid ossicle trait would be recorded as simply “present”, regardless of the side on which it appeared.

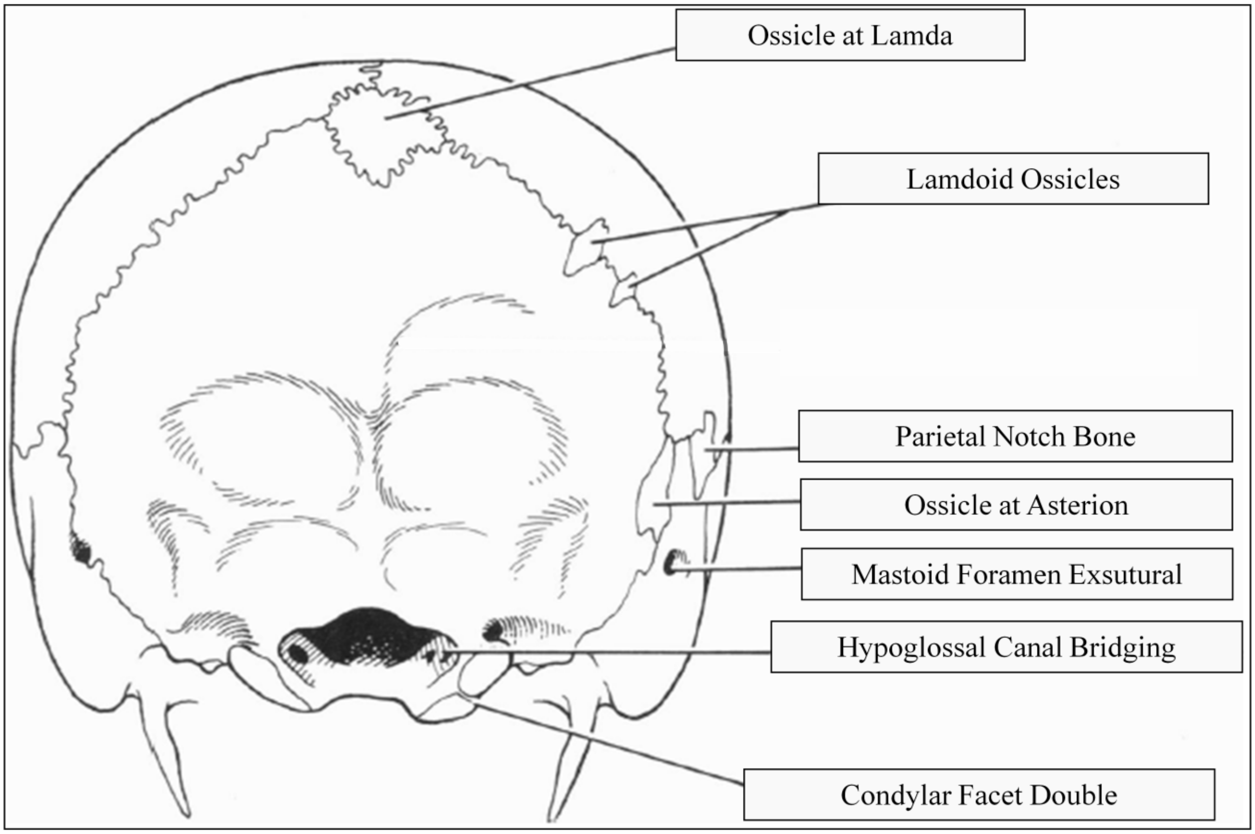

Figure 3.3: Posterior View of the Cranium and Seven Cranial Nonmetric Traits: Adapted from Berry and Berry (1967: 364).

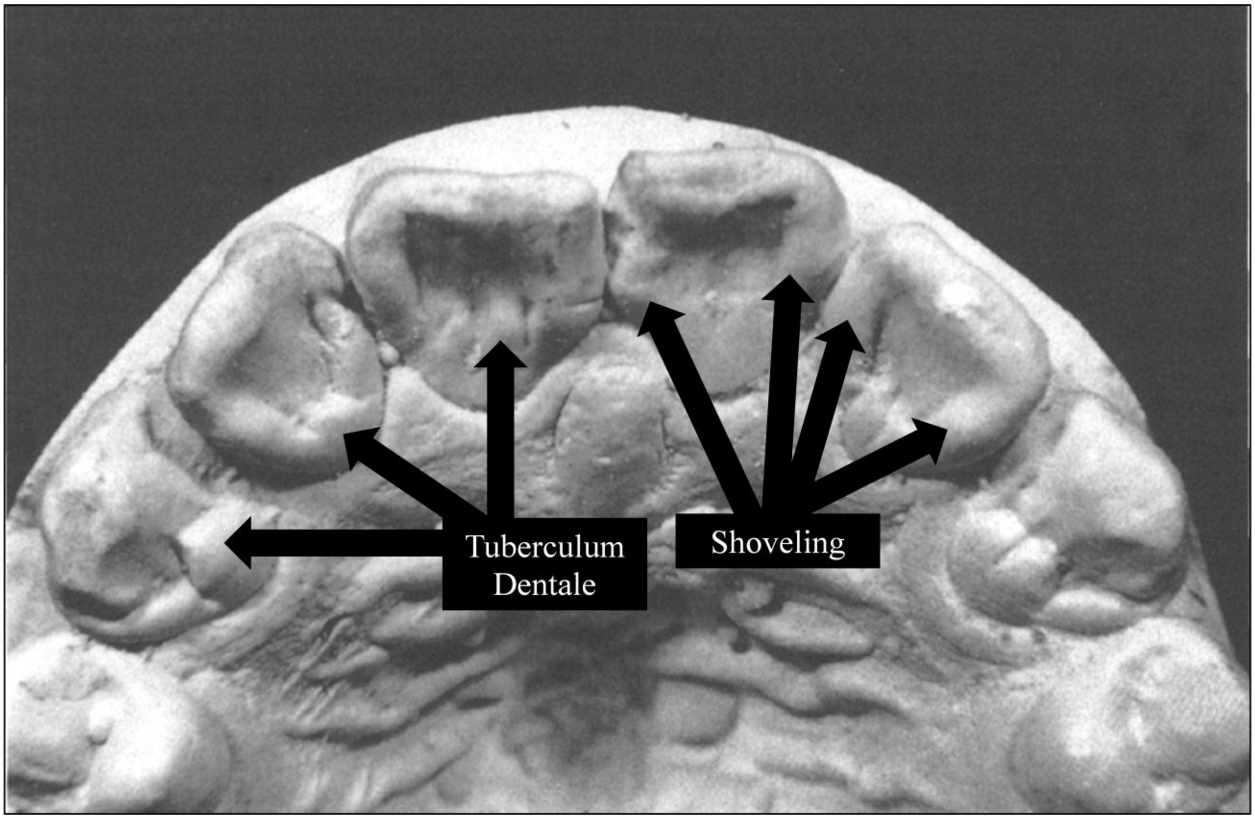

Figure 3.4: Two Dental Nonmetric Traits on the Upper Anterior Teeth: Tuberculum Dentale: occurring on the lingual surface near the medial aspect of the first and second right incisors, and on the third right premolar. Shoveling: occurring on the mesial and distal margins of the first and second left incisors. Modified from Scott (1997: 178).

Trait Manipulation and Dichotomization

Within this research, each trait was dichotomized using the "individual count" method (Scott and Turner 1977), which has four procedures (Table 3.2). Most multivariate statistical procedures require binary data sets (Sjøvold 1977; Irish and Konigsberg 2007; Mcllvaine et al. 2014: 4). The "individual count" method operates under the assumption that if a trait is present, then the genetic component is also present, and specifically addresses traits that occur bilaterally

(Sutter and Mertz 2004; Korey 1980; Mcllvaine et al. 2014). This method emphasizes the genetic basis of the traits while also maximizing sample sizes.

Table 3.2: Four Procedures of the Individual Count Method

1. All traits are counted per individual rather than per side or per tooth/bone
2. When a trait exhibits presence-absence asymmetry, it is scored as present. When multiple categories were used and asymmetry was present, the highest category/"score" is counted.
3. When an individual has only one side present (the other side worn/damaged), the available side was counted and symmetry is assumed
4. When an individual is symmetrical for a trait, the trait is counted once.

Adapted from Turner and Scott (1977: 233).

Many of the cranial and dental traits being examined in this studying occur bilaterally. Following the procedures of the "individual count" method, if an individual exhibited bilateral asymmetry for a trait (e.g., right side "present", left side "absent"), the trait was recorded as "present" in the final analysis. This dichotomization procedure is supported by research that has demonstrated the absence of side preference in nonmetric traits (Cosseddu et al. 1979; Hanihara and Ishida 2001a; 2001b; 2001c; 2001d). The third procedure of the "individual count" method (Table 3.2) requires the researcher to assume symmetry when only one side of a bilaterally occurring trait is available for observation. When only one side is available for observation and a trait is “present” the third procedure does introduce possible problematic assumptions. However, when only one side is available and the trait in question is “absent”, the third procedure may introduce error by assuming the trait is not “present”. Several individuals examined in this study exhibited bilateral asymmetry; therefore, the third procedure was not adhered to. For the purposes of this study, when one side of a bilaterally occurring trait was “absent” and the other side was “unobservable”, the trait was scored as “unobservable” (NA). This specific modification of the third procedure ensures that no assumption of trait “absent” is inserted into the final analysis.

Within this study, interobserver error was not an issue because there was only one observer. Intraobserver error was determined by rescoring 17 randomly selected individuals after all 161 individuals had been recorded. This process of reevaluation is used to identify any inconsistencies or errors between the first and second recording trials. Intraobserver errors were categorized in two ways within this study, “present/absent” errors, and “NA” errors. The “present/absent” errors occurred when, for example, the first recording trial of an individual had a score of “present” for a particular trait, and the second trial had a score of “absent” for the same trait. The “NA” errors occurred, for example, when the first recording trial was scored “present” or “absent”, and the second trial was scored as “NA”, for the same trait within a particular individual.

Molto (1979) conducted a study on rates of intraobserver error for cranial nonmetric traits. Molto found that incorporating an assessment intraobserver error within biodistance studies is critical, because such errors may play a role in distorting the interpretation of biological relationships. Nichol and Turner (1986) studied inter- and intraobserver error rates in dental nonmetric traits, finding that recording errors occur in a random fashion. In general, there is not a standardized intraobserver error level at which cranial and dental traits are excluded from the final distance analysis. Molto (1979), for example, suggested that cranial traits exceeding five percent in error rates should be excluded. Aubry (2009:121) excluded traits that exceeded a 25 percent error rate; a threshold that is admittedly "arbitrary". Sutter (1997), also using dental nonmetric data, excluded traits that exceeded a 10 percent error rate. For the purposes of this study, when a trait exceeded more than two "present/absent" errors (approximately 11 percent), *and/or* more than three "NA" errors (approximately 17 percent), the trait was excluded. This method of exclusion was adopted to maximize the sample size while simultaneously removing traits that exhibited higher than acceptable levels of error.

After recording the traits of each individual on paper recording forms, all data were entered into an Excel© spreadsheet; one individual at a time, one individual per row. Missing values were indicated with "NA", because the statistical computing software R understands "NA" as missing values. The information for each trait was entered into the spreadsheet in either one or two columns. Traits that occur bilaterally had two columns (right and left); traits that occur in midline only required one column. The "individual count" method was applied to each of the bilaterally occurring traits by a series of commands in Excel©. These commands converted the two columns into a single column, holding to the procedures of the "individual count" method.

Following the dichotomization process, biodistance methodology requires the application of statistical procedures to analyze the data. At the most fundamental level, biodistance studies rely on evolutionary theory. Evolutionary theory is a statistical theory (Sterelny and Kitcher

1988: 345), and therefore statistical procedures can be used to interpret evolutionary processes in an accurate and predictive manner (Moran 1962).

Statistical Procedures

All statistical calculations (univariate and multivariate) within this study were conducted with the computing software R (R Core Team 2014). Trait frequencies were calculated for each trait examined based on the individual count method. Trait frequencies were calculated to assess the distribution of the overall variation in trait expression exhibited between burial locations and between males and females within the site. A z-test for the difference between two proportions was used to determine if there were intrasite differences within and between the sexes, as this test makes it possible to identify where the differences are occurring in terms of specific traits. To identify possible sex difference between locations at the site the z-test statistic was applied to compare each of the subsamples being considered in a comparative manner.

Traits that exhibited an extremely high (95-100%) or low (0-5%) incidence were excluded because such traits do not aid in discriminating between groups (Irish and Konigsberg 2007). Some studies have attempted to investigate familial relationships using rare or uncommon nonmetric traits, traits that occur at or below five percent in the population (e.g., Alt and Vach 1995). Within this study, traits that occurred in low frequencies (below 5%) were excluded from the final analysis for two reasons. First, nonmetric traits have been only tentatively successful in identifying biological kinship between pairs of individuals (Ricaut et al. 2010). Second, it would be difficult to say with certainty that familial groups have been identified at Túcume because there are multiple burial contexts, spanning an approximately five hundred year period.

Traits that were found to be highly correlated, that is, traits that were often expressed together, were also excluded. Correlated traits essentially reflect the same information and this redundancy will skew biodistance measures (Constandse-Westermann 1972; Irish 2010). Several biodistance researchers have used Chi-square test of independence to identify correlated traits (Rothammer et al. 1984; Verano 1987; Donlon 2000; Sutter and Mertz 2004) or Fisher's Exact test (Ricaut et al. 2010) to identify correlated traits. In this study, a correlation matrix was generated in R, and traits exhibiting a correlation equal to or greater than 0.5 were identified. When two traits were correlated, the trait with the smallest number of total observations was excluded. The same process was used to identify traits correlated with sex and age.

The multivariate statistical methods most often used in phenotypic biodistance studies are Smith's Mean Measure of Divergence (MMD) and Mahalanobis distance (D^2) (Irish 2010). The MMD and D^2 method are both distance measures in which low values indicate groups of individuals are closely related and high values indicate they are more distantly related. Both methods can be informative depending on the samples and questions being addressed (Irish 2010). The MMD has been used in many biodistance studies (e.g., Donlon 2000; O'Brien 2003; Hanihara et al. 2003; Harris and Sjøvold 2004; Edgar 2007; Toyne 2008; Jahnke 2009; Aubry 2009; Irish 2010; Cook and Aubry 2014). However, some researchers have suggested that the MMD method has several disadvantages (Irish 2010). Perhaps the main disadvantages of the MMD method is that it often produces negative values, and the results of the MMD method may be influenced by sample size (Movsesian 2013: 499). Additionally, both the MMD and the D^2 methods cannot handle missing data, which are an unavoidable reality in "real world", biological data sets (Nakagawa and Freckleton 2008; Graham 2009), and this, in part, is the reason why a different statistical distance method was employed.

Within this study, the Gower coefficient of similarity (Gower 1966; 1971) was used, primarily because it can handle missing data (Gamble et al. 2001; McClelland 2003; Ricaut et al. 2010; Brown et al. 2012). Gower's coefficient, or distance, essentially weighs missing values as zero; thereby making the "present" values the most important values in the analysis (Gower 1966, 1971; Reyment 1991; Brown et al. 2012). While Brown et al. (2012) found that Gower's distance is one of the best methods to use when confronted with missing values, there are two significant limitations associated with it. First, Gower's distance works best when missing values do not exceed approximately 30 percent of the total number of observable variables per individual, and it is ineffective when missing values exceed 45 percent. Second, the results from Gower's distance can only reveal similarities between observations (i.e., specimens, or individuals) and cannot illuminate similarities between variables (i.e., traits). Importantly, Gower's distance cannot practically be used to investigate specific variables, and is perhaps most useful in analyses that focuses on "the relative clustering of specimens" (Brown et al 2012: 950). Gower's distance has proved useful in biodistance analysis within a single site (Stojanowski and Schillaci 2006), and it has been used to incorporate different types of biological data (e.g., molecular and nonmetric) (Ricaut et al. 2010). Within this research, several individuals exhibited a large number of missing values which made it necessary to remove these individuals (*n*=58) from the final analysis.

Using the results produced from the Gower's distance, a Ward's hierarchical cluster analysis was used to produce a dendrogram which graphically depicts the patterns of relatedness

(Howell and Kintigh 1996; Scott and Turner 1997; McClelland 2003; Murtagh and Legendre 2014) of the individuals examined in this research. Ward's method works best with large samples (*n* > 100), and it groups individuals based on shared similarities of specified characteristics (Ward 1963). Ward's method essentially minimizes variation within clusters of individuals and maximizes variation between them (Ward 1963; Ricaut et al. 2010).

The dendrograms produced within R can be compared by creating a tanglegram. A tanglegram is graphical comparison of two dendrograms with the same leaves, or nodes. In this study, the leaves of the dendrograms are the individuals examined in this study. Tanglegrams link the pairs of corresponding leaves of two dendrograms with lines. The lines drawn between the two dendrograms are used to measure the level of entanglement. The measure of entanglement falls between one and zero, where zero indicates the two dendrograms are essentially identical, and one indicates they are completely different (Venkatachalam et al. 2010). Tanglegrams have been used in biology to understand the evolutionary histories of host and parasite species, and to analyze genes within a single species (Venkatachalam et al. 2010; Scornavacca et al. 2011). To the best of my knowledge, this research represents the first time tanglegrams have been utilized within biodistance studies to compare different datasets based on the same sample.

Summary

This chapter has provided an overview of the sample examined and the methodological approach adopted for this study. The overall sample examined contained 161 individuals, 58 females, 85 males, and 18 of indeterminate sex. The burials come from five locations within the site. All individuals were examined within the museum located adjacent to the archaeology site. Nonmetric traits were recorded on paper recording forms and were later dichotomized within Excel©, following the procedures of the “individual count” method. The biological variation was analyzed within the computing software R using both univariate and multivariate statistics. Finally, this chapter provides the archaeological and methodical research questions within this study and the three hypotheses utilized to examine these questions.

CHAPTER 4: RESULTS

Introduction

This chapter details the results of the nonmetric biological distance analysis of cranial and dental remains at pre-Columbian Túcume. Certain traits and individuals were excluded from the final analysis (discussed below) due intraobserver error, large numbers of unobservable features due to damage, and intertrait correlations. The univariate analyses are used to determine if there are any sex differences, if these differences are associated with burial location, and which traits are responsible for the potential differences. The multivariate analyses are used to understand the overall nonmetric variation, and to identify cluster or groups of related individuals. The results from multivariate cluster analyses are presented in three forms: cranial, dental, and cranial and dental combined. The cranial and dental dendrograms are graphically compared with a tanglegram.

Data Analysis

Certain traits and individuals were removed from final analysis due to trait inconsistencies and missing data. Only 26 (19 cranial and seven dental) of the 123 traits examined were used in the final analysis, and 103 of the 161 individuals examined were included in the final (Appendix D). Certain traits were removed due to either high (95-100%) or low (0-5%) frequency of occurrence (30 traits). Intraobserver error was computed to identify and remove traits that were not reliably recorded. Identifying and removing traits that were correlated was done because such traits artificially inflate the distance measure. Certain individuals with a large number of missing values were removed so the Gower's distance to produce reliable results, and to make the results comparable within this study.

Intraobserver Error and Missing Data

Intraobserver error was determined by rescoring 17 randomly selected individuals. The final trait list consisting of 26 traits contained a total of 26 "NA", and 15 "present/absent" errors. Mylohyoid bridge and occipitomastoid bone, for example, contained no errors in the rescored individuals, while epipteric bone contained two "NA" errors and one "present/absent" error, for a total error rate of about 17 percent. In total, 15 traits had at least one "NA" error and 12 traits had at least one "present/absent" error. When each trait is considered individually only one trait exceeded a 20 percent error rate (accessory lesser palatine foramen), and this level of intraobserver error is generally within the acceptable range (Nichol and Turner 1986; Edgar 2002; Aubry 2009; Pilloud 2009), making there inclusion in this study acceptable.

While the statistical method selected for this study can handle missing data, when individuals and traits contained many missing values they were removed. Individuals with more than 17 missing values (65 percent) were excluded from the final analysis; this allowed for the Gower's distance to function properly while also maximizing the potential sample size (Appendix E). Eighty five percent of the individuals included in the final analysis had less than 10 missing values. In total, seventy two traits were removed from the final analysis due to either intraobserver error or missing values. Overall, the majority of the traits excluded from the final analysis were removed because of missing values (Appendix E). Several traits did not demonstrate repeatability upon rescoring, but often these traits also had a large number of missing values as well. Cusp seven on lower molar one, for example, had a 35 percent error rate but only occurred in 5 individuals overall.

Low and High Frequency Traits

Traits that occurred at an extremely low and high frequency were removed from the final analysis. Metopic suture, for example, had a frequency of 0 and thus was removed from the final analysis. Similarly, when dental shoveling was observable, it was seen in every individual and thus it was also removed from the final analysis. Traits that occurred in fewer than five percent of the individuals examined were also removed. Os Incae, for example, occurred in only four individuals was therefore excluded from the final analysis. Appendix E provides a list of the traits and the reason for their inclusion/exclusion.

Correlated Traits

Following the general procedures within nonmetric biodistance studies, correlated traits were removed. To identify correlated traits a correlation matrix was generated in R, and when two traits were correlated at an absolute value of greater than 0.5, the trait with fewer observations was removed. There were only four traits that were removed because of intertrait correlations. An unsurprising correlation was found between congenitally absent upper and lower third molars. These two traits are considered to as the same morphological feature being expressed in a different part of the mandible. The correlation matrix (see Appendix F) for the combined cranial and dental data displays the traits that were selected for the final analysis and their levels of correlation.

In four instances the correlation matrix was not able to determine if particular traits were correlated due to missing data. The traits in question (PTAB and IG-UI2, META-UM2 and TOMR-LP3, PARA-UM2 and PROTO-LM1, UCONAB-UM3 and LCSP5LM3) can be found in Appendix F. For the purposes of this study, it is assumed that these traits are not highly correlated, largely because the ASU dental system incorporates traits that are thought to be only minimally statistically correlated, (Turner et al. 1991; Scott and Turner 1997); however such correlation are likely population and/or even sample specific. Cranial traits have been found to be minimally correlated as well (Hauser and DeStefano 1989), and traits that are correlated are typically morphogenetically similar (e.g., hyperostotic traits) (Hanihara et al. 2003). Recent research, however, has suggested that dental nonmetric traits are not developmentally independent, challenging their assumed independence (Moormann et al. 2013).

Following the assessment of intertrait correlations, intraobserver error, and screening for low and high frequency traits, the final trait list was compiled. The final trait list contains 26 traits, 19 cranial and seven dental. In addition to removing traits that would be problematic for the analysis, several individuals were also removed due to high numbers of unobservable traits. Fifty-seven individuals were removed from the final analysis, leaving 103 individuals for the final analysis. Table 4.1 provides a summary of the final sample examined; this table does not include age information because it was not a factor examined in this study.

Table 4.1: Final Sample of Individuals by Sex and Location

Locations	Female	Male	Indeterminate	Total	Percent
Huaca Larga	26	8	4	**38**	***36.9%***
Huaca I	4	4	0	**8**	***7.8%***
Huaca Las Balsas, South Cemetery, South West Burials	7	5	0	**12**	***11.6%***
Temple of the Sacred Stone	0	45	0	**45**	***43.7%***
Total	**37**	**62**	**4**	**103**	
Percent	***35.9%***	***60.2%***	***3.9%***		

Univariate Statistics

The trait frequencies across the site were calculated based on the 99 individuals for whom sex could accurately be determined; individuals of indeterminate sex were removed. The trait frequencies provide the distribution of the traits among burial locations and between males and females within the site. The trait frequencies displayed in Table 4.2 exhibit relatively homogenous frequencies between males and females within the site. To determine if there is a significant difference in variability between males and females a z-test statistic used to determine the difference between two proportions was calculated for the data from which the trait frequency information (Table 4.2) was generated. Due to small sample sizes found in the Las Balsas, the Southwest burials, and the burials from the South Cemetery, these groups were combined to perform the z-test statistic. These three locations are in the south portion of the site, and are thus arbitrarily grouped together because of their proximity to each other in order to increase the samples size of the subgroups being analyzed.

Table 4.2: Male and Female Nonmetric Trait Frequencies: 99 Individuals

Trait Abbreviation	Huaca Larga		Huaca I		Huaca Las Balsas, South Cemetery, and Southwest Burials		Temple of the Sacred Stone
	Females *n*=26	Males *n*= 8	Females *n*= 4	Males *n*=4	Females *n*= 7	Males *n*=5	Males *n*=45
IOS	0.115	0.250	0.000	0.000	0.000	0.000	0.133
ZFFA	0.192	0.125	0.000	0.000	0.143	0.333	0.111
SOFO	0.423	0.125	0.750	0.500	0.571	0.333	0.378
FRG	0.462	0.125	0.000	0.000	0.143	0.167	0.178
OAL	0.154	0.125	0.000	0.250	0.429	0.167	0.133
LO	0.500	0.375	0.250	0.000	0.714	0.667	0.400
ALPF	0.308	0.750	0.500	0.250	0.571	0.333	0.511
HYP	0.385	0.625	0.250	0.250	0.571	0.333	0.467
POCS	0.846	0.625	1.000	0.500	1.000	0.833	0.822
ICC	0.346	0.500	0.250	0.000	0.143	0.167	0.311
PTAB	0.038	0.000	0.000	0.000	0.143	0.167	0.067
HSK	0.615	0.375	0.250	0.750	0.714	0.500	0.800
FOSO	0.154	0.125	0.000	0.250	0.429	0.333	0.089
AST	0.154	0.375	0.250	0.000	0.429	0.667	0.156
MFN	0.692	1.000	0.750	1.000	0.429	1.000	0.889
EPB	0.115	0.000	0.000	0.000	0.143	0.000	0.111
OMB	0.346	0.125	0.000	0.000	0.429	0.333	0.222
PNB	0.077	0.000	0.000	0.000	0.000	0.000	0.111
MYB	0.115	0.000	0.000	0.250	0.143	0.333	0.156
IG-UI2	0.154	0.375	0.500	0.000	0.286	0.000	0.156
URNUM-UP3	0.846	1.000	0.500	0.500	0.714	0.500	0.711
META-UM2	0.885	0.875	1.000	0.750	0.714	0.833	0.978
UPEG-UI2	0.077	0.000	0.250	0.000	0.000	0.167	0.022
UCONAB-UM3	0.115	0.125	0.250	0.250	0.000	0.333	0.133
LCSP5-LM3	0.462	0.125	0.000	0.500	0.857	0.333	0.422
LRNUM-LM2	0.423	0.250	0.500	0.500	0.429	0.500	0.467

Within the statistical computing software R, a z-test to determine the difference between two proportions was used to investigate potential difference between males and females (see Appendix G for generalized R script). Males and females were evaluated for differences within and between the burial locations using the trait frequency data. The males from the Temple of the Sacred Stone were also compared to all other males within the site. Using the z-test to examine trait frequencies made it possible to identify potential differences at the level of the individual trait. The only statistically significant differences were found in two traits (frontal grooves, mastoid foramen number) when all males were compared to all females (Table 4.3). Tables 4.4 through 4.9 display the results from the z-test statistic performed to examine potential sex difference within the burial different burial locations. To examine potential differences between the sacrificed males and the other individuals in the sample, three different z-tests were performed (Tables 4.7, 4.8, and 4.9). Table 4.7 displays the results from the comparison of the males from the Temple of the Sacred Stone and all other males examined in this study. In Table 4.8 the Temple of the Sacred Stone males were compared to all of the females within the sample, and in Table 4.9 the non-sacrificed males were compared to all of the females in the sample.

Table 4.3: Overall Sex Differences Based on Trait Frequency Data.

All Males Compared to All Females	
Trait	p-value
IOS	0.463
ZFFA	0.647
SOFO	0.145
FRG	***0.017**
OAL	0.565
LO	0.220
ALPF	0.361
HYP	0.733
POCS	0.065
ICC	0.941
PTAB	0.901
HSK	0.177
FOSO	0.292
AST	0.698
MFN	***0.002**
EPB	0.646
OMB	0.204
PNB	0.618
MYB	0.463
IG-UI2	0.493
URNUM-UP3	0.262
META-UM2	0.441
UPEG-UI2	0.283
UCONAB-UM3	0.463
LCSP5-LM3	0.333
LRNUM-LM2	0.853

*Statistically significant results.

Table 4.4: Sex Difference within Huaca Larga

Huaca Larga Sex Differences	
Trait	p-values
IOS	0.372
ZFFA	0.632
SOFO	0.107
FRG	0.074
OAL	0.810
LO	0.475
ALPF	0.032
HYP	0.266
POCS	0.104
ICC	0.481
PTAB	0.566
HSK	0.187
FOSO	0.810
AST	0.195
MFN	0.092
EPB	0.304
OMB	0.208
PNB	0.409
MYB	0.304
IG-UI2	0.195
URNUM-UP3	0.304
META-UM2	0.700
UPEG-UI2	0.409
UCONAB-UM3	0.970
LCSP5-LM3	0.074
LRNUM-LM2	0.338

Table 4.5: Sex Differences within Huaca I

Huaca I Sex Differences	
Trait	p-value
IOS	*NA*
ZFFA	*NA*
SOFO	0.465
FRG	*NA*
OAL	0.285
LO	0.285
ALPF	0.465
HYP	1.000
POCS	0.102
ICC	0.285
PTAB	*NA*
HSK	0.157
FOSO	0.285
AST	0.285
MFN	0.285
EPB	*NA*
OMB	*NA*
PNB	*NA*
MYB	0.285
IG-UI2	0.102
URNUM-UP3	1.000
META-UM2	0.285
UPEG-UI2	0.285
UCONAB-UM3	1.000
LCSP5-LM3	0.102
LRNUM-LM2	1.000

NA: Indicates insufficient information to perform test; zero values.

Table 4.6: Sex Differences within Southern Burial Locations

Huaca Las Balsas, South Cemetery, and Southwest Burials	
Traits	p-values
IOS	*NA*
ZFFA	0.416
SOFO	0.391
FRG	0.906
OAL	0.308
LO	0.853
ALPF	0.391
HYP	0.391
POCS	0.261
ICC	0.906
PTAB	0.906
HSK	0.429
FOSO	0.725
AST	0.391
MFN	0.026
EPB	0.335
OMB	0.725
PNB	*NA*
MYB	0.416
IG-UI2	0.155
URNUM-UP3	0.429
META-UM2	0.612
UPEG-UI2	0.261
UCONAB-UM3	0.097
LCSP5-LM3	0.053
LRNUM-LM2	0.797

NA: Indicates insufficient information to perform test; zero values.

Table 4.7: Differences Between Males: Sacraficed and Non-Sacraficed Individuals

Temple of the Scared Stone Male vs. All Other Males	
Trait	p-values
IOS	0.869
ZFFA	0.493
SOFO	0.290
FRG	0.236
OAL	0.667
LO	0.734
ALPF	0.776
HYP	0.978
POCS	0.141
ICC	0.557
PTAB	0.275
HSK	0.033
FOSO	0.331
AST	0.089
MFN	0.152
EPB	0.152
OMB	0.693
PNB	0.152
MYB	0.842
IG-UI2	0.842
URNUM-UP3	0.968
META-UM2	0.027
UPEG-UI2	0.467
UCONAB-UM3	0.330
LCSP5-LM3	0.356
LRNUM-LM2	0.698

Table 4.8: Sex Differences: All Females and the Non-Sacrificed Males

All Females vs. Non-Sacrificed Males	
Trait	p-values
IOS	0.667
ZFFA	0.896
SOFO	0.081
FRG	***0.023**
OAL	0.911
LO	0.272
ALPF	0.653
HYP	0.793
POCS	***0.013**
ICC	0.637
PTAB	0.329
HSK	0.653
FOSO	0.911
AST	0.403
MFN	***0.008**
EPB	0.159
OMB	0.260
PNB	0.329
MYB	0.487
IG-UI2	0.736
URNUM-UP3	0.389
META-UM2	0.487
UPEG-UI2	0.772
UCONAB-UM3	0.222
LCSP5-LM3	0.184
LRNUM-LM2	0.887

*Statistically significant results.

Table 4.9: Sex Differences: All Females and the Temple of the Sacred Stone Males

All Females vs. Temple of the Sacred Stone Males	
Trait	p-values
IOS	0.451
ZFFA	0.500
SOFO	0.322
FRG	0.073
OAL	0.491
LO	0.304
ALPF	0.339
HYP	0.757
POCS	0.201
ICC	0.892
PTAB	0.812
HSK	***0.042**
FOSO	0.185
AST	0.319
MFN	***0.018**
EPB	0.965
OMB	0.299
PNB	0.358
MYB	0.530
IG-UI2	0.480
URNUM-UP3	0.295
META-UM2	0.106
UPEG-UI2	0.218
UCONAB-UM3	0.728
LCSP5-LM3	0.561
LRNUM-LM2	0.757

*Statistically significant results.

Multivariate Statistical Analysis

This section includes the results of the 15 cluster analyses that were employed as well as the results of the three tanglegrams comparing the dental and cranial dendrograms. Cluster analyses within and between the documented sacrificed and non-sacrificed individuals are presented in this section. Potential sex differences are also examined in an exclusive manner in six of the dendrograms, and the last three dendrograms include all 103 individuals from across the site. The tanglegrams compare three pairs of cranial and dental dendrograms.

Each individual leaf, or node, within each dendrogram represents an individual. The label for each individual begins with an abbreviation of the chronological period (LIP, Early LIP, Late LIP, LH, ?LH, ??), Late Intermediate Period, Early-Late Intermediate Period, Late-Late Intermittent Period, Late Horizon, Possibly Late Horizon, and Unknown. Within the labels, “M”, “F”, or “?” is used to indicate sex as male, female, or indeterminate; following the sex indicator, a burial identification code is provided. The burial identification codes are an abbreviated version of the provenience information associated with each individual. Within the dendrograms, females are labeled in red to make it easier to distinguish between males and females.

Sacrificed and Non-Sacrificed Individuals

All dendrograms were produced using the statistical software R. Ward’s hierarchal cluster analysis was then applied to these distance matrices (see Appendix H for R code) to produce the dendrograms. The documented sacrificed burials from the Temple of the Sacred Stone, and several individuals from Huaca Larga that are likely part of a sacrificed group. As such, the sacrificed and non-sacrificed groups are considered separately to examine the degree of variation within these groups (Tables 4.1, 4.2, and 4.3).

The dendrogram in Figure 4.1 displays the results for the cranial nonmetric data for the sacrificed group which includes 56 individuals and is based on 19 traits. With a maximum height of 1.0, Figure 4.1 has six groups at a height of 0.4. The largest of these groups contains 15 individuals and the smallest contains four individuals. In Figure 4.2 the dendrogram again includes the 56 individuals from the sacrificed group and is based on seven dental traits. With a maximum height of approximately 1.3, Figure 4.2 has three groups at a height of 0.8. The largest of these groups contains 46 individuals and the smallest contains four. When the cranial and dental data are combined for the sacrificed group in Figure 4.3, the maximum height is 0.8. At a height of 0.4 there are four groups, the largest of which contains 21 individuals and the smallest contains six individuals. The height of the dendrogram can be thought of as the distance value between the clusters; if objects (i.e., individuals or groups of individuals) are highly correlated they will have a value close to zero. Individuals or groups of individuals that have a greater statistical distance and are not highly correlated will result in an increase in the height of the dendrogram (Saraf and Patil 2014).

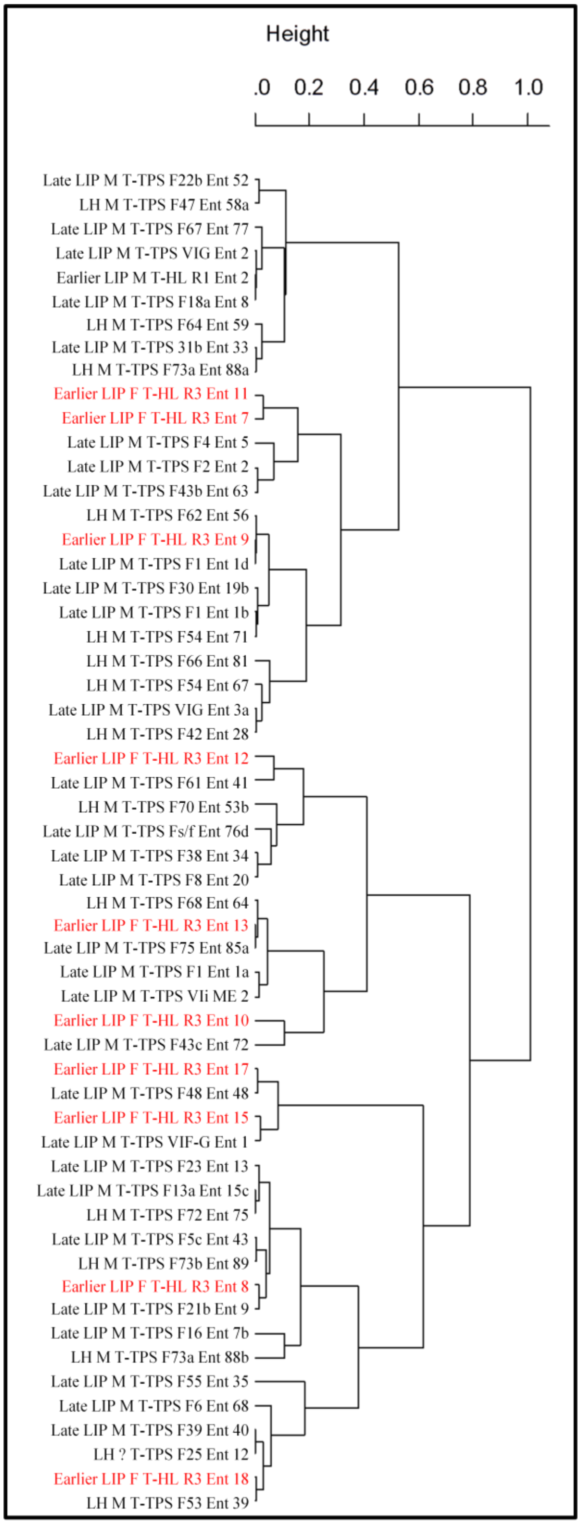

Figure 4.1: Sacrificed Burials: Based on Cranial Nonmetric Data

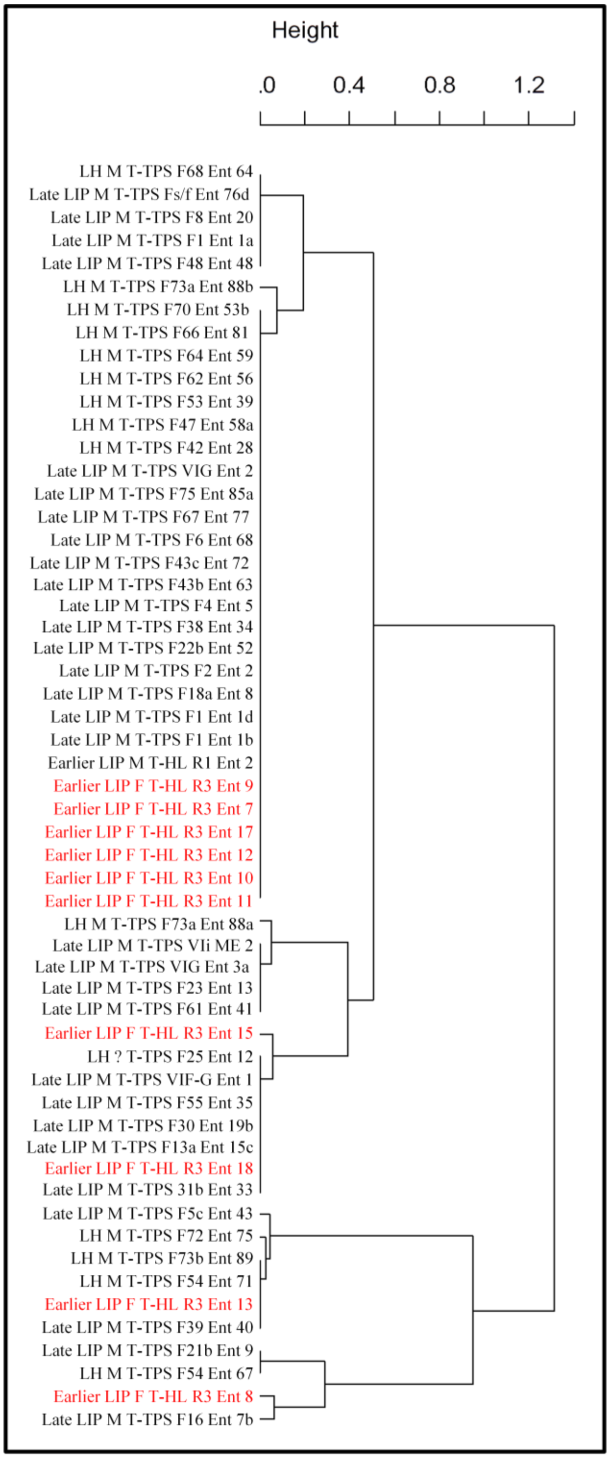

Figure 4.2: Sacrificed Burials: Based on Dental Nonmetric Data

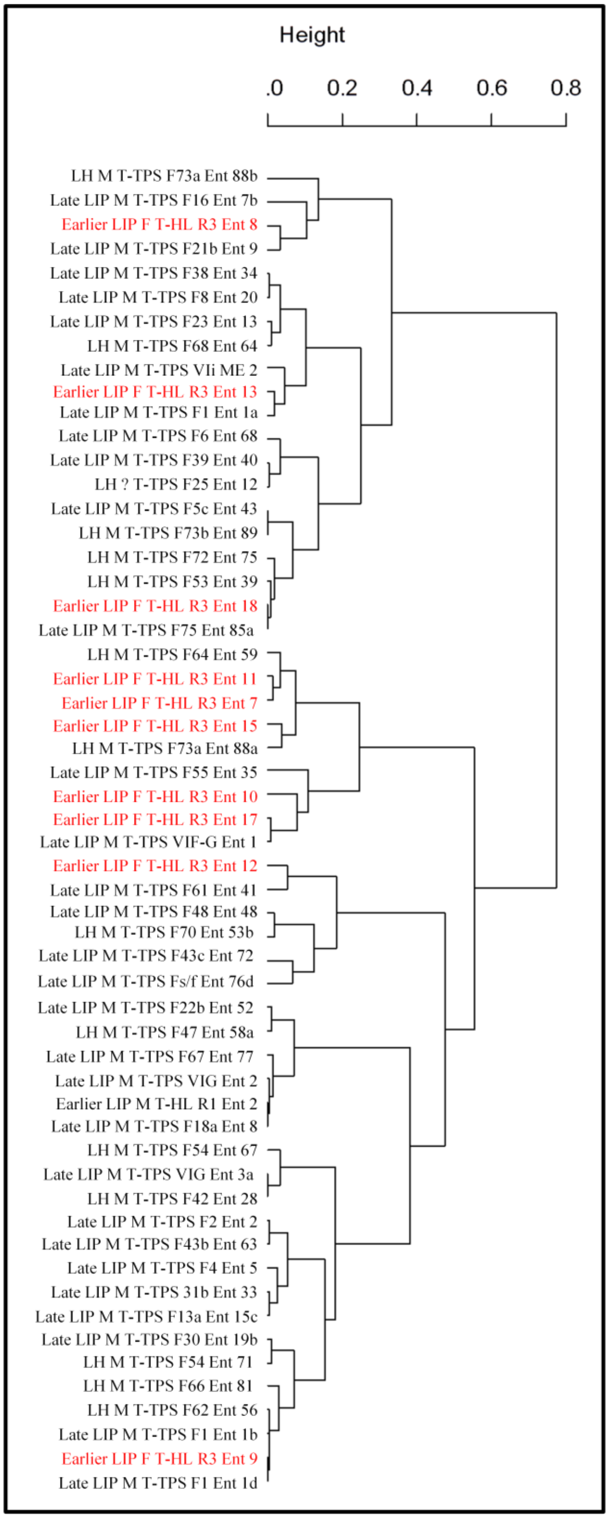

Figure 4.3: Sacrificed Burials: Based on Cranial and Dental Nonmetric Data

The dendrograms in Figures 4.4 through 4.6 contain the 47 individuals from the non-sacrificed group. The dendrogram in Figure 4.6 is based on 19 cranial traits and has a maximum height of 1.5. At a height of 0.5 there are five groups, the largest of which contains 17 individuals and the smallest contains five individuals. The dendrogram in Figure 4.5 again contains the 47 individuals from the non-sacrificed group but is based on 7 dental traits. This dendrogram has a maximum height of approximately 1.9 and at a height of 0.5 contains four groups. The largest of these groups contains 24 individuals and the smallest contains two individuals. When the cranial and dental data for the non-sacrificed group are combined, in Figure 4.6, the maximum height of the dendrogram is approximately 0.9. At a height of 0.4 there are six groups, the largest containing 11 individuals and the smallest containing six.

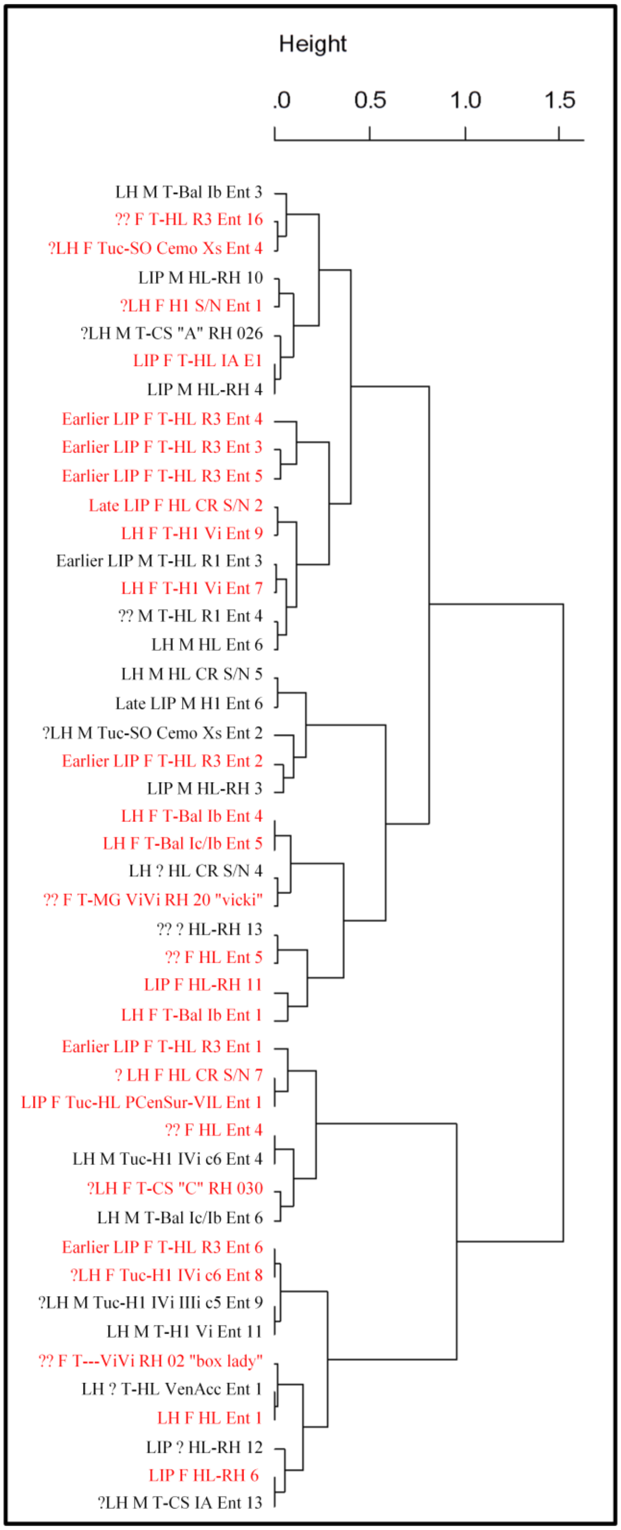

Figure 4.4: Non-Sacrificed Burials: Based on Cranial Nonmetric Data

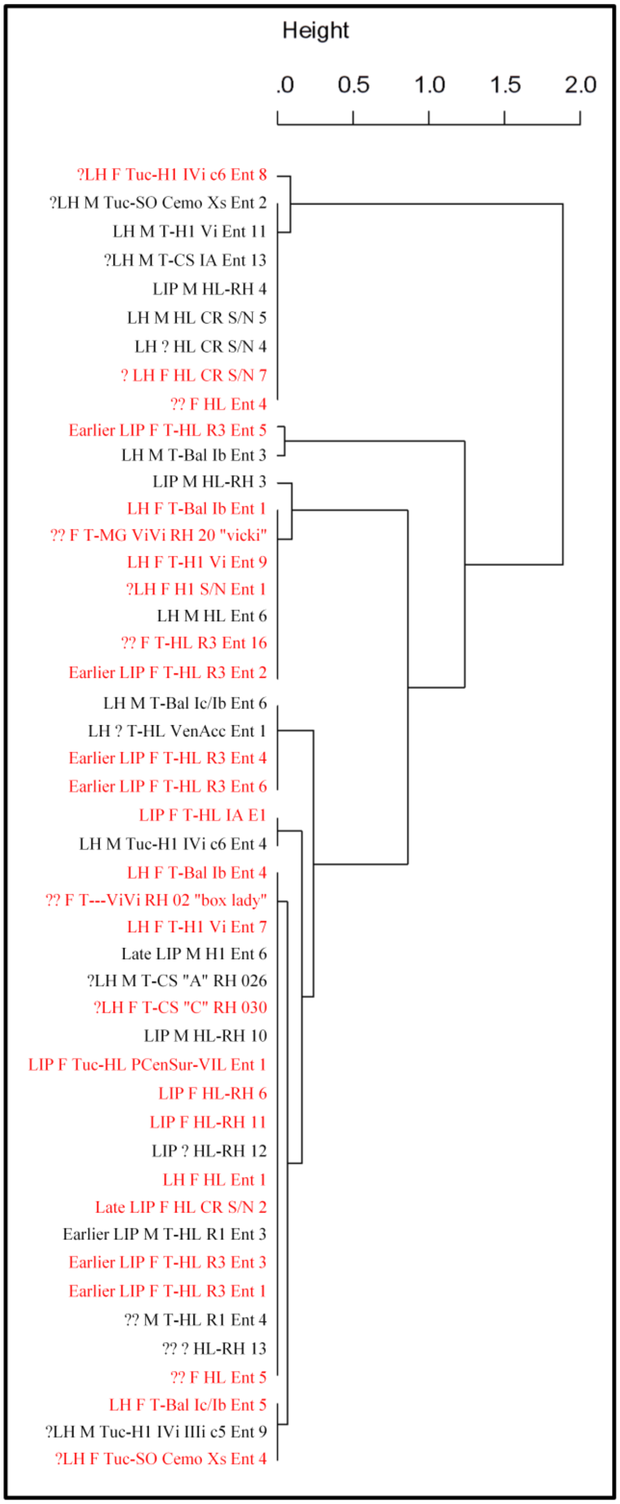

Figure 4.5: Non-Sacrificed Burials: Based on Dental Nonmetric Data

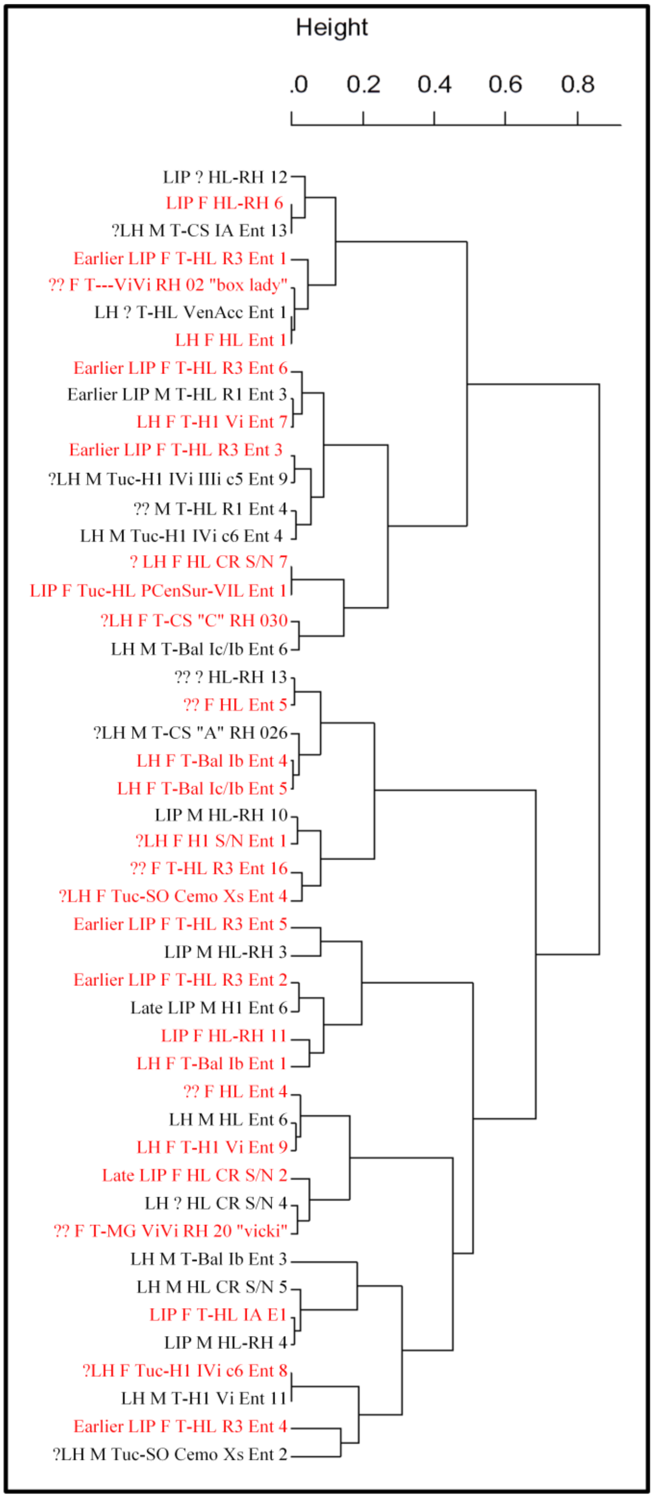

Figure 4.6: Non-Sacrificed Burials: Based on Cranial and Dental Nonmetric Data

Intrasite Sex Differences

To examine the differences within the males and females six separate cluster analyses were performed, each produced from a distance matrix. The first three dendrograms, Figure 4.7, 4.8, and 4.9, include all of the females within the sample, and the dendrograms in Figures 4.10, 4.11 and 4.12 include all of the males within the sample. The cranial and dental nonmetric data are first considered separately, and then these data are combined to produce the dendrogram in Figures 4.9 and 4.12.

The dendrogram in Figure 4.7 contains 37 female individuals and is based on 19 cranial nonmetric traits. The Figure 4.7 has a maximum height of 1.2 and at a height of 0.4 contains four groups. The largest of these groups contains 14 individuals and the smallest of which contains five individuals. The dendrogram in Figure 4.8 includes 37 female individuals found throughout the site is based on seven dental traits. Within in this dental dendrogram, the maximum height is 1.2 and at a height of 0.4 there are three groups. The largest of these groups contains 22 individuals and the smallest contains five individuals. The dendrogram in Figure 4.9 displays the combined cranial and dental nonmetric data (26 traits) again examining the 37 female individuals within the sample. This dendrogram has a maximum height of approximately 0.9. At a height of 0.2, the dendrogram in Figure 4.9 has eight groups with the largest containing 7 individuals and the smallest containing two individuals.

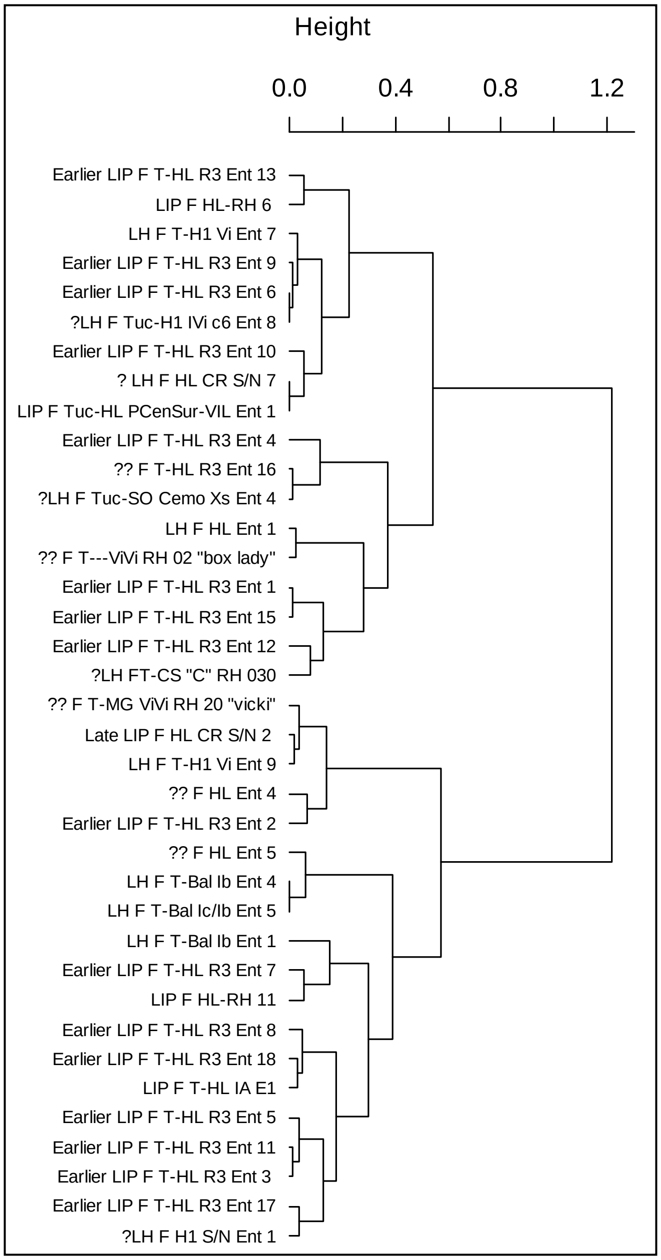

Figure 4.7: All Females: Based on Cranial Nonmetric Data

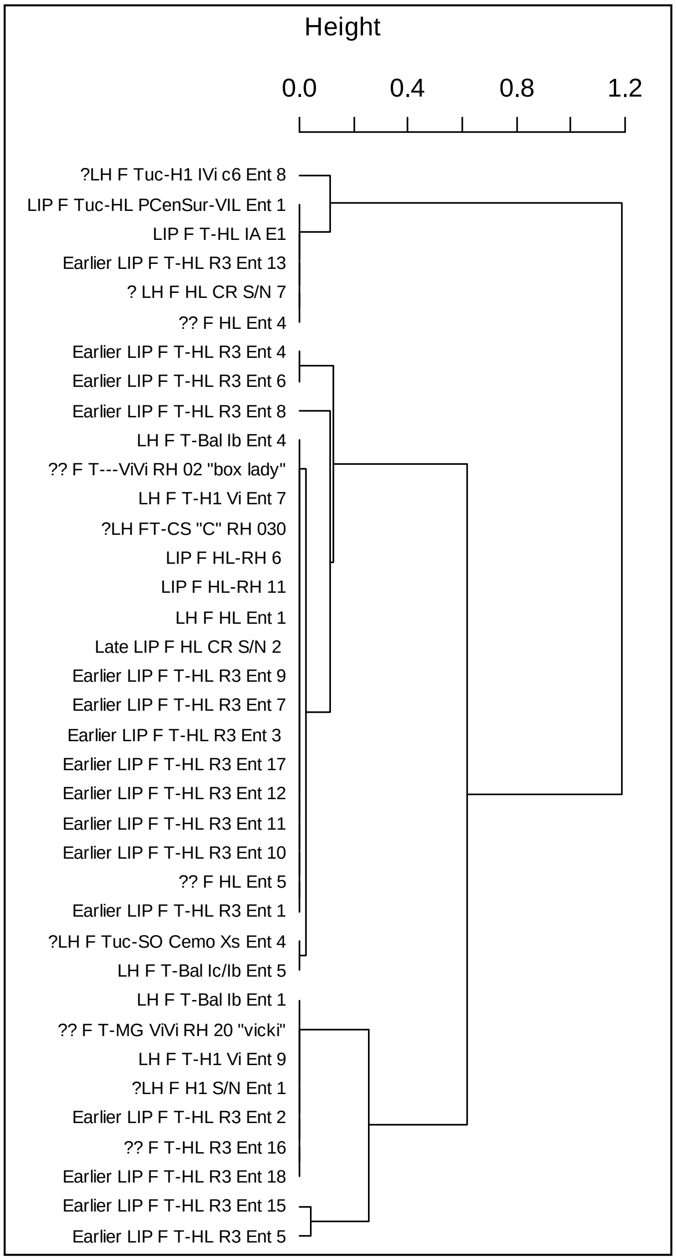

Figure 4.8: All Females: Based on Dental Nonmetric Data

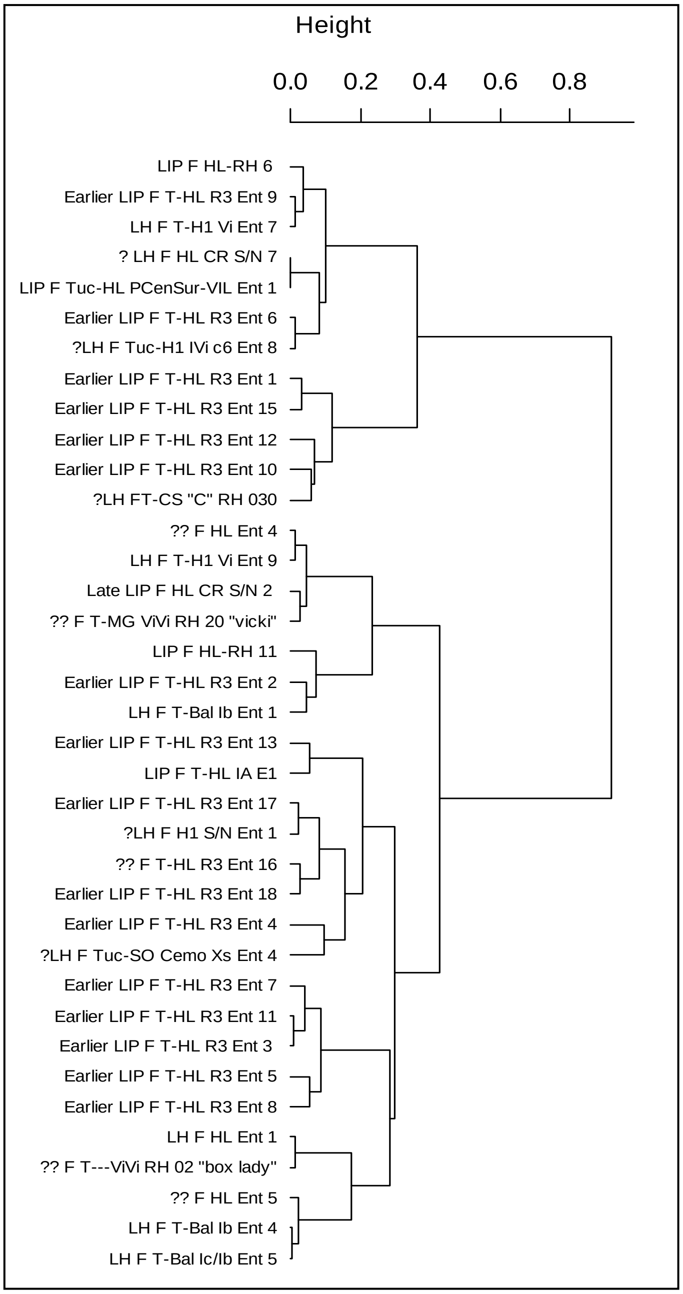

Figure 4.9: All Females: Based on Cranial and Dental Nonmetric Data

The dendrograms in Figures 4.10 through 4.12 examine the variation in the males within the sample. The cranial and dental nonmetric data are first considered separately, Figures 4.10 and 4.11, and then in tandem in Figure 4.12. The first of these dendrograms, Figure 4.10, includes 62 individuals found throughout the site and is based on 19 cranial traits. This cranial dendrogram has a maximum height of 1.2 and at height of 0.4 has six groups. The largest of these groups contains 15 individuals and the smallest contains five. The dendrogram in Figure 4.11 again contains the 62 male individuals within the sample and is based on seven dental traits. This dental dendrogram has a maximum height of 2.7 and at a height of 0.5 there are four groups. The largest of these groups contains 34 individuals and the smallest contains eight individuals. The combined cranial and dental dendrogram, Figure 4.12, includes the 62 males and is based on 26 traits. This dendrogram has a maximum height of approximately 0.9 and at a height of 0.2 contains 9 groups. The largest of these groups contains 13 individuals and the smallest contains two individuals.

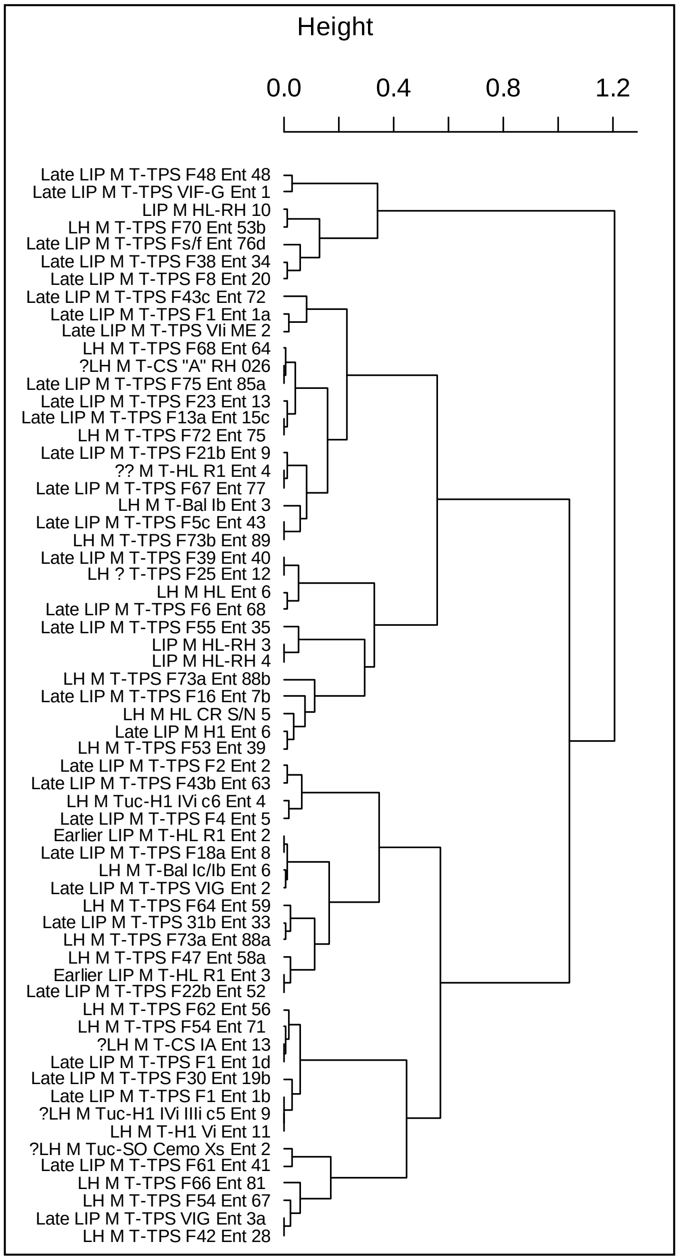

Figure 4.10: All Males: Based on Cranial Nonmetric Data

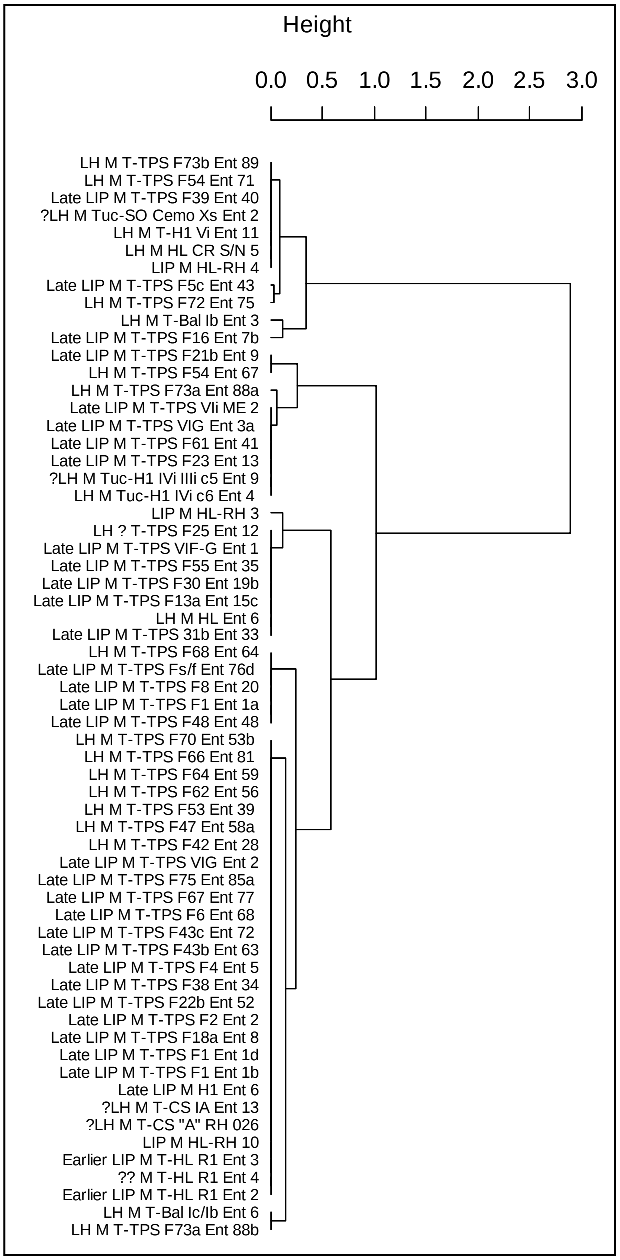

Figure 4.11: All Males: Based on Dental Nonmetric Data

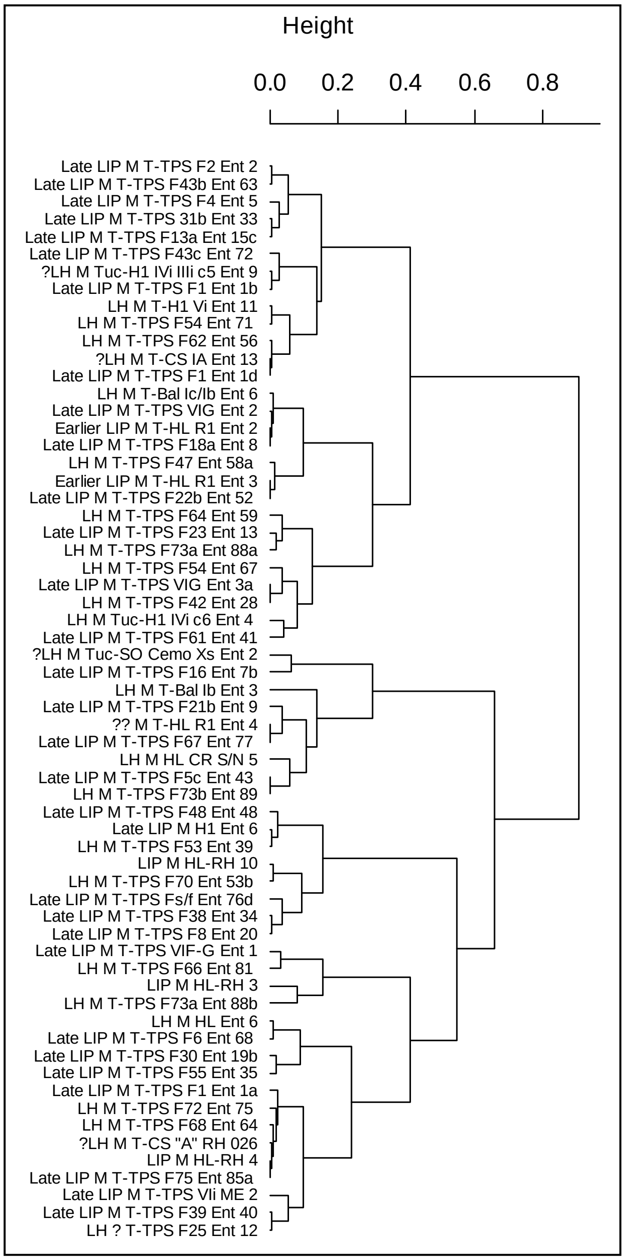

Figure 4.12: All Males: Based on Cranial and Dental Nonmetric Data

All Burial Locations: Cranial Nonmetric Results

The cranial nonmetric results below are based on 19 traits and 103 individuals (Figure 4.13). Once again, the statistical software R and the statistical package “cluster”, Gower’s distance and Ward’s hierarchical cluster analysis were applied to the data (see Appendix H for R code). The maximum height of the cranial dendrogram is 2.0. At a height of 1.0 there are five major clusters, the largest of these contains 36 individuals and the smallest contains 11 individuals.

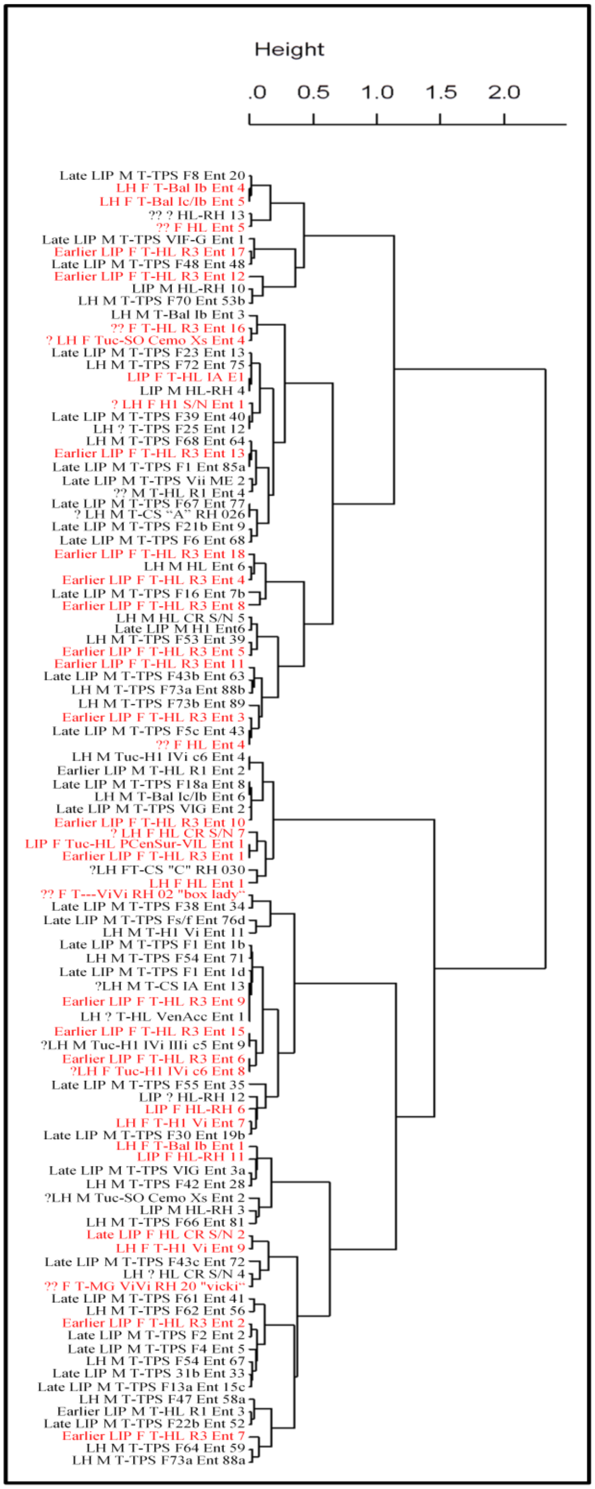

Figure 4.13: All Burial Locations: Based on Cranial Nonmetric Data.

All Burial Locations: Dental Nonmetric Results

The dental nonmetric results are based on 7 traits and 103 individuals. The same procedures applied to cranial nonmetric data were applied to the dental nonmetric data (Gower's distance and Ward's hierarchical cluster analysis). Using R and the packages previously mentioned a distance matrix and dendrogram (Figure 4.14) were generated.

There are several differences that are readily apparent when the dental dendrogram is compared to the cranial dendrogram. The maximum height of the dental dendrogram is 3.5, which is significantly larger than the cranial dendrogram. At a height of 1.0, there are four major clusters, the largest contains of which contains 58 individual and the smallest contains 14 individuals. The dental data clusters individuals more broadly than the cranial nonmetric dendrogram because there are fewer traits being considered, there is higher proportion of missing data, and there appears to be less variation in the dental traits than in the cranial traits.

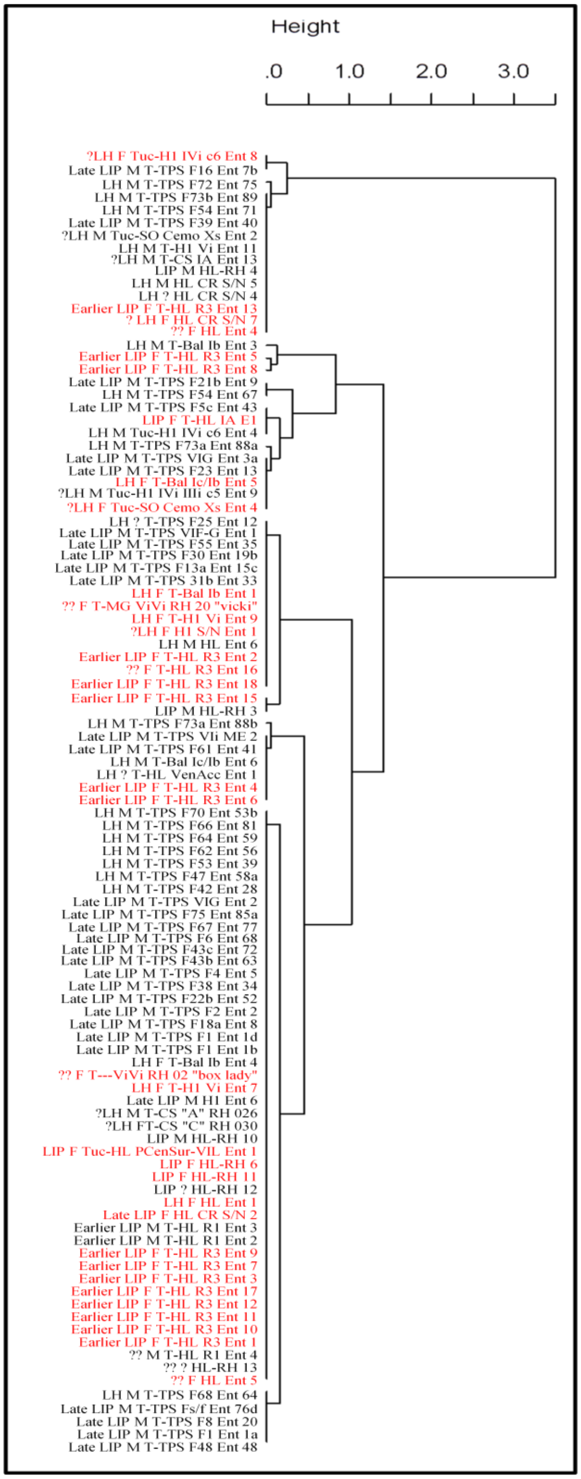

Figure 4.14: All Burial Locations: Based on Dental Nonmetric Data

All Burial Locations: Combined Cranial and Dental Results

The cranial and dental results are based on 26 traits and 103 individuals. Again, a distance matrix was generated in R using the Gower's distance and Ward's hierarchical cluster analysis. From the distance matrix a dendrogram was produced (Figure 4.15). The clusters of individuals do not correspond to burial location or sex. In contrast to the dendrogram based on dental traits alone, within the dendrogram based on the combined data most individuals have a distinct branch within the structure. The height of the combined cranial and dental dendrogram is 1.5, and at a height of 0.5 there are six major groups. The largest group contains 26 individuals and the smallest contains 11 individuals. Using a larger number of traits allows for a more refined analysis between groups simply because there are more variables (i.e., traits) being considered, there is a low proportion of missing data, and there is more variation being used to identify groups of individuals.

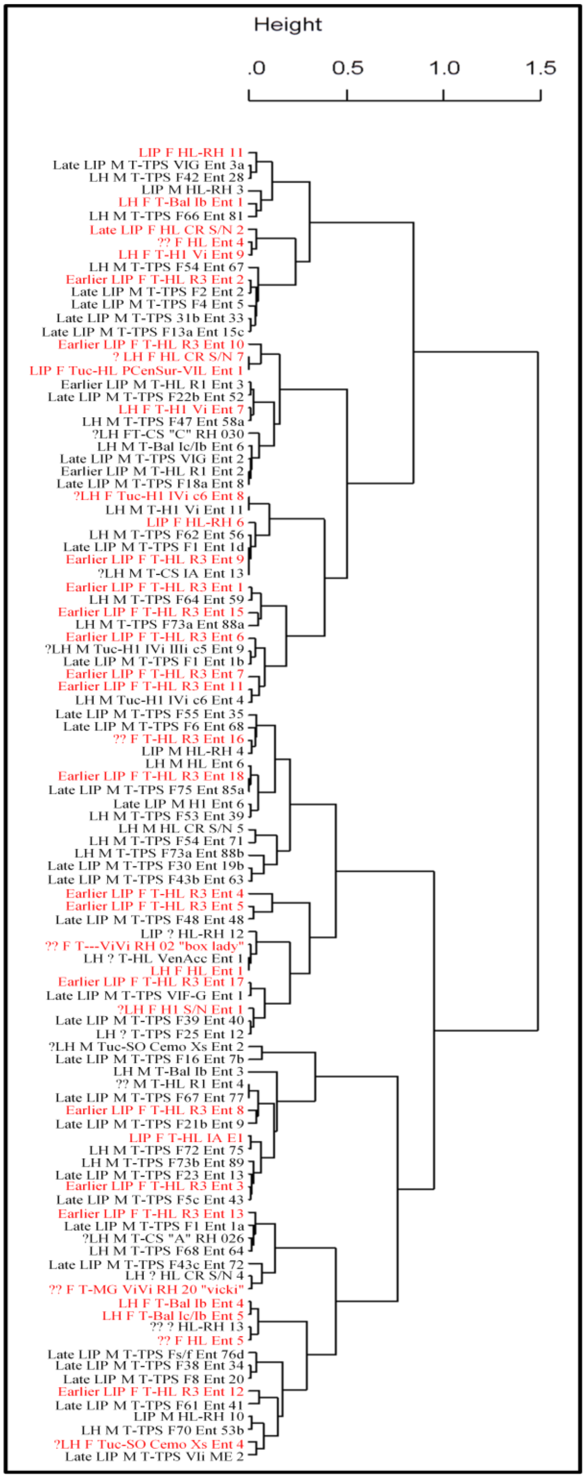

Figure 4.15: **All Burial Locations: Based on Cranial and Dental Nonmetric Data**

Tanglegram Results

The tanglegrams presented below can be used to visually compare the results of several of the dendrograms produced with cranial and dental data (Figures 4.16, 4.17, 4.18). Using the “dendextend” package within the R statistical software, the “tanglegram” function can be applied to two dendrogram that share the same leaves, or nodes. The degree of entanglement is measured between zero and one; achieving zero entanglement means that the two dendrograms being compared are essentially the same (Venkatachalam et al. 2010). Three separate tanglegrams presented are based on the cluster analyses discussed above. The first tanglegram, Figure 4.16, compares the cranial and dental nonmetric dendrograms from the subsample that includes the 37 female individuals found throughout the site. With the entanglement at 0.34, the cranial and dental nonmetric data are at 66 percent agreement in the Figure 4.16 tanglegram. The tanglegram in Figure 4.17 compares the cranial and dental nonmetric dendrograms which includes the 62 male individuals found throughout the site. The Figure 4.17 tanglegram has an entanglement of 0.37, indicating that the two dendrograms being examined are in agreement in 66 percent of cases. The final tanglegram in Figure 4.18 includes all 103 individuals within the sample. The level of entanglement in Figure 4.18 is 0.44, which indicates that the when the entire sample is considered the cranial and dental nonmetric data are in agreement in 56 percent of the cases.

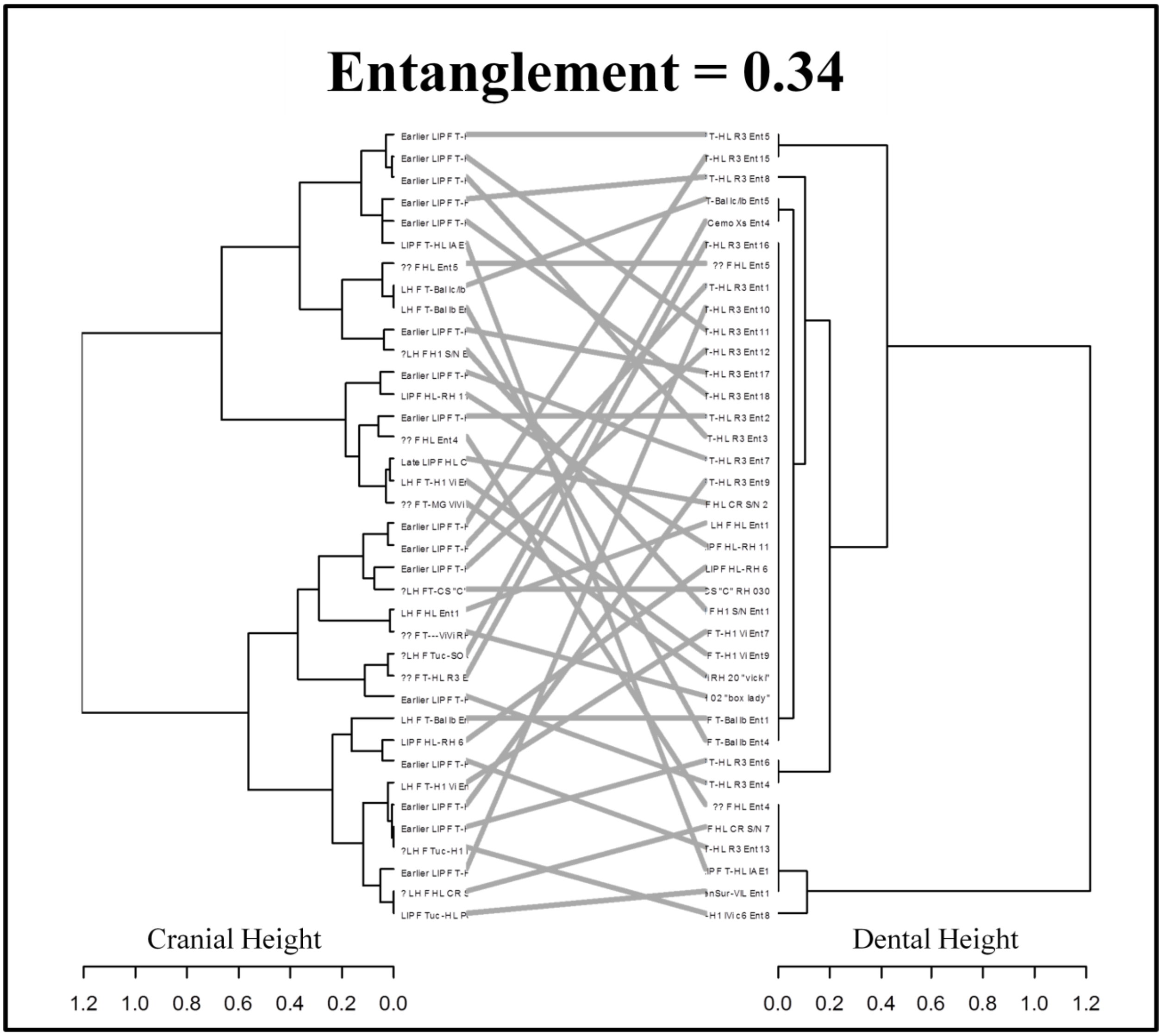

Figure 4.16: All Female Tanglegram: Cranial Dendrogram Compared to Dental Dendrogram

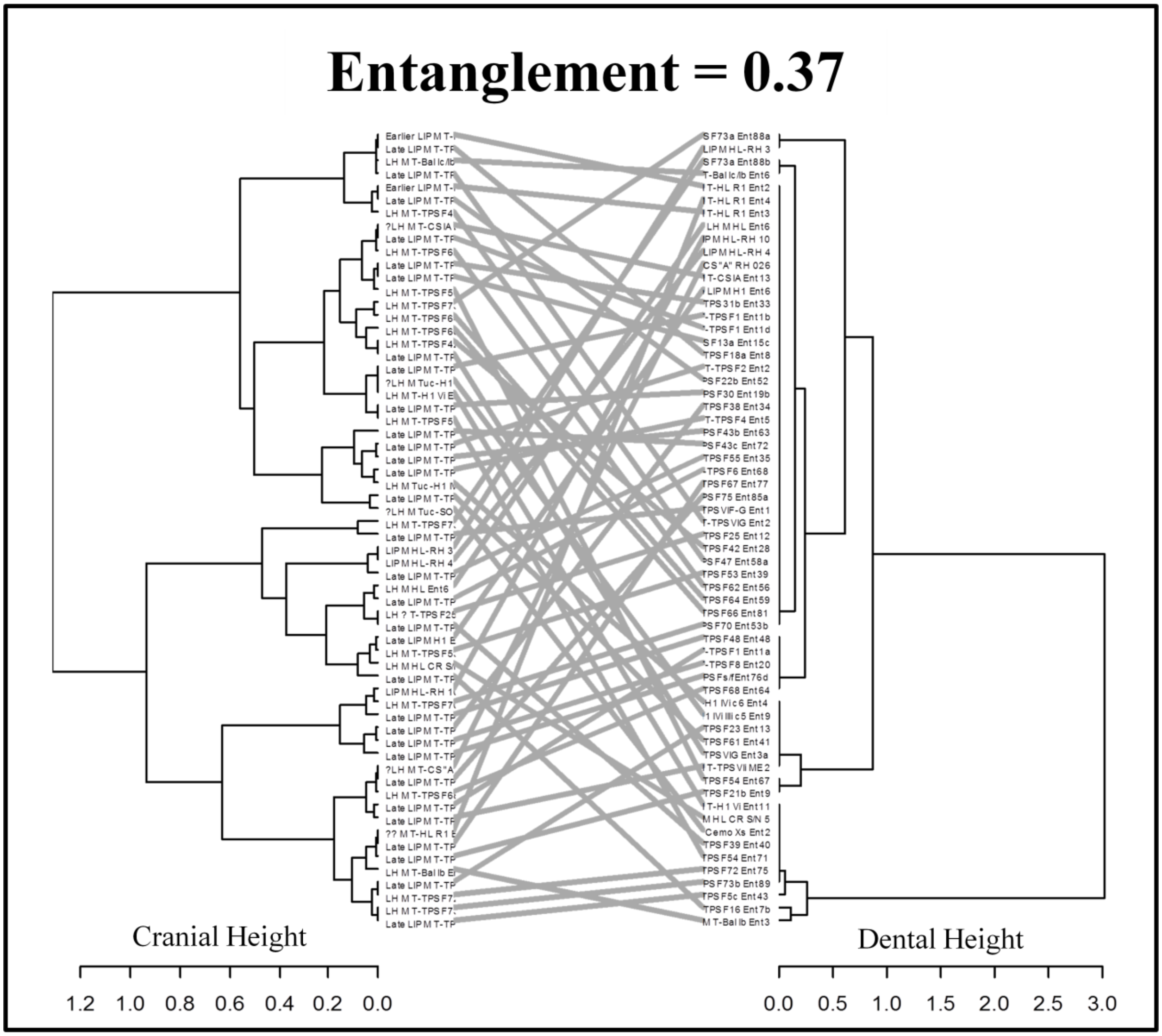

Figure 4.17: All Male Tanglegram: Cranial Dendrogram Compared to Dental Dendrogram

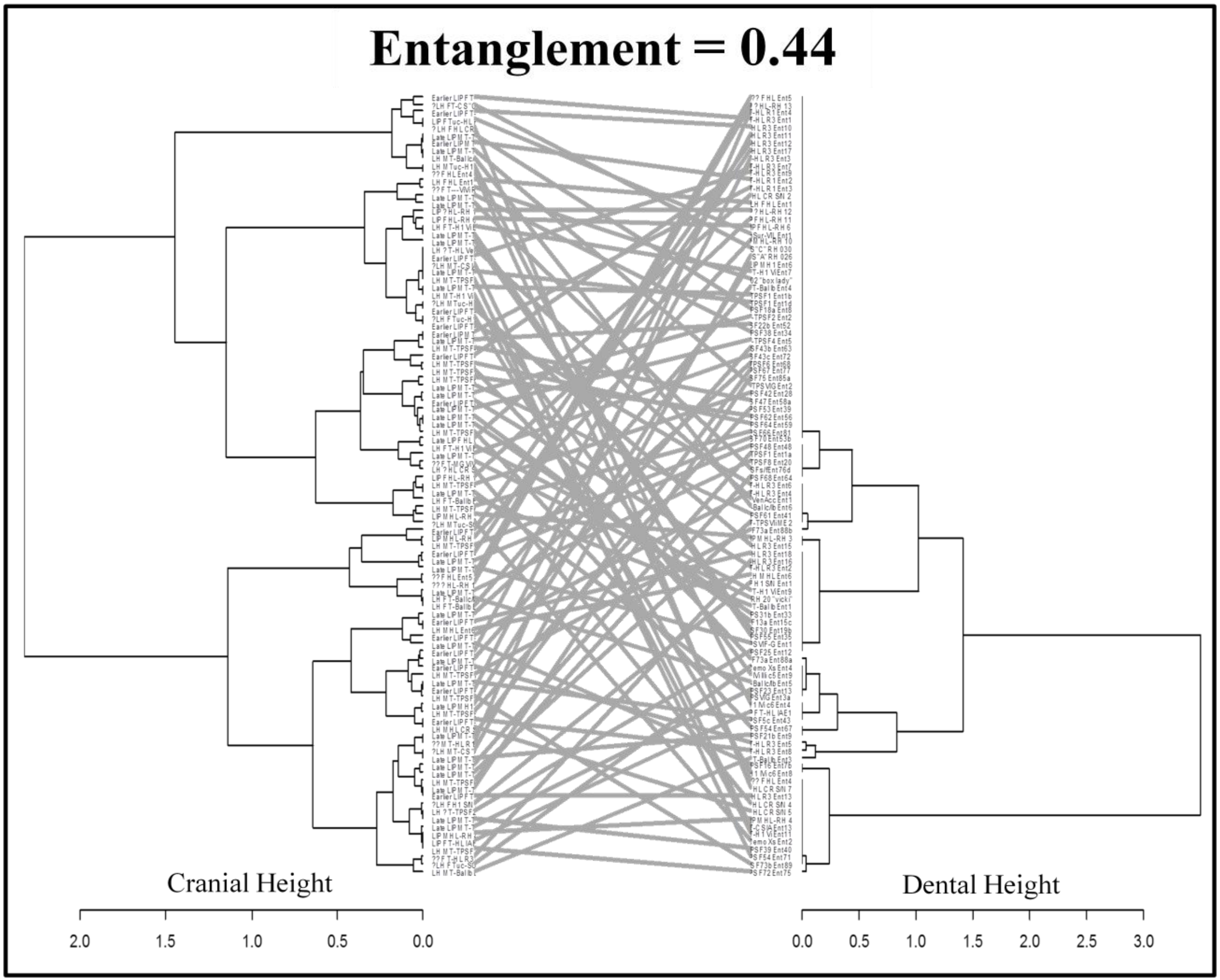

Figure 4.18: All Individuals and All Burial Locations Tanglegram: Cranial Dendrogram Compared to Dental Dendrogram.

Summary

The nonmetric data in this chapter were modified before the final analyses were conducted. Several traits were excluded due to intertrait correlations, intraobserver error and an insufficient number of observations. Several individuals were also excluded from the final analysis due to high numbers of missing values and to make the results comparable within this study. The data used to produce the trait frequencies presented in this chapter were used to investigate sex and burial location differences. Trait frequencies differences were examined with a z-test statistic for the difference between two proportions. The final dataset included 103 individuals, 19 cranial traits, and 7 dental traits. Subsamples of the final dataset were created and examined based on sex and burial context. Gower's distance and Ward's hierarchical cluster analysis were applied and nine dendrograms were produced using R statistical software. The cranial and dental nonmetric dendrograms were then compared using three tanglegrams.

CHAPTER 5: DISCUSSION

Introduction

The results of this research will be discussed in two separate sections, as this research addresses both bioarchaeological questions and methodological issues within biodistance. This chapter will discuss the results of the biodistance analysis in terms of the hypotheses and research questions within this thesis. The archaeological and biological evidence examined in this research are used to investigate communal identity within Túcume. The minimal degree of biological variation at Túcume suggests that there was a high degree of homogeneity at the site. The results have specific implications about the ancient society at Túcume, but also more general implications about human social and community identity within areas where people aggregate to participate in politico-religious and/or economic activities. Identity is a self referential, culturally constructed concept, and thus it is difficult, if not impossible, for anthropologists to *truly* discuss the social identity of ancient peoples. However, social processes influence demes in non-random ways. It is therefore possible to use biological characteristics, such as nonmetric traits, as proxies for certain aspects of identity (Nystrom 2005).

Biological Variation Within Túcume

Sex Differences

In general the results indicate that Túcume, like other Andean populations (e.g., Sutter 2004), does not have a high degree of variability within the deme. The Chimú and the Inca both controlled and maintained political influence over a large geographical area that included multiple valleys and regional centers of power, like Túcume (Dulanto 2008). Yet, Túcume does not appear to have experienced a dramatic influx of individuals from outside the region when both the trait frequency data and cluster analyses are considered. This assertion is, however, buttressed by several caveats and assumptions that will be explored further.

The first hypothesis was designed to determine if there were differences within the deme that would suggest outside genetic information was being introduced in a systematic way, particularly sex based migratory events. To examine potential sex differences within the site the univariate z-test were first performed followed by hierarchical cluster analyses. In Table 4.3, which displays the results of the z-test comparing all of the males to all of the females, two traits exhibited significant differences, the frontal grooves (FRG) with a p-value of 0.017, and mastoid foramen number (MFN) with a p-value of 0.017. To further investigate these differences each burial location was examined in isolation. No sex differences were found within the burial locations as indicated by the p-values in Tables 4.4, 4.5, and 4.6. When the Temple of the Sacred Stone males were compared to the rest of the males within the sample there were also no significant differences (Table 4.7).

To examine the sex differences found between males and females in Table 4.3 more specifically, the non-sacrificed males were compared to all of the females (Table 4.8). This was followed by a z-test to compare the sacrificed males to all of the females (Table 4.9). Interestingly, there were several traits that exhibited significant differences in Tables 4.8 and 4.9. Three traits exhibited significant differences when the non-sacrificed males were compared to all of the females in the sample (Table 4.8): the frontal grooves (p-value at 0.023), post condylar canal (p-value at 0.013), and mastoid foramen number (p-value at 0.008). When the sacrificed males were compared to all of the females in the sample (Table 4.9), two traits had significant p-values, Huschke's tympanic dehiscence (p-value at 0.042), and mastoid foramen number (p-value at 0.018). These results indicate that there are some minor difference between males and females within the sample. While the z-tests performed demonstrate that there are minor trait frequency differences between the males and females, the individuals from the Temple of the Sacred Stone are similar to the other males at the site. This suggests that these sacrificed males were perhaps selected from the local community, as the levels of variation between the Temple of the Sacred Stone individuals are similar to the rest of the individuals found throughout the site. This assertion, however, requires a more nuanced discussion.

None of the cluster analyses performed grouped individuals based on sex. In the first six dendrograms, sex differences within the sacrificed and non-sacrificed groups at the site were examined. The dendrograms in Figures 4.1, 4.2, and 4.3 examine the sacrificed burials from the Temple of the Sacred Stone and from Huaca Larga, and there are no sex based clustering patterns. The non-sacrificed group examined in the dendrograms in Figures 4.4, 4.5, and 4.6 also do not group individuals based on sex. To examine intra-sex levels of variation, and potential burial location patterns (discussed below), the males and females were considered separately in the dendrograms in Figures 4.7 through 4.12. There were no divergent groups or clustering patterns associated with the variables examined within the male only, and female only dendrograms. Finally, when all 103 individuals were examined in the dendrograms in Figures 4.13 through 4.15, once again there were no clustering patterns determined by sex.

If, for example, there was a broader range of variation or there were clustering patterns based on the variables considered in this study, this would have suggested that the people buried within the site were more distantly related, and perhaps came from outside of the deme. The degree of variation found within the sample was notably low, which indicates that the community was likely not composed of many migrants from distant regions. The trait frequency data and the z-tests indicate that there is a high degree of homogeneity between males and females, with no more than three traits exhibiting significant differences in any one test. Moreover, the cluster analyses indicate that there are no patterns based on sex within the sample examined. When both the z-test and cluster analyses results are considered, the significant p-values from the z-tests do not provide firm confirmation of substantial differences between males and females within the sample. The first hypothesis, therefore, was rejected. These results provide important information about the nature of community identity at Túcume, discussed further below.

Burial Location and Temporal Differences

The second hypothesis was developed to determine if individuals would cluster together based on burial location and documented temporal contexts using hierarchical cluster analysis. It was important to investigate these two factors because if the burials clustered together based on location or time period, it could possibly indicate that kin groups were being deliberately interred together, and/or were migrating to the site at one time. The data indicate, however, that this was not necessarily the case, as there were no clustering patterns based on burial location or time period.

Within each dendrogram, the clusters of individuals represent groups that share a higher degree of biological kinship than those from outside of their cluster. It is not possible to determine the degree of relatedness between pairs of individuals through nonmetric trait analysis. "Nonmetric traits are most likely to accurately estimate genetic kinship when the degree of relatedness among some individuals in the sample is higher than amongst others" (Ricaut et al. 2010:362). The second hypothesis is therefore rejected because the burials do not cluster together based on burial location and/or the documented temporal contexts. The major caveat being that the documented time periods are not necessarily based on firm dates.

Community Identity at Túcume: Interpretations and Implications

Intrasite Significance

The results of the nonmetric analysis within this study are similar in several respects to those of Pilloud and Larsen (2011). Using dental metric and nonmetric data, Pilloud and Larsen (2011) discovered that within Neolithic site of Çatalhöyük, Turkey, clusters of individuals that were likely related did not correspond to the burial locations. However, unlike the methods applied in this research, Pilloud and Larsen (2011) included traits that fell below five percent in occurrence. Within Túcume, the clustering patterns suggest that while biological kinship likely played a role in the social organization at Túcume, the locations of the burials do not necessarily reflect this when cranial and dental nonmetric variation is examined.

If there were large differences between males and females, or if there were divergent groups within the dendrogram based on sex, burial location, or documented time period, this might have suggested that groups of closely related kin were moving into the area from previously isolated regions (Fix 2004). This, however, was not the case, suggesting that within the archaeological complex of Túcume there was a high degree of homogeneity, biologically and perhaps socially as well. Mate exchange across social hierarchies at Túcume is one possibility, but the sample may not include many, if any, individuals of lower status, an important caveat discussed below.

While there is clearly a high degree of homogeneity within the sample, this does not entirely rule out the possibility that some migration to the site did in fact occur. The high degree of similarity between the males and females at the site is perhaps evidence of limited external gene flow, or a significant and consistent degree of in-migration from various locations. The results may in fact be congruent with the assumption that migration tends to retard micro-differentiation between populations (Fix 2004). When the previous research at Túcume is taken into consideration (Heyerdahl et al. 1995; Hewitt et al. 2008; Hewitt 2013; Toyne 2008; 2011; 2015a; 2015b;) making inferences about community identity becomes more complicated.

In the preliminary biodistance research conducted at Túcume, Toyne (2008) looked at three groups, the Temple of the Sacred Stone, Túcume, and Kuelap (a highland out-group), primarily to determine if the sacrificed individuals from the Temple of the Sacred Stone were similar to the local sample. The Túcume group within the sample consisted of other males (non-sacrificed) found at the site. The individuals from Kuelap served as an out group for the nonmetric analysis; these individuals were from the archaeology site of Kuelap, located approximately 200 kilometers east of Túcume in the highlands. The nonmetric biodistance analysis conducted by Toyne (2008) indicated that the Temple of the Sacred Stone individuals were more closely related to the Túcume group than to the Kuelap group, as would be expected. Toyne (2008; 2011; 2015a; 2015b) ultimately concluded that the sacrificed individuals from the Temple of the Sacred Stone were likely selected from the local community and may have even volunteered to be sacrificed. Moreover, there specific social identity may not have been particularly important in the context of the sacrificial ritual (Toyne 2015b).

Using oxygen and strontium isotopic analysis, Hewitt (2013) found that there were differential levels of mobility within and between three burial groups (Huaca Larga, the Temple of the Sacred Stone, and South Cemetery) at Túcume. The oxygen isotopic composition data suggested that the individuals from the Temple of the Sacred Stone likely spent their childhoods in a variety of locations, and were highly mobile in adulthood, but spent some time at Túcume (or a region with a similar isotopic signature). The Huaca Larga group, which contained the potentially sacrificed individuals, exhibited isoptopic signatures that placed them in the low to mid-level mobility category, while the South Cemetery contained individuals that likely spent much of their lives at Túcume or within the surrounding area. All of the individuals examined by Hewitt (2013) did, however, exhibit strontium isotopic ratios consistent with Lambayeque valley region. Additionally, Hewitt’s (2013) research had small sample sizes. For example, only 20 of the 116 individuals from the Temple of the Sacred Stone were examined. Concluding that all, or even most, of the individuals from the Temple of the Sacred Stone are non-local is not actually possible at this point, considering the small sample sizes and the inconsistent strontium and oxygen results presented by Hewitt (2013).

How the term “local community” is defined by archaeologists is probably not entirely congruent with how it may have been defined in the past societies being examined (Hegmon 2002). Using architectural or ecological features (e.g., the archaeology site) to delineate between local and non-local community members, at least in terms of this research project, is far too simplistic. Individuals in past social groups may have maintained multiple social identities. Moreover, in contexts where there was a frequent influx of people, where the maintenance of borders (physical and social) may have been difficult, a strict “us” and “them” situation may not have existed. Archaeological extrapolation about the “community” may, therefore, be incongruent with the lived experiences of past peoples (Schachner 2008). At Túcume, the construction, maintenance, and modification of the archaeological complex was a communal act that occurred in association with the three different cultural occupations, the Lambayeque, the Chimú, and the Inca. Communal ritual architecture (and/or activities) should perhaps be viewed as the material residue of social negotiations about the function and form of the local social network, rather than simply as an indicator of community level processes in general (Shachner 2008; Paukertat 2003). Inferences about community identity at Túcume can only be justifiably made with these theoretical caveats in mind, and in light of the previous research conducted at the site and the region.

The conclusions posited by Toyne (2008; 2011; 2015a; 2015b) and Hewitt (2013) may at first glance seem incongruent. However, the biodistance data from this study may perhaps be seen as resolving these apparently disparate conclusions, providing new information and synthesizing this previous research. Understanding how individuals/groups are integrated into cohesive social network provides crucial information about the evolution of politico-religious, economic, and cultural complexity (Stojanowski and Schillaci 2006). When other biodistance research is taken into consideration (e.g., Sutter and Verano 2007; Sutter 2009; Ricaut et al. 2010; Pilloud and Larsen 2011) Túcume does not have a high degree of variability; the results indicate quite the opposite. This study incorporates nonmetric data and uses the same distance method and clustering procedures (Gower’s distance and Ward’s hierarchical cluster analysis) as the Ricaut et al. (2010) study. The results from the current study and the Ricaut et al. (2010) study are not directly comparable, but the maximum height of the dendrogram in their study (approximately 1.2) is one indication of the low level of variability in their sample. The results from the Ricaut et al. (2010) intrasite biodistance study exhibit low levels of variability, suggesting that the population was biologically homogeneous, which is very similar to results in this thesis research.

The archaeological evidence clearly indicates that Túcume was not an isolated community within the wider Lambayeque region. During its apex, Túcume was a large urban complex that was a regional center of social importance, and people would have likely been traveling to the site. Assuming the sample examined is representative of the overall deme, the results presented in Chapter Four suggest that if migrants were traveling to the site they were quickly assimilated into the community; this assimilation would have included mate exchange between local and immigrant family groups. Community interaction was may have been very fluid, and mate exchange practices were as well. Being a member of the community at Túcume perhaps reached outward into the Lambayeque valley region, and there were perhaps kinship networks that maintained this extended community identity.

There was clearly social stratification at Túcume. However, the results suggest that social status and identity within the site was perhaps not based predominantly on biological affinity, if mate exchange occurred across the social status "barrier". The more elite burials from Huaca Larga, for example, might be expected to cluster together if these individuals were more closely related to each other than the other individuals in the sample. Yet, clustering based on burial location was not apparent in any of the statistical analyses performed. Corruccini and Shimada (2002) conducted an intracemetery dental nonmetric biodistance study on 29 individuals from a tomb in the platform mound of Huaca Loro at Batán Grande, Perú. Their results indicate that the elite individuals interred in the tomb likely represent a group of closely related kin. From the archaeological and biodistance data, Corruccini and Shimada (2002) suggest that elite status was likely inherited. It is possible that the sample considered in this thesis research is not representative of the entire social spectrum (from elites to commoners) that likely existed in ancient Túcume. Considering all of the burials examined in this study are interred within the archaeological complex itself, it is possible that these individuals represent the more elite members of the community; the non-elites may have been buried in a less conspicuous location. Even the burials from the South Cemetery, that are not considered to be part of the sites upper elite (Narváez Vargas 1995a), are still buried within the vicinity of the archaeological complex itself. The low levels of variation found within the sample may represent mate exchange between upper and lower level elite family groups, spanning the entire occupation of the site. This possibility provides a new suggestion about the sacrificed individuals found at the site. If the individuals within the sample are part of a kinship network of different elite groups at the site, inherited social status may have not necessarily been a parameter that excluded individuals from being sacrificed. These possibilities highlight the inherent limitations within this study and simultaneously provide suggestions for future research that should be conducted. One of the major limitations of this study is that while phenotypic biodistance studies provide key insights about population history and structure they do not possess the resolution necessary to determine the precise degree of biological kinship between individuals (Ricaut et al. 2010). Moreover, as an intrasite biodistance analysis this research did not incorporate an "out group" for which to compare the sample. While it is clear that there is a low level of variation within the sample, understanding the site from a regional perspective, by including a small sample of individuals from a near by site for example, may have provided a more contextualized understanding of the biological variation. The site has regional importance that must be discussed as well.

Regional Significance

Within the context of previous research conducted in the Andean north coast region, it appears that Túcume was not an isolated deme. Sutter (2009) conducted a dental nonmetric biodistance analysis that examined several mortuary samples within the Andean north coast region. The results indicated that within the Early Intermediate Period (200 BC-AD 750) the mortuary samples examined represent a coherent breeding population. All of the mortuary samples examined by Sutter (2009) predate the individuals examined thus far at Túcume by several hundred years. With this in mind, it would not be unrealistic to propose that the ancient people within the Lambayeque valley region, a region that was not included in the Sutter (2005; 2009) research, was likely a coherent geographical deme.

There has been biodistance and isotopic research conducted at other sites within the Andean north coast region to investigate the identity of sacrificed individuals specifically (e.g., Sutter and Verano 2007; Verano 2009; Turner et al. 2013; Toyne et al. 2014). The results from the current study, in part, address the different interpretations regarding the identity of the sacrificed burials at Túcume (Toyne 2008; 2011; Hewitt 2013). As Toyne et al. (2014) points out, many of the sacrificed individuals at Huacas de Moche (ca. AD 100-850) come from diverse origins. The Toyne et al. (2014) results can be paralleled to the research conducted by Hewitt (2013) at Túcume because, as previously mentioned, the isotopic evidence suggests that the individuals from the Temple of the Sacred Stone come from diverse points of origin in the region. Conversley, Turner et al. (2013) investigated the identity of sacrificed individuals at Huaca de los Sacrificios at the Chotuna-Chornancap Archaeological Complex (AD 1450–1532), a site located approximately 25 kilometers southwest of Túcume. Turner et al. (2013) found that sacrificed individuals found at this site were of local origin based on stable carbon, nitrogen, and oxygen isotope values. Chotuna-Chornancap was controlled by both the Chimú, and later the Inca, much like Túcume. The local ritual traditions on the north coast were not greatly modified by the Chimú or the Inca (Ramírez 1990). The Inca likely maintained economic control and co-opted the entrenched traditions and used them as an opportunity to extract tributes from centers of regional importance like Túcume and Chotuna-Chornancap (D’Altroy 1992; Turner et al. 2013).

These examples are pertinent because they provide a regional and temporal backdrop for a discussion of community identity at Túcume. The results suggest that the deme was generally biologically homogeneous. Within the Andes and in other parts of the world as well, geographic boundaries often operated as barriers between groups of people (e.g., Sutter 2005; O'Rouke and Enk 2012). These barriers, overtime result in genetic changes in the population (i.e., genetic drift), and understanding such evolutionary changes in populations as an inherently statistical process (Moran 1962; Sterelny and Kitcher 1988) is the fundamental, yet often unstated, assumption within biodistance and genetic distance research. The statistical results in this study suggest that Túcume was a relatively isolated deme, if the sample is in fact representative of the population. The expansion of the Chimú and Inca empires could have increased the genetic variation at Túcume and the surrounding region: previously isolated communities interacting and thus new genetic information is potentially introduced. While there is clear archaeological evidence that the Chimú and Inca exerted control over the site (Narváez Vargas 1995a; 1995b; Sandweiss 1995; Heyerdahl 1995), this does not appear to have dramatically influenced the biological variation at the site. Goods and services were exchanged, and religious syncretism may have occurred as well, however, but major gene flow does not appear to have been occurring. Being a member of the community at Túcume appears to have had a lot to do with biological kinship. The kinship networks within the site may represent the upper echelons of the social hierarchy at Túcume, and if so this suggests that elite status did not exclude individuals from human sacrifice. If elite status at Túcume was based on inheritance, similar to other contemporaneous sites (e.g., Corruccini and Shimada 2002), then being male and part of an elite lineage may have been one "inclusion factor" involved in the sacrificial process. If, however, the sample examined includes individuals from a variety of social positions, then mate exchange may have been fluid across the social hierarchy. That is, biological kinship may have been shared across social "barriers", and the practice of human sacrifice perhaps fostered integration between the community members and the dead (Toyne 2015a) precisely because there was an awareness of biological heritage within this ancient society.

Methodological Investigation: Cranial and Dental Nonmetric Data

The third hypothesis was developed to address the relationship between the cranial and dental nonmetric traits examined in this study. As discussed in Chapter Two, cranial and dental nonmetric traits are often considered in an exclusive manner. The results of the multivariate analysis suggest that the three broad forms in which the data are considered (cranial, dental, and cranial and dental combined) in this study share one major similarity. All of the dendrograms presented suggest that a high degree of homogeneity existed within and between the burial groups sampled at Túcume.

The application of the tanglegram function was used as the primary means of examining the level of agreement between cranial and dental nonmetric dendrograms. The results from the three tanglegrams indicate that there is not a high level of agreement between the cranial and dental dendrograms. When all of the females were considered in an exclusive manner there was 66 percent agreement between the cranial and dental dendrograms. When the males were examined in an exclusive manner there was 63 percent agreement. Finally, when all of the individuals in the sample were considered in tandem, there was only 56 percent agreement between the cranial and dental nonmetric dendrograms. The results suggest, tentatively, that the third hypothesis can not be rejected. However, the application of tanglegrams within this research should be considered as exploratory rather than a definitive statement about the relationship between cranial and dental nonmetric data.

The tanglegram results perhaps imply that when the dental and cranial data are considered separately, these two types of nonmetric data may offer different views of the overall genetic/biological variation within a particular deme. For example, cranial traits are thought to reveal changes within a population over only a few generations, while dental nonmetrics are thought to represent older evolutionary relationships because they have a more conservative rate of change (Hanihara et al. 2003; Lee 2007). Furthermore, nonmetric traits may not provide the resolution necessary to distinguish between very proximate groups of people (Ricaut et al. 2010; Herrera et al. 2014; Hubbard et al. 2015), an inherent methodological limitation within this study. Additionally, Herrera et al. (2014) discovered that cranial nonmetric data are highly correlated with Y-chromosome data; yet they were not able to test for dental nonmetric correlation with DNA data due to insufficient sample sizes. Due to the relatively large number of cranial traits being considered within this thesis research, the results may have an embedded patrilineal bias; yet, further research into the inheritance of nonmetric traits is required to make a definitive statement on this possibility.

The majority of individuals examined in this study exhibit cranial modification, and thus the cranial nonmetric data may exhibit a higher level of environmental influence. As discussed in Chapter Two, research has been conducted to investigate the influence cranial modification has on the occurrence of nonmetric traits. However, using a large number of traits may serve to mitigate the effects that cranial modification may have on biodistance predictions (Del Papa and

Perez 2007). Additionally, most of the cranial nonmetric traits found to be influenced by cranial modification (e.g., El-Najjaar and Dawson 1977; Verano 1987; Konigsberg et al. 1993; O'Loughlin 2004; Del Papa and Perez 2007; Perez et al. 2007) were removed from the final analysis for other reasons. Wormian bones have been found to be the most effected by cranial modification, but using wormian bones in biodistance studies does not produce inconsistencies; inconsistencies have been found when only wormian bones were used in biodistance predictions (Del Papa and Perez 2007). With these facts in mind, it is my opinion that the most reliable biodistance predictions generated in this study come from the combined cranial and dental nonmetric datasets.

Summary

The hypotheses explored within this thesis were discussed and the results of which were interpreted. Overall the cranial, dental, and cranial and dental combined data sets appear to provide complementary information. Individuals within the site do not appear to cluster together based on sex, burial location, or time period. In light of the previous research conducted at Túcume and the biodistance analyses performed, it is possible that migration to the site was occurring consistently from the surrounding area. Community identity at the site may have extended outward into the Lambayeque valley region, and was perhaps maintained through kinship networks. The biodistance results (and the archaeological evidence) potentially indicate that the sample includes upper and lower level elite family groups that participated in mate exchange over the span of occupation at the site. If, however, the sample includes individuals from the multiple levels of the social hierarchy that likely existed at Túcume, social barriers within the site may have been relatively fluid, at least in terms of mate exchange practices. The social status of the sacrificed individuals at the site, specifically the Temple of the Scared Stone individuals, is largely unknown due to the lack of grave goods. It is possible that these individuals, who make up a large portion of the sample examined in this study, come from disparate social positions within the community. If a large portion of the Temple of the Sacred Stone individuals came from elite family groups, then the results of this study suggest that being a male member of the elite may have increased your likelihood to be sacrificed. This is an intriguing but tentative assertion that requires more investigation.

The methodological aspect of this research and other nonmetric studies suggests that when possible, using both the cranial and dental nonmetric data in concert is perhaps better than using them individually. At the level of the individual, the cranial and dental dendrograms were in agreement in only a little more than half the cases. Combining these datasets will mitigate the influence of environmental factors, which cranial nonmetric traits are more susceptible to. Combining these two datasets will also provide a better snapshot of the genetic variation because dental traits likely represent older evolutionary relationships and cranial traits potentially represent more recent shifts within particular demes.

CHAPTER 6: SUMMARY AND CONCLUSIONS

The contributions made by this research will be discussed in two separate sections within this chapter, followed by potential future directions that could be explored. This research has made a significant contribution to the Andean archaeological literature and the research into bioarchaeological investigations of identity, but also explores an innovative methodological approach within biodistance studies. The research questions and the subsequent discussion of the results will be succinctly presented as well.

Biological Variation and Community Identity at Túcume

The biodistance analysis conducted in this research demonstrates that there is a high degree of biological homogeneity at Túcume. There were no major differences between males and females, nor were there any clustering patterns that corresponded with sex, burial location, and/or the documented temporal contexts. The data also indicate that the sacrificed and non-sacrificed individuals had similar levels of variation, even though the isotopic evidence (Hewitt 2013) suggests many of the sacrificed individuals may have spent their childhoods in other areas within the Lambayeque valley region. The biodistance results provide several possible conclusions regarding the nature of community identity in ancient Túcume.

When the biodistance results are considered in light of the previous research conducted at the site (e.g., Toyne 2008; 2011; 2015a; 2015b; Hewitt 2013), it is possible that kinship networks from the surrounding Lambayeque valley region maintained an extended community identity. Large urban areas of political and religious significance within the region, like Túcume, had a homogenizing effect on the deme, both biologically and socially. Such urban spaces likely drew people in to participate in everyday activities (e.g., exchange of goods) and ritual activities (e.g., sacrificial rituals) that perhaps reinforced the social ties between sites throughout the region. Alternatively, the sample may represent kin groups that held higher status in the community, which might explain the low levels of variation found in the sample. The social status/positions held by sacrificed individuals from the Temple of the Sacred Stone is not known because these individuals were not buried with any grave goods, yet these individuals were biologically indistinguishable from the rest of the sample. If the sample is predominantly composed of the upper social ranks of the community, then males sharing biological kinship with the elite may have been more likely to have been sacrificed. If, however, the sample is composed of individuals from a wide range of social positions, then it is likely that mate exchange was occurring across the social hierarchy, and that community identity was perhaps reified through the sacrificial process. Needless to say, this research has ultimately provided more questions than answers, and further research is needed to answer these intriguing questions about the ancient community at Túcume.

Cranial and Dental Nonmetric Investigation

All of the dendrograms produced in this study exhibit similar results in terms of the low levels of variability within the sample. However, when several of the cranial and dental nonmetric data were compared with the tanglegram function (Figures 4.16 - 4.18) there was not a high level of agreement between the two datasets. The highest level of agreement, at 66%, was found when all of the females within the sample were examined exclusively. Considering cranial and dental nonmetric traits exhibit different rates of change within populations (Hanihara et al

2003; Lee 2007), it is likely that the general low level of agreement between these two datasets demonstrates this differential rate of change. Using a large number of nonmetric traits will provide a more complete picture of the variability within the deme (Herrera et al. 2014), while simultaneously mitigating the influence that cranial modification may have on the biodistance predictions being made (Del Papa and Perez 2007). In light of these insights, I would tentatively argue that using cranial and dental nonmetric traits in tandem will likely provide a more accurate representation of the overall variability. The dendrograms produced from the combined cranial and dental nonmetric data are perhaps the most reliable. This assertion, however, cannot be adequately confirmed without future research into this topic.

Future Directions

There are several lines of inquiry that this research opens for future studies. Perhaps the most obvious would be an expanded biodistance study that includes samples from other arcaheological sites from the surrounding Lambayeque valley region. Using the same methodology but including individuals from other contemporaneous archaeology sites (e.g., the Chotuna-Chornancap Archaeological Complex) would further confirm/reject the extended community identity tentatively proposed within this study. Furthermore, almost half of the individuals in this study were sacrificed or are potential sacrificial inclusions. The biodistance data indicates there is a high degree of homogeneity within the sample, but what does this mean about the nature of community identity in ancient Túcume? Are the sacrificed individuals part of an elite lineage, or are they from a deme that is biologically homogenous, where mate exchange occurred across the social hierarchy at Túcume? If the social identity of the sacrificed was not of primary importance as suggested by Toyne (2015b), then what was important? Using DNA analysis (Y-chromosome and mtDNA) could be used to further investigate these questions and would serve to further confirm (or possibly reject) the findings of this study. There were minor differences found between the males and females within the site and further research using DNA analysis would undoubtedly provide a finer grain resolution of the biological relatedness between the sexes at Túcume. Using DNA analysis may also be useful in investigating the differences within and between burial locations and the documented time periods at the site.

The methodological investigation explored in this thesis certainly requires further research as well. Other studies that involve cranial and dental nonmetric traits and genetic data (e.g., Herrera et al. 2014; Hubbard et al. 2015) have demonstrated the need for more research into nonmetric traits. Future research at Túcume may allow for a better understanding of the underlying genetic components involved in nonmetric traits. As of yet, there has been no research at Túcume that has specifically incorporated genetic data. There are still many unanswered question about the ancient community at Túcume, and incorporating more lines of evidence may offer totally new interpretations about the nature of community identity at the site, as this research has attempted to demonstrate.

APPENDIX A: CRANIAL NONMETRIC TRAIT RECORDING FORM

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Location/Site Name (#): ______________________________ **Observer:** _______________ **Date (M/D/Y):** _________________

Burial/Sample Identifier (#): ________________**Age Range:** _____________ **Sex: M M? F F? ? Cultural Affiliation:** __________

*Directions: Do not record information in shaded boxes. *Note: a value of 0 is "absent"; 9 is "unobservable unless specified otherwise.*

Cranial Traits	R	M	L	Dichotomization	Comments
Frontal View	■	■	■	present= "1" absent= "0"	■
1) Metopic Suture- METO 1: partial 2: complete	■		■	2 = present	
2) Infraorbital Suture- IOS (in relation to zygomaxillary suture) 1: running medially 2: touching at one point 3: blending with it for some distance		■		2-3 = present	
3) Multiple Infraorbital Foramen - MIF 0: no true foramen 1: one 2: two 3: three or more		■		2-3 = present	Lingula or small osseous bridging?
4) *Zygomatico-Facial Foramen Absent- ZFFA 0: no true foramen 1: one large 2: one large & one small 3: two large 4: two large & one small 5: one small 6: multiple small		■		1-6 = absent 0 = present	
5)*Supraorbital Foramen- SOFO 1: one 2: multiple		■		2 = present	
6) Supraorbital Notch- SPON 1: present, < ½ occluded by spicules 2: present, > ½ occluded by spicules 3: present, but degree of occlusion unknown 4: multiple notches		■		2-4 = present	
7) Frontal Grooves- FRG 1: one 2: two 3: three or more		■		1-3 = present	
8) Trochlear Spine- TRS 1: trace 2: moderate (<2mm) 3: strong (>2mm)		■		1-3 = present	
9) *Anterior Ethmoid Extrasutural- AETH 1: sutural 2: exsutural 3: suture obliterated		■		1 = absent 2 = present 3 = unobservable	
10) Posterior Ethmoid Extrasutural- PETH 1: one 2: two 3: three or more		■		2-3 = present	
Superior and Posterior View	■	■	■	■	■
11) Bregmatic Bone- BB 1: present	■		■	1 = present	
12) Parietal Foramen Location- PFL 1: on parietal 2: in suture		■		2 = present	More than one (side)?
13) Os Inca 0: complete occipital, or partial Os Inca 1: one complete Inca bone 2: bipartite 3: tripartite	■		■	1-3 = present	
14) Ossicle at Lambda- OAL 1: present	■		■	1 = present	
15) Lambdoid Ossicle – LO 1:present		■		1 = present	
16) Coronal Ossicle - COS 1: present		■		1 = present	
17) Sagital Ossicle - SOS 1: present	■		■	1 = present	
Basal View	■	■	■	■	■
18) Maxillary Torus- MXT 1: small 2: large		■		1-2 = present	
19) Palatine Torus- PALT 1: trace 2: medium 3: strong 4: excessive		■		1-4 = present	

Location/Site Name (#): ______________________ **Observer:** ____________ **Date (M/D/Y):** ______________

Burial/Sample Identifier (#): ____________ **Age Range:** __________ **Sex: M M? F F? ? Cultural Affiliation:** ________

*Directions: Do not record information in shaded boxes. *Note: a value of 0 is "absent"; 9 is "unobservable unless specified otherwise.*

Cranial Traits	R	M	L	Dichotomization	Comments
Basal View					
20) *Accessory Lesser Palatine Foramen- ALPF 0: no true foramen 1: one foramen 2: two foramen 3: three or more foramen				2-3 = present	
21) Precondylar Tubercle- PCTB 1: bilateral weak expression 2: bilateral strong expression 3: medial tubercle with articular facet				1-3 = present	
22) Hypoglossal Canal Bridging- HYP 1: total division				1 = present	Trace or incomplete bridging?
23) Condylar Facet Double - COFD 1: partial, deep furrow 2: complete division				2 = present	
24) Postcondylar Canal -POCS 1: present				1 = present	
25) Paracondylar Process- PCP 1: small (<1mm) 2: medium (>1mm<3mm) 3: strong (>3mm)				0-1 = absent 2-3 = present	
26) Intermediate Condylar Canal- ICC 1: present (complete bridging)				1 = present	
27) *Pterygospinous Bridge- CIV 1: trace 2: incomplete 3: complete				0-2 = absent 3 = present	
28) *Pterygoalar Bridge- PTAB 1: trace 2: incomplete 3: complete				0-2 = absent 3 = present	
29) Huschke's Tympanic Dehiscence – HSK 1: trace 2: medium 3: strong 4: excessive				1-4 = present	
30) Foramen Spinosum Open - FOSO 1: present				1 = present	
31) Foramen Ovale Incomplete - FOI 1: present				1 = present	
Lateral View					
32) Asterionic Bone- AST 1: present				1 = present	
33) Marginal Foramen of Tympanic Plate - MFTP 1: present				1 = present	
34) *Mastoid Foramen Number- MFN 0: no true foramen 1: one 2: two 3: three				0-1 = absent 2-3 =present	
35) Epipteric Bone - EPB 1: one 2: two 3: three or more				1-3 = present	
36) Auditory Exostosis- AEX 1: <1/3 canal occluded 2: 1/3 – 2/3 canal occluded 3: >2/3 canal occluded				2-3 = present	
37) Occipito-Mastoid Bone- OMB 1:present				1 = present	
38) Parietal Notch Bone- PNB 1: present				1 = present	
Mandibular Traits					**Additional Comments**
39) * Multiple Mental Foramen- MMEN 0: no foramen 1:one 2: more than one				0 - 1 = absent 2 = present	
40) Mylohyoid Bridge- MYB 1: present				1 = present	
41) Mandibular Torus- MT 1: weak 2: medium 3: strong				1-3 = present	

APPENDIX B: DENTAL NONMETRIC TRAIT RECORDING FORM

Page 1 of 2

Location/Site Name (#): ______________________________ **Observer:** ______________ **Date (M/D/Y):**________________

Burial/Sample Identifier (#): ________________ **Age Range:** ______________ **Sex: M M? F F? ? Cultural Affiliation:** ________

Directions: Do <u>not</u> record information in shaded boxes. *See Dental Nonmetric Recording Sheet Key for scoring values for each trait.

<u>Dental Nonmetric Recording Sheet</u>

Upper Jaw	**RI1**	**LI1**	**RI2**	**LI2**	**RC**	**LC**	**RP3**	**LP3**	**RP4**	**LP4**	**RM1**	**LM1**	**RM2**	**LM2**	**RM3**	**LM3**
Status/ Wear																
Caries																
Trait – Abbreviation																
Winging - WING			▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
Labial Curve - LABC			▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
U. Shovel - USHOV							▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
U. Double Shovel - UDBS									▨	▨	▨	▨	▨	▨	▨	▨
Interrup. Groove - IG					▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
Tuberculum Den. - TB							▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
Me. Ridge - MRIG	▨	▨	▨	▨			▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
Dis. Acc. Ridge - DAR	▨	▨	▨	▨			▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
Me. & Di. Acc. Csp. - MDAC	▨	▨	▨	▨	▨	▨					▨	▨	▨	▨	▨	▨
Distal Sagital Ridge - DSR	▨	▨	▨	▨	▨	▨			▨	▨	▨	▨	▨	▨	▨	▨
Root Number- URNUM	▨	▨	▨	▨	▨	▨					▨	▨	▨	▨	▨	▨
Metacone - META	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Hypocone – HYPO	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Cusp 5 - UCSP5	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Carabelli's Trait - CARA	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Parastyle - PARA	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Enamel Ext. - UENEX	▨	▨	▨	▨	▨	▨										
Odontome - UODON	▨	▨	▨	▨	▨	▨					▨	▨	▨	▨	▨	▨
Peg/reduce - UPEG	▨	▨			▨	▨	▨	▨	▨	▨	▨	▨	▨	▨		
Cong. Absence - UCONAB	▨	▨			▨	▨	▨	▨			▨	▨	▨	▨		
Extra Teeth -																
Comments:																

Adapted from (Turner et al. 1991: 29; Sutter 1997: 151)

Page 2 of 2

Location/Site Name (#): ____ **Observer:** __________________ **Date (M/D/Y):** ____________________

Burial/Sample Identifier (#): _____________________ **Age Range:** _________________ **Sex: M M? F F? ? Cultural Affiliation:** __________

Directions: Do <u>not</u> record information in shaded boxes. *See Dental Nonmetric Recording Sheet Key for scoring values for each trait.

Dental Nonmetric Recording Sheet

Lower Jaw	**RI1**	**LI1**	**RI2**	**LI2**	**RC**	**LC**	**RP3**	**LP3**	**RP4**	**LP4**	**RM1**	**LM1**	**RM2**	**LM2**	**RM3**	**LM3**
Status/ Wear																
Caries																
Trait - Abbreviation																
L. Shovel - LSHOV					▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
L. Double Shovel - LDBS					▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
L. Dis. Acc. Ridge - LDAR	▨	▨	▨	▨			▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
Canine Root Num. CRN	▨	▨	▨	▨			▨	▨	▨	▨	▨	▨	▨	▨	▨	▨
Tome's Root - TOMR	▨	▨	▨	▨	▨	▨			▨	▨	▨	▨	▨	▨	▨	▨
Lingual Csp. Var. LCV	▨	▨	▨	▨	▨	▨					▨	▨	▨	▨	▨	▨
Protostylid - PROTO	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Cusp Num. - CSPNM	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Cusp 5 - LCSP5	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Cusp 6 - LCSP6	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Cusp 7 – LCSP7	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Root Number - LRNUM	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Groove Pattern – GRVPT	▨	▨	▨	▨	▨	▨	▨	▨	▨	▨						
Odontome - LODON	▨	▨	▨	▨	▨	▨					▨	▨	▨	▨	▨	▨
Cong. Absence - LCONAB			▨	▨	▨	▨	▨	▨			▨	▨	▨	▨		
Extra Teeth																
Comments:																

Adapted from (Turner et al. 1991: 29; Sutter 1997: 151)

APPENDIX C: TRAIT ABBREVIATION AND DICHOTOMIZATION

Nonmetric Trait	Abbreviation	Range	Dichotomization	Trait Description/Reference
Metopic Suture	METO	0-2	2 = present	Ossenberg 1969: 24 Hauser and DeStefano 1989: 46 Berry and Berry 1967: 367
Infraorbital Suture	IOS	0-3	2-3 = present	Ossenberg 1969: 31 Hauser and DeStefano 1989: 67
Multiple Infraorbital Foramen	MIF	0-3	2-3 = present	Berry and Berry 1967: 370 Hauser and DeStefano 1989: 70
Zygomatico-Facial Foramen Absent	ZFFA	0-6	0 = present	Berry and Berry 1967: 369 Hauser and DeStefano 1989: 224
Supraorbital Foramen	SOFO	0-2	1-2 = present	Hauser and DeStefano 1989: 50 Buikstra and Ubelaker 1994: 87
Supraorbital Notch	SPON	0-4	2-4 = present	Berry and Berry 1967: 369 Hauser and DeStefano 1989: 50 Buikstra and Ubelaker 1994: 87
Frontal Grooves	FRG	0-3	1-3 = present	Ossenberg 1969: 131 Hauser and DeStefano 1989: 48
Trochlear Spine	TRS	0-3	1-3 = present	Ossenberg 1969: 131 Hauser and DeStefano 1989: 48
Anterior Ethmoid Extrasutural	AETH	0-3	2 = present	Berry and Berry 1967: 370 Hauser and DeStefano 1989: 59
Posterior Ethmoid Extrasutural	PETH	0-3	2-3 = present	Berry and Berry 1967: 370 Hauser and DeStefano 1989: 59
Bregmatic Bone	BB	0-1	1 = present	Berry and Berry 1967: 367 Hauser and DeStefano 1989: 84
Parietal Foramen Location	PFL	0-2	2 = present	Berry and Berry 1967: 366 Hauser and DeStefano 1989: 78
Os Incae	OSINC	0-3	1-3 = present	Ossenberg 1969: 80 Hauser and DeStefano 1989: 99
Ossicle at Lambda	OAL	0-1	1 = present	Berry and Berry 1967: 365 Hauser and DeStefano 1989: 84
Lambdoid Ossicle	LO	0-1	1 = present	Berry and Berry 1967: 366 Hauser and DeStefano 1989: 84
Coronal Ossicle	COS	0-1	1 = present	Berry and Berry 1967: 367 Hauser and DeStefano 1989: 84
Sagital Ossicle	SOS	0-1	1 = present	Hauser and DeStefano 1989: 84
Maxillary Torus	MXT	0-2	1-2 = present	Berry and Berry 1967: 369 Hauser and DeStefano 1989: 180
Palatine Torus	PALT	0-4	1-4 = present	Hauser and DeStefano 1989: 174
Accessory Lesser Palatine Foramen	ALPF	0-3	2-3 = present	Berry and Berry 1967: 369
Precondylar Tubercle	PCTB	0-3	1-3 = present	Berry and Berry 1967: 368 Ossenberg 1969: 161 Hauser and DeStefano 1989: 134
Hypoglossal Canal Bridging	HYP	0-1	1 = present	Berry and Berry 1967: 368 Ossenberg 1969: 147 Hauser and DeStefano 1989: 125
Condylar Facet Double	COFD	0-2	2 = present	Berry and Berry 1967: 368 Hauser and DeStefano 1989: 116

Nonmetric Trait	Abbreviation	Range	Dichotomization	Trait Description/Reference
Postcondylar Canal	POCS	0-1	1 = present	Berry and Berry 1967: 368 Ossenberg 1969: 104 Hauser and DeStefano 1989: 114
Paracondylar Process	PCP	0-3	2-3 = present	Ossenberg 1969: 151 Hauser and DeStefano 1989: 128
Intermediate Condylar Canal	ICC	0-1	1 = present	Ossenberg 1969: 74 Hauser and DeStefano 1989: 126
Pterygospinous Bridge	CIV	0-3	3 = present	Ossenberg 1969: 50 Hauser and DeStefano 1989: 156
Pterygoalar Bridge	PTAB	0-3	3 = present	Ossenberg 1969: 53 Hauser and DeStefano 1989: 156
Huschke's Tympanic Dehiscence	HSK	0-4	1-4 = present	Berry and Berry 1967: 368 Ossenberg 1969: 34 Hauser and DeStefano 1989: 143
Foramen Spinosum Open	FOSO	0-1	1 = present	Berry and Berry 1967: 369 Hauser and DeStefano 1989: 149
Foramen Ovale Incomplete	FOI	0-1	1 = present	Berry and Berry 1967: 369 Hauser and DeStefano 1989: 149
Asterionic Bone	AST	0-1	1 = present	Berry and Berry 1967: 368 Hauser and DeStefano 1989: 196
Marginal Foramen of Tympanic Plate	MFTP	0-1	1 = present	Ossenberg 1969: 47 Hauser and DeStefano 1989: 143
Mastoid Foramen Number	MFN	0-3	2-3 =present	Berry and Berry 1967: 368 Hauser and DeStefano 1989: 202
Epipteric Bone	EPB	0-3	1-3 = present	Berry and Berry 1967: 367 Ossenberg 1969: 91 Hauser and DeStefano 1989: 212
Auditory Exostosis	AEX	0-3	2-3 = present	Berry and Berry 1967: 368 Ossenberg 1969: 69 Hauser and DeStefano 1989: 186
Occipito-Mastoid Bone	OMB	0-1	1 = present	Ossenberg 1969: 86 Hauser and DeStefano 1989: 197
Parietal Notch Bone	PNB	0-1	1 = present	Berry and Berry 1967: 368 Ossenberg 1969: 86 Hauser and DeStefano 1989: 207
Multiple Mental Foramen	MMEN	0-2	2 = present	Ossenberg 1969: 140 Hauser and DeStefano 1989: 230
Mylohyoid Bridge	MYB	0-1	1 = present	Ossenberg 1969: 66 Hauser and DeStefano 1989: 234
Mandibular Torus	MT	0-3	1-3 = present	Hauser and DeStefano 1989: 183
Winging-Maxillary Incisors 1	WING-UI1	0-1	1 = present	Turner et al. 1991: 14
Labial Curve- Maxillary Incisors 1	LABC-UI1	0-4	1-4 = present	Turner et al. 1991: 15
Shoveling- Maxillary Incisors 1	USHOV-UI1	0-7	2-7 = present	Turner et al. 1991: 14
Shoveling- Maxillary Incisors 2	USHOV-UI2	0-7	2-7 = present	Turner et al. 1991: 14
Shoveling- Maxillary Canines	USHOV-UC	0-7	2-7 = present	Turner et al. 1991: 14

Nonmetric Trait	Abbreviation	Range	Dichotomization	Trait Description/Reference
Double Shoveling- Maxillary Incisors 1	UDBS-UI1	0-6	2-6 = present	Turner et al. 1991: 15
Double Shoveling- Maxillary Incisors 2	UDBS-UI2	0-6	2-6 = present	Turner et al. 1991: 15
Double Shoveling- Maxillary Canines	UDBS-UC	0-6	2-6 = present	Turner et al. 1991: 15
Double Shoveling- Maxillary Premolars 3	UDBS-UP3	0-6	2-6 = present	Turner et al. 1991: 15
Interruption Groove- Maxillary Incisors 1	IG-UI1	0-1	1 = present	Turner et al. 1991: 16
Interruption Groove- Maxillary Incisors 2	IG-UI2	0-1	1 = present	Turner et al. 1991: 16
Tuberculum Dentale- Maxillary Incisors 1	TB-UI1	0-6	1-6 = present	Turner et al. 1991: 16
Tuberculum Dentale- Maxillary Incisors 2	TB-UI2	0-6	1-6 = present	Turner et al. 1991: 16
Tuberculum Dentale- Maxillary Canines	TB-UC	0-6	1-6 = present	Turner et al. 1991: 16
Mesial Ridge- Maxillary Canines	MRIG-UC	0-3	1-3 = present	Turner et al. 1991: 16
Distal Accessory Ridge- Maxillary Canines	DAR-UC	0-5	1-5 = present	Turner et al. 1991: 17
Mesial and Distal Accessory Cusp Maxillary Premolars 3	MDAC-UP3	0-1	1 = present	Turner et al. 1991: 17
Mesial and Distal Accessory Cusp Maxillary Premolars 4	MDAC-UP4	0-1	1 = present	Turner et al. 1991: 17
Distal Sagital Ridge- Maxillary Premolars 3	DSR-UP1	0-1	1 = present	Turner et al. 1991: 18
Root Number- Maxillary Premolars 3	URNUM-UP3	1-3	1 = present	Turner et al. 1991: 20
Root Number- Maxillary Premolars 4	URNUM-UP4	1-3	1 = present	Turner et al. 1991: 20
Metacone- Maxillary Molars 1	META-UM1	0-6	5-6 = present	Turner et al. 1991: 18
Metacone- Maxillary Molars 2	META-UM2	0-6	5-6 = present	Turner et al. 1991: 18
Metacone- Maxillary Molars 3	META-UM3	0-6	5-6 = present	Turner et al. 1991: 18
Hypocone- Maxillary Molars 1	HYPO-UM1	0-6	5-6 = present	Turner et al. 1991: 18
Hypocone- Maxillary Molars 2	HYPO-UM2	0-6	5-6 = present	Turner et al. 1991: 18
Hypocone- Maxillary Molars 3	HYPO-UM3	0-6	5-6 = present	Turner et al. 1991: 18
Cusp 5- Maxillary Molars 1	UCSP5-UM1	0-5	1-5 = present	Turner et al. 1991: 18
Cusp 5- Maxillary Molars 2	UCSP5-UM2	0-5	1-5 = present	Turner et al. 1991: 18
Cusp 5- Maxillary Molars 3	UCSP5-UM3	0-5	1-5 = present	Turner et al. 1991: 18

Nonmetric Trait	Abbreviation	Range	Dichotomization	Trait Description/Reference
Carabelli's Trait- Maxillary Molars 1	CARA-UM1	0-7	2-7 = present	Turner et al. 1991: 19
Carabelli's Trait- Maxillary Molars 2	CARA-UM2	0-7	2-7 = present	Turner et al. 1991: 19
Carabelli's Trait- Maxillary Molars 3	CARA-UM3	0-7	2-7 = present	Turner et al. 1991: 19
Parastyle- Maxillary Molars 1	PARA-UM1	0-5	1-5 = present	Turner et al. 1991: 19
Parastyle- Maxillary Molars 2	PARA-UM2	0-5	1-5 = present	Turner et al. 1991: 19
Parastyle- Maxillary Molars 3	PARA-UM3	0-5	1-5 = present	Turner et al. 1991: 19
Enamel Extensions- Maxillary Premolars 3	UENEX-UP3	0-3	2-3 = present	Turner et al. 1991: 19
Enamel Extensions- Maxillary Premolars 4	UENEX-UP4	0-3	2-3 = present	Turner et al. 1991: 19
Enamel Extensions- Maxillary Molars 1	UENEX-UM1	0-3	2-3 = present	Turner et al. 1991: 19
Enamel Extensions- Maxillary Molars 2	UENEX-UM2	0-3	2-3 = present	Turner et al. 1991: 19
Enamel Extensions- Maxillary Molars 3	UENEX-UM3	0-3	2-3 = present	Turner et al. 1991: 19
Odontome- Maxillary Premolars 3	UODON-UP3	0-1	1 = present	Turner et al. 1991: 21
Odontome- Maxillary Premolars 4	UODON-UP4	0-1	1 = present	Turner et al. 1991: 21
Peg/Reduced- Maxillary Incisors 2	UPEG-UI2	0-2	1-2 = present	Turner et al. 1991: 20
Peg/Reduced- Maxillary Molars 3	UPEG-UM3	0-2	1-2 = present	Turner et al. 1991: 21
Congenitally Absent- Maxillary Incisors 2	UCONAB-UI2	0-1	1 = present	Turner et al. 1991: 21
Congenitally Absent- Maxillary Premolars 4	UCONAB-UP4	0-1	1 = present	Turner et al. 1991: 21
Congenitally Absent- Maxillary Molars 3	UCONAB-UM3	0-1	1 = present	Turner et al. 1991: 21
Shoveling- Mandibular Incisors 1 and 2	LSHOV-LI1-2	0-3	1-3 = present	Turner et al. 1991: 14
Double Shoveling- Mandibular Incisors 1	LDBS-LI1	0-4	1-4 = present	Turner et al. 1991: 14
Double Shoveling- Mandibular Incisors 1	LDBS-LI2	0-4	1-4 = present	Turner et al. 1991: 17
Distal Accessory Ridge- Mandibular Canines	LDAR-LC	0-5	2-5 = present	Turner et al. 1991: 17
Canine Root Number- Mandibular Canines	CRN-LC	1-2	2 = present	Turner et al. 1991: 24
Tome's Root- Mandibular Premolars 3	TOMR-LP3	0-7	4-7 = present	Turner et al. 1991: 24
Lingual Cusp Variation- Mandibular Premolars 3	LCV-LP3	0-3	2-3 = present	Turner et al. 1991: 21 Bollini et al. 2009: 1065

Nonmetric Trait	Abbreviation	Range	Dichotomization	Trait Description/Reference
Lingual Cusp Variation- Mandibular Premolars 4	LCV-LP4	0-3	2-3 = present	Turner et al. 1991: 21 Bollini et al. 2009: 1065
Protostylid- Mandibular Molars 1	PROTO-LM1	0-7	2-7 = present	Turner et al. 1991: 23
Protostylid- Mandibular Molars 2	PROTO-LM2	0-7	2-7 = present	Turner et al. 1991: 23
Protostylid-Mandibular Molars 3	PROTO-LM3	0-7	2-7 = present	Turner et al. 1991: 23
Cusp Number- Mandibular Molars 1	CSPNM-LM1	4-6	6 = present	Turner et al. 1991: 23
Cusp Number- Mandibular Molars 2	CSPNM-LM2	4-6	4 = present	Turner et al. 1991: 23
Cusp Number- Mandibular Molars 3	CSPNM-LM3	4-6	4 = present	Turner et al. 1991: 23
Cusp Five- Mandibular Molars 1	LCSP5-LM1	0-5	1-5 = present	Turner et al. 1991: 24
Cusp Five- Mandibular Molars 2	LCSP5-LM2	0-5	1-5 = present	Turner et al. 1991: 24
Cusp Five- Mandibular Molars 3	LCSP5-LM3	0-5	1-5 = present	Turner et al. 1991: 24
Cusp Six- Mandibular Molars 1	LCSP6-LM1	0-5	1-5 = present	Turner et al. 1991: 24
Cusp Six- Mandibular Molars 2	LCSP6-LM2	0-5	1-5 = present	Turner et al. 1991: 24
Cusp Six- Mandibular Molars 3	LCSP6-LM3	0-5	1-5 = present	Turner et al. 1991: 24
Cusp Seven- Mandibular Molars 1	LCSP7-LM1	0-4	1-4 = present	Turner et al. 1991: 24
Cusp Seven- Mandibular Molars 2	LCSP7-LM2	0-4	1-4 = present	Turner et al. 1991: 24
Cusp Seven- Mandibular Molars 3	LCSP7-LM3	0-4	1-4 = present	Turner et al. 1991: 24
Root Number- Mandibular Molars 1	LRNUM-LM1	1-3	3 = present	Turner et al. 1991: 25
Root Number- Mandibular Molars 2	LRNUM-LM2	1-3	2 = present	Turner et al. 1991: 25
Root Number- Mandibular Molars 3	LRNUM-LM3	1-3	2 = present	Turner et al. 1991: 25
Groove Pattern- Mandibular Molars 1	GRVPT-LM1	Y = 1 + = 2 X = 3	1 = present	Turner et al. 1991: 22
Groove Pattern- Mandibular Molars 2	GRVPT-LM2	Y = 1 + = 2 X = 3	1 = present	Turner et al. 1991: 22
Groove Pattern- Mandibular Molars 3	GRVPT-LM3	Y = 1 + = 2 X = 3	1 = present	Turner et al. 1991: 22
Odontome- Mandibular Premolars 3	LODON-LP3	0-1	1 = present	Turner et al. 1991: 21

Nonmetric Trait	Abbreviation	Range	Dichotomization	Trait Description/Reference
Odontome- Mandibular Premolars 4	LODON-LP4	0-1	1 = present	Turner et al. 1991: 21
Congenitally Absent- Mandibular Incisors 1	LCONAB-LI1	0-1	1 = present	Turner et al. 1991: 21
Congenitally Absent- Mandibular Premolars 4	LCONAB-LP4	0-1	1 = present	Turner et al. 1991: 21
Congenitally Absent- Mandibular Molars 3	LCONAB-LM3	0-1	1 = present	Turner et al. 1991: 21

APPENDIX D: FINAL SAMPLE DATA SET

Chronology/Sex/Burial Identifier	IOS	ZFFA	SOFO
? LH F HL CR S/N 7	1	0	NA
?? ? HL-RH 13	0	1	1
?? F HL Ent 4	NA	NA	0
?? F HL Ent 5	0	1	1
?? F T-HL R3 Ent 16	0	0	1
?? M T-HL R1 Ent 4	0	0	0
Earlier LIP F T-HL R3 Ent 1	1	0	1
Earlier LIP F T-HL R3 Ent 10	0	0	1
Earlier LIP F T-HL R3 Ent 11	0	0	0
Earlier LIP F T-HL R3 Ent 12	0	0	0
Earlier LIP F T-HL R3 Ent 13	0	0	0
Earlier LIP F T-HL R3 Ent 15	0	0	1
Earlier LIP F T-HL R3 Ent 17	0	0	1
Earlier LIP F T-HL R3 Ent 18	NA	0	0
Earlier LIP F T-HL R3 Ent 2	1	0	0
Earlier LIP F T-HL R3 Ent 3	0	0	0
Earlier LIP F T-HL R3 Ent 4	0	1	1
Earlier LIP F T-HL R3 Ent 5	0	0	0
Earlier LIP F T-HL R3 Ent 6	0	0	1
Earlier LIP F T-HL R3 Ent 7	0	0	0
Earlier LIP F T-HL R3 Ent 8	0	0	0
Earlier LIP F T-HL R3 Ent 9	0	0	1
Earlier LIP M T-HL R1 Ent 2	0	0	0
Earlier LIP M T-HL R1 Ent 3	0	0	0
Late LIP F HL CR S/N 2	0	1	0
LH ? HL CR S/N 4	0	0	0
LH ? T-HL VenAcc Ent 1	NA	NA	1
LH F HL Ent 1	1	0	1
LH M HL CR S/N 5	1	NA	0
LH M HL Ent 6	NA	0	0
LIP ? HL-RH 12	0	1	1
LIP F HL-RH 11	0	1	0
LIP F HL-RH 6	0	0	1
LIP F T-HL IA E1	0	1	0
LIP F Tuc-HL PCenSur-VIL Ent 1	NA	0	1
LIP M HL-RH 10	0	0	1
LIP M HL-RH 3	1	1	0
LIP M HL-RH 4	NA	NA	NA
?LH FT-CS "C" RH 030	0	0	1
?LH M T-CS "A" RH 026	0	0	0
?LH M T-CS IA Ent 13	NA	NA	1
?LH F H1 S/N Ent 1	0	0	1
?LH F Tuc-H1 IVi c6 Ent 8	NA	0	1

Chronology/Sex/Burial Identifier	IOS	ZFFA	SOFO
?LH M Tuc-H1 IVi IIIi c5 Ent 9	0	0	1
Late LIP M H1 Ent 6	NA	0	0
LH F T-H1 Vi Ent 7	0	0	1
LH F T-H1 Vi Ent 9	0	0	0
LH M T-H1 Vi Ent 11	NA	NA	1
LH M Tuc-H1 IVi c6 Ent 4	NA	0	0
?? F T-MG ViVi RH 20 "vicki"	0	0	0
?? F T---ViVi RH 02 "box lady"	NA	0	1
?LH F Tuc-SO Cemo Xs Ent 4	0	0	1
?LH M Tuc-SO Cemo Xs Ent 2	NA	1	0
LH F T-Bal Ib Ent 1	NA	1	1
LH F T-Bal Ib Ent 4	0	0	0
LH F T-Bal Ic/Ib Ent 5	0	0	0
LH M T-Bal Ib Ent 3	0	1	0
LH M T-Bal Ic/Ib Ent 6	0	0	0
Late LIP M T-TPS 31b Ent 33	NA	0	0
Late LIP M T-TPS F1 Ent 1a	0	0	0
Late LIP M T-TPS F1 Ent 1b	0	0	1
Late LIP M T-TPS F1 Ent 1d	0	0	1
Late LIP M T-TPS F13a Ent 15c	0	0	0
Late LIP M T-TPS F16 Ent 7b	0	1	0
Late LIP M T-TPS F18a Ent 8	NA	0	0
Late LIP M T-TPS F2 Ent 2	1	0	0
Late LIP M T-TPS F21b Ent 9	0	NA	0
Late LIP M T-TPS F22b Ent 52	0	0	0
Late LIP M T-TPS F23 Ent 13	0	0	0
Late LIP M T-TPS F30 Ent 19b	0	0	1
Late LIP M T-TPS F38 Ent 34	NA	0	1
Late LIP M T-TPS F39 Ent 40	NA	0	1
Late LIP M T-TPS F4 Ent 5	1	0	0
Late LIP M T-TPS F43b Ent 63	NA	0	0
Late LIP M T-TPS F43c Ent 72	0	0	NA
Late LIP M T-TPS F48 Ent 48	0	0	1
Late LIP M T-TPS F55 Ent 35	1	NA	1
Late LIP M T-TPS F5c Ent 43	0	0	0
Late LIP M T-TPS F6 Ent 68	1	0	1
Late LIP M T-TPS F61 Ent 41	0	0	0
Late LIP M T-TPS F67 Ent 77	0	0	0
Late LIP M T-TPS F75 Ent 85a	0	0	0
Late LIP M T-TPS F8 Ent 20	NA	0	0
Late LIP M T-TPS Fs/f Ent 76d	NA	0	1
Late LIP M T-TPS VIF-G Ent 1	0	0	1
Late LIP M T-TPS VIG Ent 2	0	0	0

Chronology/Sex/Burial Identifier	IOS	ZFFA	SOFO
Late LIP M T-TPS VIG Ent 3a	0	1	0
Late LIP M T-TPS VIi ME 2	0	0	1
LH ? T-TPS F25 Ent 12	0	0	1
LH M T-TPS F42 Ent 28	0	1	0
LH M T-TPS F47 Ent 58a	NA	0	1
LH M T-TPS F53 Ent 39	NA	0	0
LH M T-TPS F54 Ent 67	1	1	0
LH M T-TPS F54 Ent 71	NA	0	1
LH M T-TPS F62 Ent 56	0	0	1
LH M T-TPS F64 Ent 59	1	0	0
LH M T-TPS F66 Ent 81	NA	1	1
LH M T-TPS F68 Ent 64	0	0	0
LH M T-TPS F70 Ent 53b	0	0	1
LH M T-TPS F72 Ent 75	0	0	0
LH M T-TPS F73a Ent 88a	0	0	0
LH M T-TPS F73a Ent 88b	0	0	0
LH M T-TPS F73b Ent 89	0	0	0

Chronology/Sex/Burial Identifier	**FRG**	**OAL**	**LO**
? LH F HL CR S/N 7	0	0	1
?? ? HL-RH 13	0	1	0
?? F HL Ent 4	1	0	1
?? F HL Ent 5	0	NA	1
?? F T-HL R3 Ent 16	0	0	NA
?? M T-HL R1 Ent 4	0	0	0
Earlier LIP F T-HL R3 Ent 1	1	0	1
Earlier LIP F T-HL R3 Ent 10	1	0	1
Earlier LIP F T-HL R3 Ent 11	1	0	0
Earlier LIP F T-HL R3 Ent 12	1	1	1
Earlier LIP F T-HL R3 Ent 13	0	0	1
Earlier LIP F T-HL R3 Ent 15	1	0	0
Earlier LIP F T-HL R3 Ent 17	1	0	0
Earlier LIP F T-HL R3 Ent 18	1	0	0
Earlier LIP F T-HL R3 Ent 2	0	0	1
Earlier LIP F T-HL R3 Ent 3	0	0	0
Earlier LIP F T-HL R3 Ent 4	1	1	0
Earlier LIP F T-HL R3 Ent 5	1	1	0
Earlier LIP F T-HL R3 Ent 6	0	0	0
Earlier LIP F T-HL R3 Ent 7	1	0	0
Earlier LIP F T-HL R3 Ent 8	0	0	0
Earlier LIP F T-HL R3 Ent 9	0	0	1
Earlier LIP M T-HL R1 Ent 2	0	0	1
Earlier LIP M T-HL R1 Ent 3	0	0	NA
Late LIP F HL CR S/N 2	0	0	0
LH ? HL CR S/N 4	0	0	1
LH ? T-HL VenAcc Ent 1	NA	0	NA
LH F HL Ent 1	1	0	1
LH M HL CR S/N 5	0	0	0
LH M HL Ent 6	1	0	0
LIP ? HL-RH 12	1	0	1
LIP F HL-RH 11	1	1	1
LIP F HL-RH 6	0	0	1
LIP F T-HL IA E1	0	0	1
LIP F Tuc-HL PCenSur-VIL Ent 1	0	NA	1
LIP M HL-RH 10	0	1	1
LIP M HL-RH 3	NA	0	NA
LIP M HL-RH 4	0	0	1
?LH FT-CS "C" RH 030	1	0	1
?LH M T-CS "A" RH 026	0	0	1
?LH M T-CS IA Ent 13	0	0	1
?LH F H1 S/N Ent 1	NA	0	1
?LH F Tuc-H1 IVi c6 Ent 8	NA	0	NA

Chronology/Sex/Burial Identifier	FRG	OAL	LO
?LH M Tuc-H1 IVi IIIi c5 Ent 9	NA	0	0
Late LIP M H1 Ent 6	NA	1	NA
LH F T-H1 Vi Ent 7	0	0	NA
LH F T-H1 Vi Ent 9	NA	0	0
LH M T-H1 Vi Ent 11	NA	0	0
LH M Tuc-H1 IVi c6 Ent 4	NA	NA	NA
?? F T-MG ViVi RH 20 "vicki"	0	0	1
?? F T---ViVi RH 02 "box lady"	NA	0	NA
?LH F Tuc-SO Cemo Xs Ent 4	0	1	1
?LH M Tuc-SO Cemo Xs Ent 2	0	1	0
LH F T-Bal Ib Ent 1	0	1	1
LH F T-Bal Ib Ent 4	0	NA	NA
LH F T-Bal Ic/Ib Ent 5	0	1	1
LH M T-Bal Ib Ent 3	0	0	NA
LH M T-Bal Ic/Ib Ent 6	0	0	1
Late LIP M T-TPS 31b Ent 33	0	0	NA
Late LIP M T-TPS F1 Ent 1a	0	0	NA
Late LIP M T-TPS F1 Ent 1b	0	0	0
Late LIP M T-TPS F1 Ent 1d	0	0	1
Late LIP M T-TPS F13a Ent 15c	0	0	1
Late LIP M T-TPS F16 Ent 7b	1	NA	NA
Late LIP M T-TPS F18a Ent 8	0	0	NA
Late LIP M T-TPS F2 Ent 2	0	NA	NA
Late LIP M T-TPS F21b Ent 9	0	0	NA
Late LIP M T-TPS F22b Ent 52	0	0	1
Late LIP M T-TPS F23 Ent 13	NA	0	1
Late LIP M T-TPS F30 Ent 19b	0	0	0
Late LIP M T-TPS F38 Ent 34	0	NA	1
Late LIP M T-TPS F39 Ent 40	1	0	1
Late LIP M T-TPS F4 Ent 5	NA	0	NA
Late LIP M T-TPS F43b Ent 63	0	1	0
Late LIP M T-TPS F43c Ent 72	0	0	0
Late LIP M T-TPS F48 Ent 48	1	1	0
Late LIP M T-TPS F55 Ent 35	NA	0	0
Late LIP M T-TPS F5c Ent 43	0	0	0
Late LIP M T-TPS F6 Ent 68	1	0	NA
Late LIP M T-TPS F61 Ent 41	0	1	1
Late LIP M T-TPS F67 Ent 77	0	0	0
Late LIP M T-TPS F75 Ent 85a	NA	0	NA
Late LIP M T-TPS F8 Ent 20	0	1	1
Late LIP M T-TPS Fs/f Ent 76d	0	1	1
Late LIP M T-TPS VIF-G Ent 1	1	NA	NA
Late LIP M T-TPS VIG Ent 2	0	0	1

Chronology/Sex/Burial Identifier	FRG	OAL	LO
Late LIP M T-TPS VIG Ent 3a	0	NA	NA
Late LIP M T-TPS VIi ME 2	0	0	1
LH ? T-TPS F25 Ent 12	1	0	1
LH M T-TPS F42 Ent 28	0	0	1
LH M T-TPS F47 Ent 58a	0	0	0
LH M T-TPS F53 Ent 39	1	NA	NA
LH M T-TPS F54 Ent 67	0	0	1
LH M T-TPS F54 Ent 71	0	NA	NA
LH M T-TPS F62 Ent 56	0	0	1
LH M T-TPS F64 Ent 59	1	0	NA
LH M T-TPS F66 Ent 81	0	0	0
LH M T-TPS F68 Ent 64	0	0	1
LH M T-TPS F70 Ent 53b	0	1	1
LH M T-TPS F72 Ent 75	0	0	1
LH M T-TPS F73a Ent 88a	0	0	0
LH M T-TPS F73a Ent 88b	0	0	0
LH M T-TPS F73b Ent 89	0	0	0

Chronology/Sex/Burial Identifier	ALPF	HYP	POCS
? LH F HL CR S/N 7	0	NA	1
?? ? HL-RH 13	NA	1	1
?? F HL Ent 4	NA	0	1
?? F HL Ent 5	0	1	1
?? F T-HL R3 Ent 16	1	1	1
?? M T-HL R1 Ent 4	1	1	1
Earlier LIP F T-HL R3 Ent 1	0	0	1
Earlier LIP F T-HL R3 Ent 10	0	0	1
Earlier LIP F T-HL R3 Ent 11	0	0	1
Earlier LIP F T-HL R3 Ent 12	1	0	1
Earlier LIP F T-HL R3 Ent 13	1	1	1
Earlier LIP F T-HL R3 Ent 15	0	0	1
Earlier LIP F T-HL R3 Ent 17	0	1	1
Earlier LIP F T-HL R3 Ent 18	1	1	1
Earlier LIP F T-HL R3 Ent 2	NA	0	1
Earlier LIP F T-HL R3 Ent 3	0	1	1
Earlier LIP F T-HL R3 Ent 4	1	1	1
Earlier LIP F T-HL R3 Ent 5	0	1	1
Earlier LIP F T-HL R3 Ent 6	0	0	1
Earlier LIP F T-HL R3 Ent 7	0	0	0
Earlier LIP F T-HL R3 Ent 8	NA	1	1
Earlier LIP F T-HL R3 Ent 9	NA	0	1
Earlier LIP M T-HL R1 Ent 2	1	0	1
Earlier LIP M T-HL R1 Ent 3	1	0	1
Late LIP F HL CR S/N 2	1	0	NA
LH ? HL CR S/N 4	NA	0	0
LH ? T-HL VenAcc Ent 1	1	NA	NA
LH F HL Ent 1	1	0	1
LH M HL CR S/N 5	1	1	NA
LH M HL Ent 6	1	1	1
LIP ? HL-RH 12	1	0	1
LIP F HL-RH 11	0	0	1
LIP F HL-RH 6	1	0	1
LIP F T-HL IA E1	1	1	1
LIP F Tuc-HL PCenSur-VIL Ent 1	NA	0	NA
LIP M HL-RH 10	1	1	1
LIP M HL-RH 3	0	NA	NA
LIP M HL-RH 4	NA	1	NA
?LH FT-CS "C" RH 030	1	0	1
?LH M T-CS "A" RH 026	1	1	1
?LH M T-CS IA Ent 13	NA	0	NA
?LH F H1 S/N Ent 1	0	1	1
?LH F Tuc-H1 IVi c6 Ent 8	NA	0	1

Chronology/Sex/Burial Identifier	**ALPF**	**HYP**	**POCS**
?LH M Tuc-H1 IVi IIIi c5 Ent 9	NA	NA	NA
Late LIP M H1 Ent 6	NA	1	1
LH F T-H1 Vi Ent 7	1	0	1
LH F T-H1 Vi Ent 9	1	0	1
LH M T-H1 Vi Ent 11	1	0	1
LH M Tuc-H1 IVi c6 Ent 4	NA	0	NA
?? F T-MG ViVi RH 20 "vicki"	1	0	1
?? F T---ViVi RH 02 "box lady"	1	1	1
?LH F Tuc-SO Cemo Xs Ent 4	1	1	1
?LH M Tuc-SO Cemo Xs Ent 2	NA	0	1
LH F T-Bal Ib Ent 1	0	0	1
LH F T-Bal Ib Ent 4	NA	1	1
LH F T-Bal Ic/Ib Ent 5	0	1	1
LH M T-Bal Ib Ent 3	NA	1	1
LH M T-Bal Ic/Ib Ent 6	NA	0	1
Late LIP M T-TPS 31b Ent 33	1	0	1
Late LIP M T-TPS F1 Ent 1a	1	1	0
Late LIP M T-TPS F1 Ent 1b	1	0	1
Late LIP M T-TPS F1 Ent 1d	NA	0	1
Late LIP M T-TPS F13a Ent 15c	1	0	1
Late LIP M T-TPS F16 Ent 7b	1	1	1
Late LIP M T-TPS F18a Ent 8	NA	0	1
Late LIP M T-TPS F2 Ent 2	1	0	NA
Late LIP M T-TPS F21b Ent 9	NA	1	1
Late LIP M T-TPS F22b Ent 52	1	0	0
Late LIP M T-TPS F23 Ent 13	0	1	1
Late LIP M T-TPS F30 Ent 19b	1	NA	1
Late LIP M T-TPS F38 Ent 34	NA	1	1
Late LIP M T-TPS F39 Ent 40	1	1	1
Late LIP M T-TPS F4 Ent 5	1	0	0
Late LIP M T-TPS F43b Ent 63	NA	0	1
Late LIP M T-TPS F43c Ent 72	1	0	0
Late LIP M T-TPS F48 Ent 48	NA	1	1
Late LIP M T-TPS F55 Ent 35	NA	1	1
Late LIP M T-TPS F5c Ent 43	0	1	1
Late LIP M T-TPS F6 Ent 68	1	1	1
Late LIP M T-TPS F61 Ent 41	1	0	1
Late LIP M T-TPS F67 Ent 77	NA	1	1
Late LIP M T-TPS F75 Ent 85a	1	1	1
Late LIP M T-TPS F8 Ent 20	NA	1	1
Late LIP M T-TPS Fs/f Ent 76d	1	0	NA
Late LIP M T-TPS VIF-G Ent 1	0	NA	NA
Late LIP M T-TPS VIG Ent 2	0	0	1

Chronology/Sex/Burial Identifier	ALPF	HYP	POCS
Late LIP M T-TPS VIG Ent 3a	0	0	1
Late LIP M T-TPS VIi ME 2	NA	1	1
LH ? T-TPS F25 Ent 12	1	1	1
LH M T-TPS F42 Ent 28	0	0	1
LH M T-TPS F47 Ent 58a	NA	0	0
LH M T-TPS F53 Ent 39	1	1	1
LH M T-TPS F54 Ent 67	1	0	1
LH M T-TPS F54 Ent 71	1	0	1
LH M T-TPS F62 Ent 56	1	0	1
LH M T-TPS F64 Ent 59	0	0	1
LH M T-TPS F66 Ent 81	0	0	1
LH M T-TPS F68 Ent 64	1	1	1
LH M T-TPS F70 Ent 53b	1	1	1
LH M T-TPS F72 Ent 75	1	1	1
LH M T-TPS F73a Ent 88a	0	0	1
LH M T-TPS F73a Ent 88b	0	1	1
LH M T-TPS F73b Ent 89	0	1	1

Chronology/Sex/Burial Identifier	ICC	PTAB	HSK
? LH F HL CR S/N 7	1	NA	0
?? ? HL-RH 13	0	0	1
?? F HL Ent 4	0	NA	0
?? F HL Ent 5	0	NA	1
?? F T-HL R3 Ent 16	0	0	0
?? M T-HL R1 Ent 4	NA	0	0
Earlier LIP F T-HL R3 Ent 1	1	0	NA
Earlier LIP F T-HL R3 Ent 10	1	0	0
Earlier LIP F T-HL R3 Ent 11	0	0	1
Earlier LIP F T-HL R3 Ent 12	1	0	1
Earlier LIP F T-HL R3 Ent 13	1	0	1
Earlier LIP F T-HL R3 Ent 15	1	0	1
Earlier LIP F T-HL R3 Ent 17	0	0	1
Earlier LIP F T-HL R3 Ent 18	0	0	1
Earlier LIP F T-HL R3 Ent 2	0	0	1
Earlier LIP F T-HL R3 Ent 3	0	0	1
Earlier LIP F T-HL R3 Ent 4	0	0	0
Earlier LIP F T-HL R3 Ent 5	1	0	1
Earlier LIP F T-HL R3 Ent 6	0	0	0
Earlier LIP F T-HL R3 Ent 7	0	0	1
Earlier LIP F T-HL R3 Ent 8	1	0	1
Earlier LIP F T-HL R3 Ent 9	0	0	1
Earlier LIP M T-HL R1 Ent 2	1	0	0
Earlier LIP M T-HL R1 Ent 3	1	0	0
Late LIP F HL CR S/N 2	0	0	0
LH ? HL CR S/N 4	0	0	1
LH ? T-HL VenAcc Ent 1	NA	NA	1
LH F HL Ent 1	1	0	1
LH M HL CR S/N 5	1	NA	1
LH M HL Ent 6	0	0	0
LIP ? HL-RH 12	1	0	1
LIP F HL-RH 11	0	0	1
LIP F HL-RH 6	1	1	1
LIP F T-HL IA E1	0	0	1
LIP F Tuc-HL PCenSur-VIL Ent 1	NA	NA	0
LIP M HL-RH 10	1	0	1
LIP M HL-RH 3	NA	0	1
LIP M HL-RH 4	NA	NA	NA
?LH FT-CS "C" RH 030	1	1	0
?LH M T-CS "A" RH 026	0	0	1
?LH M T-CS IA Ent 13	NA	NA	1
?LH F H1 S/N Ent 1	NA	0	1
?LH F Tuc-H1 IVi c6 Ent 8	0	NA	NA

Chronology/Sex/Burial Identifier	ICC	PTAB	HSK
?LH M Tuc-H1 IVi IIIi c5 Ent 9	NA	NA	1
Late LIP M H1 Ent 6	NA	NA	1
LH F T-H1 Vi Ent 7	1	0	0
LH F T-H1 Vi Ent 9	0	0	0
LH M T-H1 Vi Ent 11	0	0	1
LH M Tuc-H1 IVi c6 Ent 4	0	NA	0
?? F T-MG ViVi RH 20 "vicki"	0	0	1
?? F T---ViVi RH 02 "box lady"	0	0	1
?LH F Tuc-SO Cemo Xs Ent 4	0	0	0
?LH M Tuc-SO Cemo Xs Ent 2	0	0	1
LH F T-Bal Ib Ent 1	NA	0	1
LH F T-Bal Ib Ent 4	NA	NA	1
LH F T-Bal Ic/Ib Ent 5	0	0	1
LH M T-Bal Ib Ent 3	0	NA	0
LH M T-Bal Ic/Ib Ent 6	NA	NA	0
Late LIP M T-TPS 31b Ent 33	1	NA	1
Late LIP M T-TPS F1 Ent 1a	0	0	1
Late LIP M T-TPS F1 Ent 1b	0	0	1
Late LIP M T-TPS F1 Ent 1d	0	0	1
Late LIP M T-TPS F13a Ent 15c	0	0	1
Late LIP M T-TPS F16 Ent 7b	0	1	1
Late LIP M T-TPS F18a Ent 8	1	NA	0
Late LIP M T-TPS F2 Ent 2	0	0	1
Late LIP M T-TPS F21b Ent 9	0	0	NA
Late LIP M T-TPS F22b Ent 52	1	0	0
Late LIP M T-TPS F23 Ent 13	NA	NA	1
Late LIP M T-TPS F30 Ent 19b	1	0	1
Late LIP M T-TPS F38 Ent 34	0	0	1
Late LIP M T-TPS F39 Ent 40	0	0	1
Late LIP M T-TPS F4 Ent 5	0	0	1
Late LIP M T-TPS F43b Ent 63	NA	NA	1
Late LIP M T-TPS F43c Ent 72	0	0	1
Late LIP M T-TPS F48 Ent 48	NA	NA	1
Late LIP M T-TPS F55 Ent 35	1	0	0
Late LIP M T-TPS F5c Ent 43	0	0	1
Late LIP M T-TPS F6 Ent 68	0	1	0
Late LIP M T-TPS F61 Ent 41	0	0	1
Late LIP M T-TPS F67 Ent 77	1	0	0
Late LIP M T-TPS F75 Ent 85a	NA	NA	1
Late LIP M T-TPS F8 Ent 20	0	NA	1
Late LIP M T-TPS Fs/f Ent 76d	0	0	1
Late LIP M T-TPS VIF-G Ent 1	NA	NA	1
Late LIP M T-TPS VIG Ent 2	1	0	0

Chronology/Sex/Burial Identifier	ICC	PTAB	HSK
Late LIP M T-TPS VIG Ent 3a	0	0	1
Late LIP M T-TPS VIi ME 2	0	0	NA
LH ? T-TPS F25 Ent 12	0	0	1
LH M T-TPS F42 Ent 28	0	0	1
LH M T-TPS F47 Ent 58a	1	NA	0
LH M T-TPS F53 Ent 39	NA	0	1
LH M T-TPS F54 Ent 67	0	0	1
LH M T-TPS F54 Ent 71	1	0	1
LH M T-TPS F62 Ent 56	0	0	1
LH M T-TPS F64 Ent 59	1	0	1
LH M T-TPS F66 Ent 81	NA	0	1
LH M T-TPS F68 Ent 64	1	0	1
LH M T-TPS F70 Ent 53b	1	0	1
LH M T-TPS F72 Ent 75	0	0	1
LH M T-TPS F73a Ent 88a	1	0	1
LH M T-TPS F73a Ent 88b	1	1	1
LH M T-TPS F73b Ent 89	0	0	1

Chronology/Sex/Burial Identifier	FOSO	AST	MFN
? LH F HL CR S/N 7	0	NA	1
?? ? HL-RH 13	0	1	0
?? F HL Ent 4	NA	NA	NA
?? F HL Ent 5	NA	NA	0
?? F T-HL R3 Ent 16	1	0	1
?? M T-HL R1 Ent 4	0	1	1
Earlier LIP F T-HL R3 Ent 1	1	0	1
Earlier LIP F T-HL R3 Ent 10	0	1	1
Earlier LIP F T-HL R3 Ent 11	0	0	1
Earlier LIP F T-HL R3 Ent 12	1	1	1
Earlier LIP F T-HL R3 Ent 13	0	1	1
Earlier LIP F T-HL R3 Ent 15	1	0	1
Earlier LIP F T-HL R3 Ent 17	0	1	0
Earlier LIP F T-HL R3 Ent 18	0	0	1
Earlier LIP F T-HL R3 Ent 2	NA	0	1
Earlier LIP F T-HL R3 Ent 3	0	0	1
Earlier LIP F T-HL R3 Ent 4	0	0	1
Earlier LIP F T-HL R3 Ent 5	0	0	1
Earlier LIP F T-HL R3 Ent 6	0	0	1
Earlier LIP F T-HL R3 Ent 7	0	0	0
Earlier LIP F T-HL R3 Ent 8	0	0	1
Earlier LIP F T-HL R3 Ent 9	0	0	1
Earlier LIP M T-HL R1 Ent 2	1	1	1
Earlier LIP M T-HL R1 Ent 3	0	0	1
Late LIP F HL CR S/N 2	0	0	0
LH ? HL CR S/N 4	0	1	0
LH ? T-HL VenAcc Ent 1	NA	NA	NA
LH F HL Ent 1	NA	0	0
LH M HL CR S/N 5	0	0	1
LH M HL Ent 6	0	0	1
LIP ? HL-RH 12	NA	0	1
LIP F HL-RH 11	0	0	0
LIP F HL-RH 6	0	0	1
LIP F T-HL IA E1	0	0	1
LIP F Tuc-HL PCenSur-VIL Ent 1	NA	NA	NA
LIP M HL-RH 10	0	1	1
LIP M HL-RH 3	NA	0	1
LIP M HL-RH 4	0	0	1
?LH FT-CS "C" RH 030	1	1	1
?LH M T-CS "A" RH 026	0	1	1
?LH M T-CS IA Ent 13	NA	NA	1
?LH F H1 S/N Ent 1	0	1	1
?LH F Tuc-H1 IVi c6 Ent 8	NA	NA	1

Chronology/Sex/Burial Identifier	FOSO	AST	MFN
?LH M Tuc-H1 IVi IIIi c5 Ent 9	NA	NA	1
Late LIP M H1 Ent 6	NA	0	1
LH F T-H1 Vi Ent 7	0	NA	1
LH F T-H1 Vi Ent 9	0	0	0
LH M T-H1 Vi Ent 11	1	0	1
LH M Tuc-H1 IVi c6 Ent 4	NA	NA	1
?? F T-MG ViVi RH 20 "vicki"	0	0	0
?? F T---ViVi RH 02 "box lady"	1	0	0
?LH F Tuc-SO Cemo Xs Ent 4	1	1	1
?LH M Tuc-SO Cemo Xs Ent 2	0	1	1
LH F T-Bal Ib Ent 1	0	0	1
LH F T-Bal Ib Ent 4	NA	NA	0
LH F T-Bal Ic/Ib Ent 5	0	1	0
LH M T-Bal Ib Ent 3	1	NA	1
LH M T-Bal Ic/Ib Ent 6	NA	1	1
Late LIP M T-TPS 31b Ent 33	NA	0	1
Late LIP M T-TPS F1 Ent 1a	0	NA	1
Late LIP M T-TPS F1 Ent 1b	0	0	1
Late LIP M T-TPS F1 Ent 1d	0	0	1
Late LIP M T-TPS F13a Ent 15c	0	0	1
Late LIP M T-TPS F16 Ent 7b	0	0	1
Late LIP M T-TPS F18a Ent 8	NA	NA	1
Late LIP M T-TPS F2 Ent 2	0	0	1
Late LIP M T-TPS F21b Ent 9	0	1	1
Late LIP M T-TPS F22b Ent 52	0	0	1
Late LIP M T-TPS F23 Ent 13	0	0	1
Late LIP M T-TPS F30 Ent 19b	0	0	1
Late LIP M T-TPS F38 Ent 34	NA	0	1
Late LIP M T-TPS F39 Ent 40	NA	NA	1
Late LIP M T-TPS F4 Ent 5	1	0	1
Late LIP M T-TPS F43b Ent 63	NA	0	1
Late LIP M T-TPS F43c Ent 72	0	1	1
Late LIP M T-TPS F48 Ent 48	NA	NA	NA
Late LIP M T-TPS F55 Ent 35	NA	0	1
Late LIP M T-TPS F5c Ent 43	0	0	1
Late LIP M T-TPS F6 Ent 68	0	0	1
Late LIP M T-TPS F61 Ent 41	0	1	1
Late LIP M T-TPS F67 Ent 77	0	1	1
Late LIP M T-TPS F75 Ent 85a	NA	NA	1
Late LIP M T-TPS F8 Ent 20	NA	NA	NA
Late LIP M T-TPS Fs/f Ent 76d	0	0	0
Late LIP M T-TPS VIF-G Ent 1	NA	NA	NA
Late LIP M T-TPS VIG Ent 2	0	1	1

Chronology/Sex/Burial Identifier	FOSO	AST	MFN
Late LIP M T-TPS VIG Ent 3a	0	0	1
Late LIP M T-TPS VIi ME 2	0	1	1
LH ? T-TPS F25 Ent 12	0	0	1
LH M T-TPS F42 Ent 28	0	0	1
LH M T-TPS F47 Ent 58a	0	0	1
LH M T-TPS F53 Ent 39	1	0	1
LH M T-TPS F54 Ent 67	0	0	1
LH M T-TPS F54 Ent 71	NA	0	1
LH M T-TPS F62 Ent 56	0	0	1
LH M T-TPS F64 Ent 59	0	NA	1
LH M T-TPS F66 Ent 81	0	0	1
LH M T-TPS F68 Ent 64	0	0	NA
LH M T-TPS F70 Ent 53b	0	1	1
LH M T-TPS F72 Ent 75	0	0	1
LH M T-TPS F73a Ent 88a	0	0	1
LH M T-TPS F73a Ent 88b	1	0	1
LH M T-TPS F73b Ent 89	1	0	1

Chronology/Sex/Burial Identifier	EPB %	OMB	PNB
? LH F HL CR S/N 7	1	NA	NA
?? ? HL-RH 13	0	1	0
?? F HL Ent 4	NA	NA	NA
?? F HL Ent 5	NA	NA	0
?? F T-HL R3 Ent 16	0	0	0
?? M T-HL R1 Ent 4	0	0	0
Earlier LIP F T-HL R3 Ent 1	0	0	0
Earlier LIP F T-HL R3 Ent 10	0	1	1
Earlier LIP F T-HL R3 Ent 11	0	1	0
Earlier LIP F T-HL R3 Ent 12	0	0	1
Earlier LIP F T-HL R3 Ent 13	1	1	0
Earlier LIP F T-HL R3 Ent 15	0	0	0
Earlier LIP F T-HL R3 Ent 17	NA	1	0
Earlier LIP F T-HL R3 Ent 18	0	0	0
Earlier LIP F T-HL R3 Ent 2	NA	0	0
Earlier LIP F T-HL R3 Ent 3	0	1	0
Earlier LIP F T-HL R3 Ent 4	0	1	0
Earlier LIP F T-HL R3 Ent 5	NA	1	0
Earlier LIP F T-HL R3 Ent 6	NA	0	0
Earlier LIP F T-HL R3 Ent 7	NA	0	0
Earlier LIP F T-HL R3 Ent 8	0	0	0
Earlier LIP F T-HL R3 Ent 9	NA	0	NA
Earlier LIP M T-HL R1 Ent 2	0	0	0
Earlier LIP M T-HL R1 Ent 3	0	0	0
Late LIP F HL CR S/N 2	0	1	0
LH ? HL CR S/N 4	NA	1	0
LH ? T-HL VenAcc Ent 1	NA	NA	NA
LH F HL Ent 1	0	1	0
LH M HL CR S/N 5	0	0	0
LH M HL Ent 6	0	0	0
LIP ? HL-RH 12	0	1	0
LIP F HL-RH 11	0	0	0
LIP F HL-RH 6	1	1	0
LIP F T-HL IA E1	0	0	0
LIP F Tuc-HL PCenSur-VIL Ent 1	NA	NA	NA
LIP M HL-RH 10	0	NA	0
LIP M HL-RH 3	NA	1	0
LIP M HL-RH 4	NA	NA	0
?LH FT-CS "C" RH 030	0	0	0
?LH M T-CS "A" RH 026	0	1	0
?LH M T-CS IA Ent 13	NA	NA	NA
?LH F H1 S/N Ent 1	0	0	0
?LH F Tuc-H1 IVi c6 Ent 8	NA	NA	NA

Chronology/Sex/Burial Identifier	EPB %	OMB	PNB
?LH M Tuc-H1 IVi IIIi c5 Ent 9	NA	NA	NA
Late LIP M H1 Ent 6	NA	0	0
LH F T-H1 Vi Ent 7	0	NA	0
LH F T-H1 Vi Ent 9	0	0	0
LH M T-H1 Vi Ent 11	NA	0	0
LH M Tuc-H1 IVi c6 Ent 4	NA	NA	NA
?? F T-MG ViVi RH 20 "vicki"	0	1	0
?? F T---ViVi RH 02 "box lady"	0	1	0
?LH F Tuc-SO Cemo Xs Ent 4	0	0	0
?LH M Tuc-SO Cemo Xs Ent 2	0	1	0
LH F T-Bal Ib Ent 1	1	0	0
LH F T-Bal Ib Ent 4	NA	NA	NA
LH F T-Bal Ic/Ib Ent 5	0	1	0
LH M T-Bal Ib Ent 3	NA	NA	NA
LH M T-Bal Ic/Ib Ent 6	NA	NA	0
Late LIP M T-TPS 31b Ent 33	NA	0	0
Late LIP M T-TPS F1 Ent 1a	1	1	0
Late LIP M T-TPS F1 Ent 1b	0	0	0
Late LIP M T-TPS F1 Ent 1d	NA	0	0
Late LIP M T-TPS F13a Ent 15c	0	0	0
Late LIP M T-TPS F16 Ent 7b	NA	NA	0
Late LIP M T-TPS F18a Ent 8	NA	NA	NA
Late LIP M T-TPS F2 Ent 2	1	1	0
Late LIP M T-TPS F21b Ent 9	0	0	0
Late LIP M T-TPS F22b Ent 52	0	0	0
Late LIP M T-TPS F23 Ent 13	NA	0	0
Late LIP M T-TPS F30 Ent 19b	0	1	0
Late LIP M T-TPS F38 Ent 34	0	1	1
Late LIP M T-TPS F39 Ent 40	0	NA	0
Late LIP M T-TPS F4 Ent 5	0	0	0
Late LIP M T-TPS F43b Ent 63	0	1	0
Late LIP M T-TPS F43c Ent 72	0	1	1
Late LIP M T-TPS F48 Ent 48	NA	NA	NA
Late LIP M T-TPS F55 Ent 35	1	1	0
Late LIP M T-TPS F5c Ent 43	0	NA	0
Late LIP M T-TPS F6 Ent 68	0	0	0
Late LIP M T-TPS F61 Ent 41	0	0	0
Late LIP M T-TPS F67 Ent 77	0	0	0
Late LIP M T-TPS F75 Ent 85a	NA	NA	NA
Late LIP M T-TPS F8 Ent 20	NA	NA	NA
Late LIP M T-TPS Fs/f Ent 76d	0	0	1
Late LIP M T-TPS VIF-G Ent 1	NA	NA	NA
Late LIP M T-TPS VIG Ent 2	0	0	0

Chronology/Sex/Burial Identifier	EPB %	OMB	PNB
Late LIP M T-TPS VIG Ent 3a	0	0	0
Late LIP M T-TPS VIi ME 2	1	1	0
LH ? T-TPS F25 Ent 12	0	0	0
LH M T-TPS F42 Ent 28	0	0	1
LH M T-TPS F47 Ent 58a	NA	0	0
LH M T-TPS F53 Ent 39	NA	0	0
LH M T-TPS F54 Ent 67	0	0	0
LH M T-TPS F54 Ent 71	0	0	0
LH M T-TPS F62 Ent 56	NA	0	0
LH M T-TPS F64 Ent 59	0	0	0
LH M T-TPS F66 Ent 81	0	0	0
LH M T-TPS F68 Ent 64	0	1	0
LH M T-TPS F70 Ent 53b	1	0	1
LH M T-TPS F72 Ent 75	0	0	0
LH M T-TPS F73a Ent 88a	0	0	0
LH M T-TPS F73a Ent 88b	0	1	0
LH M T-TPS F73b Ent 89	0	0	0

Chronology/Sex/Burial Identifier	MYB	IG-UI2	URNUM-UP3
? LH F HL CR S/N 7	NA	NA	1
?? ? HL-RH 13	NA	NA	1
?? F HL Ent 4	NA	NA	1
?? F HL Ent 5	1	0	1
?? F T-HL R3 Ent 16	0	1	1
?? M T-HL R1 Ent 4	0	0	1
Earlier LIP F T-HL R3 Ent 1	0	0	1
Earlier LIP F T-HL R3 Ent 10	0	NA	1
Earlier LIP F T-HL R3 Ent 11	0	0	1
Earlier LIP F T-HL R3 Ent 12	0	NA	1
Earlier LIP F T-HL R3 Ent 13	0	NA	1
Earlier LIP F T-HL R3 Ent 15	0	1	1
Earlier LIP F T-HL R3 Ent 17	0	NA	1
Earlier LIP F T-HL R3 Ent 18	0	1	1
Earlier LIP F T-HL R3 Ent 2	1	1	1
Earlier LIP F T-HL R3 Ent 3	0	0	1
Earlier LIP F T-HL R3 Ent 4	0	NA	1
Earlier LIP F T-HL R3 Ent 5	0	0	NA
Earlier LIP F T-HL R3 Ent 6	0	0	1
Earlier LIP F T-HL R3 Ent 7	0	0	1
Earlier LIP F T-HL R3 Ent 8	1	0	0
Earlier LIP F T-HL R3 Ent 9	0	0	1
Earlier LIP M T-HL R1 Ent 2	0	NA	1
Earlier LIP M T-HL R1 Ent 3	0	NA	1
Late LIP F HL CR S/N 2	NA	NA	1
LH ? HL CR S/N 4	NA	1	1
LH ? T-HL VenAcc Ent 1	0	NA	1
LH F HL Ent 1	NA	0	1
LH M HL CR S/N 5	NA	NA	1
LH M HL Ent 6	0	1	1
LIP ? HL-RH 12	NA	NA	1
LIP F HL-RH 11	NA	NA	1
LIP F HL-RH 6	NA	NA	1
LIP F T-HL IA E1	0	0	1
LIP F Tuc-HL PCenSur-VIL Ent 1	0	0	NA
LIP M HL-RH 10	NA	NA	1
LIP M HL-RH 3	NA	1	1
LIP M HL-RH 4	NA	1	1
?LH FT-CS "C" RH 030	NA	NA	1
?LH M T-CS "A" RH 026	NA	NA	1
?LH M T-CS IA Ent 13	0	NA	NA
?LH F H1 S/N Ent 1	0	1	NA
?LH F Tuc-H1 IVi c6 Ent 8	NA	NA	NA

Chronology/Sex/Burial Identifier	MYB	IG-UI2	URNUM-UP3
?LH M Tuc-H1 IVi IIIi c5 Ent 9	0	0	NA
Late LIP M H1 Ent 6	1	NA	1
LH F T-H1 Vi Ent 7	0	0	1
LH F T-H1 Vi Ent 9	NA	1	1
LH M T-H1 Vi Ent 11	0	NA	1
LH M Tuc-H1 IVi c6 Ent 4	0	0	NA
?? F T-MG ViVi RH 20 "vicki"	0	1	NA
?? F T---ViVi RH 02 "box lady"	0	0	1
?LH F Tuc-SO Cemo Xs Ent 4	0	0	NA
?LH M Tuc-SO Cemo Xs Ent 2	1	NA	NA
LH F T-Bal Ib Ent 1	0	1	1
LH F T-Bal Ib Ent 4	NA	0	1
LH F T-Bal Ic/Ib Ent 5	1	0	1
LH M T-Bal Ib Ent 3	0	0	NA
LH M T-Bal Ic/Ib Ent 6	1	NA	1
Late LIP M T-TPS 31b Ent 33	0	1	1
Late LIP M T-TPS F1 Ent 1a	0	0	1
Late LIP M T-TPS F1 Ent 1b	0	0	1
Late LIP M T-TPS F1 Ent 1d	0	0	1
Late LIP M T-TPS F13a Ent 15c	0	1	1
Late LIP M T-TPS F16 Ent 7b	1	NA	0
Late LIP M T-TPS F18a Ent 8	0	NA	1
Late LIP M T-TPS F2 Ent 2	NA	NA	1
Late LIP M T-TPS F21b Ent 9	1	0	0
Late LIP M T-TPS F22b Ent 52	0	0	NA
Late LIP M T-TPS F23 Ent 13	0	0	1
Late LIP M T-TPS F30 Ent 19b	0	1	1
Late LIP M T-TPS F38 Ent 34	0	0	1
Late LIP M T-TPS F39 Ent 40	NA	NA	1
Late LIP M T-TPS F4 Ent 5	0	NA	NA
Late LIP M T-TPS F43b Ent 63	0	NA	1
Late LIP M T-TPS F43c Ent 72	0	NA	NA
Late LIP M T-TPS F48 Ent 48	0	0	1
Late LIP M T-TPS F55 Ent 35	0	1	1
Late LIP M T-TPS F5c Ent 43	0	0	1
Late LIP M T-TPS F6 Ent 68	0	NA	1
Late LIP M T-TPS F61 Ent 41	1	NA	1
Late LIP M T-TPS F67 Ent 77	0	0	1
Late LIP M T-TPS F75 Ent 85a	0	NA	NA
Late LIP M T-TPS F8 Ent 20	0	0	1
Late LIP M T-TPS Fs/f Ent 76d	0	NA	NA
Late LIP M T-TPS VIF-G Ent 1	1	1	1
Late LIP M T-TPS VIG Ent 2	0	0	NA

Chronology/Sex/Burial Identifier	MYB	IG-UI2	URNUM-UP3
Late LIP M T-TPS VIG Ent 3a	0	NA	1
Late LIP M T-TPS VIi ME 2	0	NA	1
LH ? T-TPS F25 Ent 12	0	1	1
LH M T-TPS F42 Ent 28	0	0	1
LH M T-TPS F47 Ent 58a	0	0	1
LH M T-TPS F53 Ent 39	0	0	1
LH M T-TPS F54 Ent 67	0	NA	0
LH M T-TPS F54 Ent 71	0	1	NA
LH M T-TPS F62 Ent 56	1	NA	1
LH M T-TPS F64 Ent 59	0	NA	NA
LH M T-TPS F66 Ent 81	1	NA	1
LH M T-TPS F68 Ent 64	0	0	1
LH M T-TPS F70 Ent 53b	0	0	NA
LH M T-TPS F72 Ent 75	0	0	1
LH M T-TPS F73a Ent 88a	0	0	1
LH M T-TPS F73a Ent 88b	1	NA	1
LH M T-TPS F73b Ent 89	0	NA	NA

Chronology/Sex/Burial Identifier	META-UM2	UPEG-UI2	UCONAB-UM3
? LH F HL CR S/N 7	1	NA	1
?? ? HL-RH 13	1	NA	0
?? F HL Ent 4	1	0	NA
?? F HL Ent 5	1	0	0
?? F T-HL R3 Ent 16	1	0	0
?? M T-HL R1 Ent 4	1	0	0
Earlier LIP F T-HL R3 Ent 1	1	0	0
Earlier LIP F T-HL R3 Ent 10	1	NA	0
Earlier LIP F T-HL R3 Ent 11	1	0	0
Earlier LIP F T-HL R3 Ent 12	1	NA	0
Earlier LIP F T-HL R3 Ent 13	1	NA	1
Earlier LIP F T-HL R3 Ent 15	0	0	0
Earlier LIP F T-HL R3 Ent 17	1	0	0
Earlier LIP F T-HL R3 Ent 18	1	0	0
Earlier LIP F T-HL R3 Ent 2	1	0	0
Earlier LIP F T-HL R3 Ent 3	1	0	0
Earlier LIP F T-HL R3 Ent 4	1	1	0
Earlier LIP F T-HL R3 Ent 5	0	0	0
Earlier LIP F T-HL R3 Ent 6	1	1	0
Earlier LIP F T-HL R3 Ent 7	1	0	0
Earlier LIP F T-HL R3 Ent 8	1	0	0
Earlier LIP F T-HL R3 Ent 9	1	0	0
Earlier LIP M T-HL R1 Ent 2	1	NA	0
Earlier LIP M T-HL R1 Ent 3	1	NA	0
Late LIP F HL CR S/N 2	1	NA	0
LH ? HL CR S/N 4	1	NA	NA
LH ? T-HL VenAcc Ent 1	1	NA	0
LH F HL Ent 1	1	0	0
LH M HL CR S/N 5	1	NA	1
LH M HL Ent 6	1	0	0
LIP ? HL-RH 12	1	NA	0
LIP F HL-RH 11	1	NA	0
LIP F HL-RH 6	1	NA	0
LIP F T-HL IA E1	1	0	1
LIP F Tuc-HL PCenSur-VIL Ent 1	1	0	NA
LIP M HL-RH 10	1	NA	0
LIP M HL-RH 3	0	NA	0
LIP M HL-RH 4	1	0	NA
?LH FT-CS "C" RH 030	1	NA	0
?LH M T-CS "A" RH 026	1	NA	0
?LH M T-CS IA Ent 13	1	NA	NA
?LH F H1 S/N Ent 1	1	0	0
?LH F Tuc-H1 IVi c6 Ent 8	1	1	1

Chronology/Sex/Burial Identifier	META-UM2	UPEG-UI2	UCONAB-UM3
?LH M Tuc-H1 IVi IIIi c5 Ent 9	1	0	0
Late LIP M H1 Ent 6	1	0	0
LH F T-H1 Vi Ent 7	1	0	0
LH F T-H1 Vi Ent 9	1	0	0
LH M T-H1 Vi Ent 11	NA	NA	1
LH M Tuc-H1 IVi c6 Ent 4	1	0	NA
?? F T-MG ViVi RH 20 "vicki"	NA	0	0
?? F T---ViVi RH 02 "box lady"	1	0	0
?LH F Tuc-SO Cemo Xs Ent 4	1	0	0
?LH M Tuc-SO Cemo Xs Ent 2	1	NA	1
LH F T-Bal Ib Ent 1	NA	0	0
LH F T-Bal Ib Ent 4	1	0	0
LH F T-Bal Ic/Ib Ent 5	1	0	0
LH M T-Bal Ib Ent 3	0	0	1
LH M T-Bal Ic/Ib Ent 6	1	1	0
Late LIP M T-TPS 31b Ent 33	1	0	0
Late LIP M T-TPS F1 Ent 1a	1	0	0
Late LIP M T-TPS F1 Ent 1b	1	0	0
Late LIP M T-TPS F1 Ent 1d	1	0	0
Late LIP M T-TPS F13a Ent 15c	1	0	0
Late LIP M T-TPS F16 Ent 7b	1	NA	1
Late LIP M T-TPS F18a Ent 8	1	NA	0
Late LIP M T-TPS F2 Ent 2	1	NA	0
Late LIP M T-TPS F21b Ent 9	1	0	0
Late LIP M T-TPS F22b Ent 52	1	0	0
Late LIP M T-TPS F23 Ent 13	1	0	0
Late LIP M T-TPS F30 Ent 19b	1	0	0
Late LIP M T-TPS F38 Ent 34	1	0	0
Late LIP M T-TPS F39 Ent 40	1	NA	1
Late LIP M T-TPS F4 Ent 5	1	NA	0
Late LIP M T-TPS F43b Ent 63	1	0	0
Late LIP M T-TPS F43c Ent 72	1	NA	0
Late LIP M T-TPS F48 Ent 48	1	0	0
Late LIP M T-TPS F55 Ent 35	1	0	0
Late LIP M T-TPS F5c Ent 43	1	0	1
Late LIP M T-TPS F6 Ent 68	1	0	0
Late LIP M T-TPS F61 Ent 41	1	NA	0
Late LIP M T-TPS F67 Ent 77	1	0	NA
Late LIP M T-TPS F75 Ent 85a	1	0	0
Late LIP M T-TPS F8 Ent 20	1	0	0
Late LIP M T-TPS Fs/f Ent 76d	1	0	0
Late LIP M T-TPS VIF-G Ent 1	1	0	0
Late LIP M T-TPS VIG Ent 2	1	0	0

Chronology/Sex/Burial Identifier	META-UM2	UPEG-UI2	UCONAB-UM3
Late LIP M T-TPS VIG Ent 3a	1	0	0
Late LIP M T-TPS VIi ME 2	1	NA	0
LH ? T-TPS F25 Ent 12	1	0	0
LH M T-TPS F42 Ent 28	1	0	0
LH M T-TPS F47 Ent 58a	1	0	0
LH M T-TPS F53 Ent 39	1	0	NA
LH M T-TPS F54 Ent 67	1	NA	0
LH M T-TPS F54 Ent 71	1	0	1
LH M T-TPS F62 Ent 56	1	NA	0
LH M T-TPS F64 Ent 59	1	0	0
LH M T-TPS F66 Ent 81	1	0	0
LH M T-TPS F68 Ent 64	1	0	0
LH M T-TPS F70 Ent 53b	1	NA	0
LH M T-TPS F72 Ent 75	1	0	1
LH M T-TPS F73a Ent 88a	0	0	0
LH M T-TPS F73a Ent 88b	1	1	0
LH M T-TPS F73b Ent 89	1	0	1

Chronology/Sex/Burial Identifier	LCSP5-LM3	LRNUM-LM2
? LH F HL CR S/N 7	NA	NA
?? ? HL-RH 13	NA	NA
?? F HL Ent 4	NA	1
?? F HL Ent 5	NA	NA
?? F T-HL R3 Ent 16	1	1
?? M T-HL R1 Ent 4	NA	NA
Earlier LIP F T-HL R3 Ent 1	1	NA
Earlier LIP F T-HL R3 Ent 10	NA	NA
Earlier LIP F T-HL R3 Ent 11	1	NA
Earlier LIP F T-HL R3 Ent 12	NA	NA
Earlier LIP F T-HL R3 Ent 13	NA	1
Earlier LIP F T-HL R3 Ent 15	NA	1
Earlier LIP F T-HL R3 Ent 17	1	1
Earlier LIP F T-HL R3 Ent 18	1	1
Earlier LIP F T-HL R3 Ent 2	1	NA
Earlier LIP F T-HL R3 Ent 3	1	NA
Earlier LIP F T-HL R3 Ent 4	1	NA
Earlier LIP F T-HL R3 Ent 5	NA	1
Earlier LIP F T-HL R3 Ent 6	NA	NA
Earlier LIP F T-HL R3 Ent 7	1	1
Earlier LIP F T-HL R3 Ent 8	1	1
Earlier LIP F T-HL R3 Ent 9	1	1
Earlier LIP M T-HL R1 Ent 2	NA	1
Earlier LIP M T-HL R1 Ent 3	NA	1
Late LIP F HL CR S/N 2	NA	NA
LH ? HL CR S/N 4	NA	NA
LH ? T-HL VenAcc Ent 1	NA	0
LH F HL Ent 1	NA	NA
LH M HL CR S/N 5	NA	NA
LH M HL Ent 6	1	NA
LIP ? HL-RH 12	NA	NA
LIP F HL-RH 11	NA	NA
LIP F HL-RH 6	NA	NA
LIP F T-HL IA E1	NA	NA
LIP F Tuc-HL PCenSur-VIL Ent 1	1	1
LIP M HL-RH 10	NA	NA
LIP M HL-RH 3	NA	NA
LIP M HL-RH 4	NA	NA
?LH FT-CS "C" RH 030	NA	NA
?LH M T-CS "A" RH 026	NA	NA
?LH M T-CS IA Ent 13	1	1
?LH F H1 S/N Ent 1	NA	1
?LH F Tuc-H1 IVi c6 Ent 8	NA	1

Chronology/Sex/Burial Identifier	LCSP5-LM3	LRNUM-LM2
?LH M Tuc-H1 IVi IIIi c5 Ent 9	1	0
Late LIP M H1 Ent 6	NA	1
LH F T-H1 Vi Ent 7	NA	NA
LH F T-H1 Vi Ent 9	NA	NA
LH M T-H1 Vi Ent 11	NA	1
LH M Tuc-H1 IVi c6 Ent 4	1	0
?? F T-MG ViVi RH 20 "vicki"	1	1
?? F T---ViVi RH 02 "box lady"	1	NA
?LH F Tuc-SO Cemo Xs Ent 4	1	0
?LH M Tuc-SO Cemo Xs Ent 2	NA	1
LH F T-Bal Ib Ent 1	1	1
LH F T-Bal Ib Ent 4	1	1
LH F T-Bal Ic/Ib Ent 5	1	0
LH M T-Bal Ib Ent 3	NA	1
LH M T-Bal Ic/Ib Ent 6	1	NA
Late LIP M T-TPS 31b Ent 33	NA	NA
Late LIP M T-TPS F1 Ent 1a	0	1
Late LIP M T-TPS F1 Ent 1b	1	1
Late LIP M T-TPS F1 Ent 1d	1	1
Late LIP M T-TPS F13a Ent 15c	1	NA
Late LIP M T-TPS F16 Ent 7b	NA	1
Late LIP M T-TPS F18a Ent 8	1	1
Late LIP M T-TPS F2 Ent 2	NA	NA
Late LIP M T-TPS F21b Ent 9	0	0
Late LIP M T-TPS F22b Ent 52	1	1
Late LIP M T-TPS F23 Ent 13	NA	0
Late LIP M T-TPS F30 Ent 19b	1	1
Late LIP M T-TPS F38 Ent 34	NA	NA
Late LIP M T-TPS F39 Ent 40	NA	NA
Late LIP M T-TPS F4 Ent 5	1	1
Late LIP M T-TPS F43b Ent 63	NA	1
Late LIP M T-TPS F43c Ent 72	NA	1
Late LIP M T-TPS F48 Ent 48	0	1
Late LIP M T-TPS F55 Ent 35	1	1
Late LIP M T-TPS F5c Ent 43	NA	0
Late LIP M T-TPS F6 Ent 68	1	NA
Late LIP M T-TPS F61 Ent 41	1	0
Late LIP M T-TPS F67 Ent 77	NA	1
Late LIP M T-TPS F75 Ent 85a	1	1
Late LIP M T-TPS F8 Ent 20	0	NA
Late LIP M T-TPS Fs/f Ent 76d	0	1
Late LIP M T-TPS VIF-G Ent 1	1	NA
Late LIP M T-TPS VIG Ent 2	NA	NA

Chronology/Sex/Burial Identifier	LCSP5-LM3	LRNUM-LM2
Late LIP M T-TPS VIG Ent 3a	1	0
Late LIP M T-TPS VIi ME 2	1	0
LH ? T-TPS F25 Ent 12	NA	NA
LH M T-TPS F42 Ent 28	NA	NA
LH M T-TPS F47 Ent 58a	1	NA
LH M T-TPS F53 Ent 39	NA	NA
LH M T-TPS F54 Ent 67	NA	0
LH M T-TPS F54 Ent 71	NA	NA
LH M T-TPS F62 Ent 56	1	1
LH M T-TPS F64 Ent 59	1	1
LH M T-TPS F66 Ent 81	1	1
LH M T-TPS F68 Ent 64	0	NA
LH M T-TPS F70 Ent 53b	NA	1
LH M T-TPS F72 Ent 75	NA	1
LH M T-TPS F73a Ent 88a	1	0
LH M T-TPS F73a Ent 88b	NA	1
LH M T-TPS F73b Ent 89	NA	NA

APPENDIX E: NONMETRIC INCLUSION AND EXCLUSION TABLE

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Metopic Suture			✓	
Infraorbital Suture	✓			
Multiple Infraorbital Foramen		✓		
Zygomatico-Facial Foramen Absent	✓			
Supraorbital Foramen	✓			
Supraorbital Notch		✓		
Frontal Grooves	✓			
Trochlear Spine		✓		
Anterior Ethmoid Extrasutural				✓
Posterior Ethmoid Extrasutural		✓		
Bregmatic Bone			✓	
Parietal Foramen Location		✓		
Os Incae			✓	
Ossicle at Lambda	✓			
Lambdoid Ossicle	✓			
Coronal Ossicle			✓	

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Sagital Ossicle			✓	
Maxillary Torus			✓	✓
Palatine Torus			✓	✓
Accessory Lesser Palatine Foramen	✓			
Precondylar Tubercle			✓	
Hypoglossal Canal Bridging	✓			
Condylar Facet Double			✓	
Postcondylar Canal	✓			
Paracondylar Process		✓		
Intermediate Condylar Canal	✓			
Pterygospinous Bridge		✓		
Pterygoalar Bridge	✓			
Huschke’s Tympanic Dehiscence	✓			
Foramen Spinosum Open	✓			

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Foramen Ovale Incomplete			✓	
Asterionic Bone	✓			
Marginal Foramen of Tympanic Plate		✓		
Mastoid Foramen Number	✓			
Epipteric Bone	✓			
Auditory Exostosis			✓	
Occipito-Mastoid Bone	✓			
Parietal Notch Bone	✓			
Multiple Mental Foramen		✓		
Mylohyoid Bridge	✓			
Mandibular Torus			✓	
Winging-Maxillary Incisors 1		✓		
Labial Curve-Maxillary Incisors 1		✓		
Shoveling-Maxillary Incisors 1			✓	

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Shoveling- Maxillary Incisors 2			✓	
Shoveling- Maxillary Canines			✓	
Double Shoveling- Maxillary Incisors 1			✓	
Double Shoveling- Maxillary Incisors 2			✓	
Double Shoveling- Maxillary Canines			✓	
Double Shoveling- Maxillary Premolars 3			✓	
Interruption Groove- Maxillary Incisors 1		✓	✓	
Interruption Groove- Maxillary Incisors 2	✓			
Tuberculum Dentale- Maxillary Incisors 1		✓		
Tuberculum Dentale- Maxillary Incisors 2		✓		

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	**Low or High Frequency**	**Intertrait Correlations**
Tuberculum Dentale- Maxillary Canines		✓		
Mesial Ridge- Maxillary Canines		✓		
Distal Accessory Ridge- Maxillary Canines		✓		
Mesial and Distal Accessory Cusp- Maxillary Premolars 3		✓		
Mesial and Distal Accessory Cusp- Maxillary Premolars 4		✓		
Distal Sagital Ridge- Maxillary Premolars 3		✓		
Root Number- Maxillary Premolars 3	✓			
Root Number- Maxillary Premolars 4		✓		
Metacone- Maxillary Molars 1		✓		

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Metacone- Maxillary Molars 2	✓			
Metacone- Maxillary Molars 3		✓		
Hypocone- Maxillary Molars 1		✓	✓	
Hypocone- Maxillary Molars 2		✓		
Hypocone- Maxillary Molars 3		✓		
Cusp 5- Maxillary Molars 1		✓		
Cusp 5- Maxillary Molars 2		✓		
Cusp 5- Maxillary Molars 3		✓		
Carabelli's Trait- Maxillary Molars 1		✓		
Carabelli's Trait- Maxillary Molars 2		✓		
Carabelli's Trait- Maxillary Molars 3		✓		

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Parastyle-Maxillary Molars 1		✓		
Parastyle-Maxillary Molars 2		✓		
Parastyle-Maxillary Molars 3		✓		
Enamel Extensions-Maxillary Premolars 3		✓		
Enamel Extensions-Maxillary Premolars 4		✓		
Enamel Extensions-Maxillary Molars 1		✓		
Enamel Extensions-Maxillary Molars 2		✓		
Enamel Extensions-Maxillary Molars 3		✓		

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Odontome- Maxillary Premolars 3		✓	✓	
Odontome- Maxillary Premolars 4		✓	✓	
Peg/Reduced- Maxillary Incisors 2	✓			
Peg/Reduced- Maxillary Molars 3		✓		
Congenitally Absent- Maxillary Incisors 2		✓		
Congenitally Absent- Maxillary Premolars 4		✓		
Congenitally Absent- Maxillary Molars 3	✓			
Shoveling- Mandibular Incisors 1 and 2			✓	
Double Shoveling- Mandibular Incisors 1		✓	✓	

Trait	**Included**	**Excluded**		
		Intraobserver Error and/or Missing Data	**Low or High Frequency**	**Intertrait Correlations**
Double Shoveling- Mandibular Incisors 1		✓	✓	
Distal Accessory Ridge- Mandibular Canines		✓		
Canine Root Number- Mandibular Canines		✓		
Tome’s Root- Mandibular Premolars 3			✓	
Lingual Cusp Variation- Mandibular Premolars 3		✓		
Lingual Cusp Variation- Mandibular Premolars 4		✓		
Protostylid- Mandibular Molars 1			✓	
Protostylid- Mandibular Molars 2			✓	

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Protostylid- Mandibular Molars 3		✓		
Cusp Number- Mandibular Molars 1		✓		
Cusp Number- Mandibular Molars 2		✓		
Cusp Number- Mandibular Molars 3		✓		
Cusp Five- Mandibular Molars 1		✓		
Cusp Five- Mandibular Molars 2		✓		
Cusp Five- Mandibular Molars 3	✓			

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Cusp Six-Mandibular Molars 1		✓		
Cusp Six-Mandibular Molars 2		✓		
Cusp Six-Mandibular Molars 3		✓		
Cusp Seven-Mandibular Molars 1		✓		
Cusp Seven-Mandibular Molars 2		✓		
Cusp Seven-Mandibular Molars 3		✓		
Root Number-Mandibular Molars 1		✓		
Root Number-Mandibular Molars 2	✓			
Root Number-Mandibular Molars 3		✓		

Trait	Included	Excluded		
		Intraobserver Error and/or Missing Data	Low or High Frequency	Intertrait Correlations
Groove Pattern- Mandibular Molars 1		✓		
Groove Pattern- Mandibular Molars 2		✓		
Groove Pattern- Mandibular Molars 3		✓		
Odontome- Mandibular Premolars 3		✓		
Odontome- Mandibular Premolars 4		✓		
Congenitally Absent- Mandibular Incisors 1		✓		
Congenitally Absent- Mandibular Premolars 4		✓		
Congenitally Absent- Mandibular Molars 3				✓

APPENDIX F: NONMETRIC TRAIT CORRELATION MATRI

Trait	IOS	ZFFA	SOFO	FRG	OAL	LO	ALPF	HYP	POCS	ICC	PTAB
IOS	1	0.028	-0.026	0.149	-0.18	0.085	-0.003	-0.154	-0.038	0.133	0.04
ZFFA	0.028	1	-0.041	-0.007	0.194	-0.013	-0.158	-0.05	0.13	-0.267	0.011
SOFO	-0.026	-0.041	1	0.155	0.043	0.08	0.06	-0.046	0.136	0.08	0.087
FRG	0.149	-0.007	0.155	1	0.053	-0.104	-0.134	0.03	0.074	0.049	0.185
OAL	-0.18	0.194	0.043	0.053	1	0.054	-0.01	0.127	0.146	-0.076	-0.112
LO	0.085	-0.013	0.08	-0.104	0.054	1	0.198	-0.131	0.107	0.014	0.04
ALPF	-0.003	-0.158	0.06	-0.134	-0.01	0.198	1	0.059	-0.098	-0.04	0.086
HYP	-0.154	-0.05	-0.046	0.03	0.127	-0.131	0.059	1	0.199	-0.14	0.077
POCS	-0.038	0.13	0.136	0.074	0.146	0.107	-0.098	0.199	1	0.06	0.079
ICC	0.133	-0.267	0.08	0.049	-0.076	0.014	-0.04	-0.14	0.06	1	0.138
PTAB	0.04	0.011	0.087	0.185	-0.112	0.04	0.086	0.077	0.079	0.138	1
HSK	-0.006	0.077	-0.028	0.013	0.174	0.055	-0.133	0.118	0.014	-0.193	-0.102
FOSO	0.083	-0.123	0.107	0.198	-0.029	0	0.064	0.019	0.043	0.104	0.154
AST	-0.293	-0.145	0.002	-0.112	0.252	0.224	0.043	0.137	-0.022	0.096	-0.055
MFN	0.091	-0.121	-0.008	-0.076	-0.17	-0.007	0.083	0.024	0.127	0.266	0.112
EPB..	0.215	-0.055	0.155	-0.218	0.047	0.211	0.024	0.109	-0.099	0.155	0.1
OMB	-0.019	0.088	0.035	0.003	0.068	-0.117	-0.015	0.176	-0.055	-0.016	0.06
PNB	-0.12	-0.032	0.143	0.012	0.228	0.192	0.012	-0.111	-0.081	0.031	-0.082
MYB	-0.032	0.214	-0.129	-0.104	0.186	0.045	-0.184	0.051	0.133	-0.138	0.313
IG.UI2	0.246	0.022	0.093	0.149	-0.161	0.008	0.162	-0.139	0.072	-0.006	NA
URNUM.UP3	-0.067	-0.251	0.197	0.025	0.09	0.028	-0.138	-0.12	-0.056	0.061	-0.166
META.UM2	-0.032	-0.155	0.105	-0.11	-0.013	0.243	0.323	-0.009	-0.064	-0.174	0.063
UPEG.UI2	-0.104	0.071	0.096	-0.017	0.031	-0.148	-0.101	-0.073	0.074	-0.046	0.379
UCONAB.UM3	0.065	0.16	-0.108	-0.095	-0.113	-0.056	0.08	0.183	0.114	-0.085	0.054
LCSP5.LM3..	0.158	0.11	0.11	0.088	-0.325	-0.149	-0.26	-0.307	0.092	0.056	0.06
LRNUM.LM2	0.009	-0.068	0.115	0.243	-0.078	-0.164	0.207	-0.084	-0.163	0.276	0.117

Trait	HSK	FOSO	AST	MFN	EPB..	OMB	PNB	MYB	IG.UI2	URNUM.UP
IOS	-0.006	0.083	-0.293	0.091	0.215	-0.019	-0.12	-0.032	0.246	-0.067
ZFFA	0.077	-0.123	-0.145	-0.121	-0.055	0.088	-0.032	0.214	0.022	-0.251
SOFO	-0.028	0.107	0.002	-0.008	0.155	0.035	0.143	-0.129	0.093	0.197
FRG	0.013	0.198	-0.112	-0.076	-0.218	0.003	0.012	-0.104	0.149	0.025
OAL	0.174	-0.029	0.252	-0.17	0.047	0.068	0.228	0.186	-0.161	0.09
LO	0.055	0	0.224	-0.007	0.211	-0.117	0.192	0.045	0.008	0.028
ALPF	-0.133	0.064	0.043	0.083	0.024	-0.015	0.012	-0.184	0.162	-0.138
HYP	0.118	0.019	0.137	0.024	0.109	0.176	-0.111	0.051	-0.139	-0.12
POCS	0.014	0.043	-0.022	0.127	-0.099	-0.055	-0.081	0.133	0.072	-0.056
ICC	-0.193	0.104	0.096	0.266	0.155	-0.016	0.031	-0.138	-0.006	0.061
PTAB	-0.102	0.154	-0.055	0.112	0.1	0.06	-0.082	0.313	NA	-0.166
HSK	1	-0.115	-0.198	-0.117	0.019	0.162	0.07	0.186	0.071	-0.117
FOSO	-0.115	1	0.002	0.099	-0.179	-0.178	-0.007	-0.093	-0.009	0.113
AST	-0.198	0.002	1	-0.049	0.088	0.148	0.198	0.159	-0.152	-0.004
MFN	-0.117	0.099	-0.049	1	0.153	-0.276	0.007	-0.099	0	-0.102
EPB..	0.019	-0.179	0.088	0.153	1	0.278	0.027	-0.134	0.108	0.097
OMB	0.162	-0.178	0.148	-0.276	0.278	1	0.04	0.001	-0.006	0.17
PNB	0.07	-0.007	0.198	0.007	0.027	0.04	1	-0.157	-0.189	0.058
MYB	0.186	-0.093	0.159	-0.099	-0.134	0.001	-0.157	1	0.04	-0.35
IG.UI2	0.071	-0.009	-0.152	0	0.108	-0.006	-0.189	0.04	1	0.151
URNUM.UP3	-0.117	0.113	-0.004	-0.102	0.097	0.17	0.058	-0.35	0.151	1
META.UM2	-0.039	-0.204	0.146	-0.096	0.065	-0.066	0.067	0.106	-0.069	-0.045
UPEG.UI2	-0.261	0.103	0.067	0.123	-0.058	0.199	-0.062	0.246	-0.089	0.054
UCONAB.UM3	0.084	0.104	-0.057	0.176	0.083	-0.08	-0.119	0.02	-0.083	-0.097
LCSP5.LM3..	-0.213	0.147	-0.106	0.127	-0.135	-0.131	-0.479	0.024	0.279	0.255
LRNUM.LM2	-0.049	0.122	-0.237	-0.051	0.094	0.09	0.147	-0.066	0.348	0.189

Trait	META.UM	UPEG.UI	UCONAB.UM3	LCSP5.LM	LRNUM.LM2
IOS	-0.032	-0.104	0.065	0.158	0.009
ZFFA	-0.155	0.071	0.16	0.11	-0.068
SOFO	0.105	0.096	-0.108	0.11	0.115
FRG	-0.11	-0.017	-0.095	0.088	0.243
OAL	-0.013	0.031	-0.113	-0.325	-0.078
LO	0.243	-0.148	-0.056	-0.149	-0.164
ALPF	0.323	-0.101	0.08	-0.26	0.207
HYP	-0.009	-0.073	0.183	-0.307	-0.084
POCS	-0.064	0.074	0.114	0.092	-0.163
ICC	-0.174	-0.046	-0.085	0.056	0.276
PTAB	0.063	0.379	0.054	0.06	0.117
HSK	-0.039	-0.261	0.084	-0.213	-0.049
FOSO	-0.204	0.103	0.104	0.147	0.122
AST	0.146	0.067	-0.057	-0.106	-0.237
MFN	-0.096	0.123	0.176	0.127	-0.051
EPB..	0.065	-0.058	0.083	-0.135	0.094
OMB	-0.066	0.199	-0.08	-0.131	0.09
PNB	0.067	-0.062	-0.119	-0.479	0.147
MYB	0.106	0.246	0.02	0.024	-0.066
IG.UI2	-0.069	-0.089	-0.083	0.279	0.348
URNUM.UP3	-0.045	0.054	-0.097	0.255	0.189
META.UM2	1	0.069	-0.04	-0.058	0.006
UPEG.UI2	0.069	1	0.086	0.091	0.12
UCONAB.UM3	-0.04	0.086	1	NA	0.107
LCSP5.LM3..	-0.058	0.091	NA	1	-0.012
LRNUM.LM2	0.006	0.12	0.107	-0.012	1

APPENDIX G: UNIVARIATE R CODE

```
Overall<-read.csv("IMPORT FILE NAME",header=TRUE);Overall
x1<- Overall[,1]
 x1
 x2<- Overall[,2]
 x2
 n1<- 45
 n2<- 17
 p1<- x1/n1
 p2<- x2/n2
 phat<- (x1+x2)/(n1+n2)
 sd.test<- sqrt(phat*(1-phat)*(1/n1+1/n2))
 p1
 p2
 sd.test
 z.stat<- (p1-p2)/sd.test
 z.stat
 pnorm(z.stat);
PVALS<-1-abs(2*pnorm(z.stat)-1);PVALS
write.csv(PVALS, "EXPORT FILE NAME")
```

APPEDIX H: MULTIVARIATE R CODE

```
Z<-read.csv("Dental 103.csv",header=TRUE,row.names=1, na.strings="NA");Z
Zmydata<- apply(Z,2,as.numeric);Zmydata
####Dimension Check####
dim(Zmydata)
C<-read.csv("Cranial 103.csv",header=TRUE,row.names=1, na.strings="NA");C
Cmydata<- apply(C,2,as.numeric);Cmydata
####Dimension Check####
dim(Cmydata)
####################
CD<-read.csv("All peeps 4-17-15.csv",header=TRUE,row.names=1, na.strings="NA");CD
CDmydata<- apply(CD,2,as.numeric);CDmydata
#####Correlation Matrix#####
CDcor<-cor(CDmydata, use="pairwise.complete.obs");CDcor
CDCORR<-round(CDcor, digits=3);CDCORR
write.csv(CDCORR, "All Peeps CORR.csv")
#####Gower Distance + Ward's Cluster####
Zdist<-daisy(Z,metric="gower");Zdist
Cdist<-daisy(C,metric="gower");Cdist
RndZdist<-round(Zdist,digits=3);RndZdist
DdistM<-as.matrix(RndZdist)
write.csv(DdistM, "Dental 7 103.csv")
RndCdist<-round(Cdist,digits=3);RndCdist
CdistM<-as.matrix(RndCdist);CdistM
write.csv(CdistM, "Cranial 7 103.csv")
Zfit<-hclust((Zdist^2),method="ward");Zfit
Zdend<-plot(Zfit,cex=.7,hang=-1, main="D")
```

```
Cfit<-hclust((Cdist^2),method="ward");Cfit

Cdend<-plot(Cfit,cex=.7,hang=-1, main="TITLE")

Tang<-tanglegram(Cfit,Zfit)

utg<-Tang %>% untangle(method = "step2side");utg

utg %>% set("labels_cex", .5) %>% plot(main = paste("1 entanglement =", round(entanglement(utg), 2)))

utg2<-utg %>% untangle(method = "random");utg2

utg2 %>% set("labels_cex", .5) %>% plot(main = paste("2 entanglement =", round(entanglement(utg), 2)))

###Cranial and dentanl combined#####

CD<-read.csv("104 peeps chron sex 26 traits total den cran sperate 2-17-15.csv",header=TRUE,row.names=1, na.strings="NA");CD

CDmydata<- apply(CD,2,as.numeric);CDmydata

dim(CDmydata)

CDdist<-daisy(CD,metric="gower");CDdist

RndCDdist<-round(CDdist,digits=3);RndCDdist

CDdistM<-as.matrix(RndCDdist)

write.csv(CDdistM, " Cranial and Dental 26 103.csv")

CDfit<-hclust((CDdist^2),method="ward");CDfit

CDdend<-plot(CDfit,cex=.7,hang=-1, main="CD")
```

APPENDIX I: FIGURE REUSE PERMISSIONS

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To whom it may concern,
I am a writing my masters thesis and I would like to use an image from the book, "Biological Anthropology of the Human Skeleton, Second Edition" in Chapter 17, page 534. I need the image as a visual aid as an example of the background information for my research.
Best,

Wesley E. Garrett,
Master's Student and Graduate Teaching Assistant,
Anthropology Department,
The University of Central Florida

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