5-2013

Striking out and digging in: A bioarchaeological perspective on the impacts of the Wari expansion on populations in the Peruvian central highlands.

Christine M. Pink
cpink@utk.edu

Recommended Citation

Pink, Christine M., "Striking out and digging in: A bioarchaeological perspective on the impacts of the Wari expansion on populations in the Peruvian central highlands.. " PhD diss., University of Tennessee, 2013.
https://trace.tennessee.edu/utk_graddiss/1802

To the Graduate Council:

I am submitting herewith a dissertation written by Christine M. Pink entitled "Striking out and digging in: A bioarchaeological perspective on the impacts of the Wari expansion on populations in the Peruvian central highlands.." I have examined the final electronic copy of this dissertation for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Doctor of Philosophy, with a major in Anthropology.

Lyle W. Konigsberg, Major Professor

We have read this dissertation and recommend its acceptance:

Richard Jantz, Graciela Cabana, Chad Black, Tiffiny Tung

Accepted for the Council:
Dixie L. Thompson

Vice Provost and Dean of the Graduate School

(Original signatures are on file with official student records.)

Striking out and digging in: A bioarchaeological perspective on the impacts of the Wari expansion on populations in the Peruvian central highlands.

A Dissertation Presented for
The Doctor of Philosophy
Degree
The University of Tennessee, Knoxville

Christine M. Pink
May 2013

DEDICATION

To my grandparents:

Frank and Dolores Pink

and

John Louis and Caroline Murrel

ACKNOWLEDGEMENTS

The completion of this dissertation is due to the efforts and support of so many more people than me. I am forever grateful to my committee members for their patience and sage advice. Together you have fostered my love of this field. I can only hope that one day I can take what I learned from your mentorship and use it to encourage my future students. Dr. Konigsberg even from afar you guided me in the way only a truly gifted mentor could. Your ability to make clear the most complicated of theoretical concepts (to me anyhow), not to mention the formulas that defined them, kept me moving forward and helped me to become a producer rather than just a consumer of knowledge. I could never thank you enough for your guidance.

I have never been pushed to expand my thinking as much as by you Dr. Cabana. At times I thought I would never be able to articulate a good argument, but your dedication to making me work outside of my comfort zone has made me a better anthropologist. All researchers should hold themselves to the standards that you demonstrate in your own work and expect of your students.

Dr. Tung, if it were not for you I might still be standing lost on the side of the Pan-American Highway somewhere in Peru. You taught me the ropes of archaeological research in South America. You expected nothing but the best from me, you had patience with my broken Spanish, you have been one of my fiercest advocates, and you were a friend when I really needed it. I feel that you have mentored me not only in the technical aspects of theory and method, but also as a professional woman. You are a role model for all female graduate students aspiring to balance a career as an academic and a field bioarchaeologist.

Dr. Jantz I am so grateful to have had the opportunity to learn from you. I think they call it the “Jantz Effect,” but your way of calming anxious graduate students is amazing. Your door was always open and you always listened patiently. I have always enjoyed the banter with regard to statistical approaches between you and Dr. Konigsberg. And I was even more excited when I got the joke.

I think the power of an outside perspective is often lost on graduate students caught up in their theses and dissertations. Dr. Black, your insightful comments helped me to step back and appreciate the historical record and the interpretive power it had to offer this project.

This project also benefited from substantial financial support. The McClure Scholarship for Summer Research supported the initial travel and data collection to explore the feasibility of the dissertation project. The William M. Bass Endowment financed multiple trips to Peru for data collection. The Diversity Enhancement Fellowship for Summer Dissertation Research supported an extended data collection trip to Peru in 2010. Without these grants and scholarships this project could not have been completed.

I must thank Patricia Maita from the Museo Nacional de Antropológia, Arqueológia, e Historia del Peru for her assistance for the month I was in residence doing data collection. Your willingness to go to great lengths to facilitate this project will forever be appreciated. Thanks are also owed to Dr. Jose Ochatoma from the Universidad de San Cristóbol Huamanga in Ayacucho, Peru. You are a true scholar and your dedication and support of a novice researcher was remarkable.

Chris Philipp, curator at the Field Museum of Natural History in Chicago, I am forever grateful for your assistance. You were beyond busy when I visited yet you always made yourself available to me to ensure that I was able to collect the most and best quality data possible.

I have had the honor of collaborating with two remarkable archaeological programs in Peru in recent years. Dr. Danielle Kurin, thank you so much. The Proyecto Bioarqueológico Andahuaylas is amazing and I am lucky to have had the chance to work with you and Enmanuel Gomez Choque. I do not look forward to all the 12 hour bus rides to Andahuaylas; however, I do look forward to many more years of collaboration in the future.

I have put a lot of my own blood, sweat, and tears into the Proyecto de Investigación Arqueológico Regional Ancash (PIARA). But, I have nothing on Rebecca Bria, Kathryn Rua DeTore, and Elizabeth Cruzado. I will always remember fondly archaeological survey with "team girlie". PIARA has been and adventure to say the least and I am so excited as the fruits of our labor at the Hualcayan are starting to be recognized. Rebecca especially, thank you. Our late night talks about Andean archaeology and cultures in the Callejón de Huaylas helped me develop my interpretations derived from this study. I truly look forward to a long career of collaboration and figuring out just what was going on up in the north-central highlands.

Lastly, but perhaps most importantly I need to acknowledge my friends and family. I would never have made it thought graduate school without the "circle of trust." Kathleen Thompson Alsup, Angela Dautartas, Miriam Soto, and Shauna McNulty you ladies were my family in Tennessee and kept me sane. Without the support of my family though all the years I probably would have quit a long time ago. Mom you always reminded me how much I really love anthropology, and would not enjoy working in a cubicle. Even though it meant sending your little girl to far off places without phones and internet, you always supported me in achieving my goals. Dad, thank you for understanding. It is hard to describe the challenges of graduate school to someone that has not been through it. You were always encouraging, and reminded me that “all this” would be worth it. To my sister and brother, Jennifer and Eric, thank you for your patience. Jennifer especially thank you for all of the supportive phone calls and little messages. I also thank my family for understanding all of the times that I was not around for birthdays, holidays, or special events. Without your support and consideration I could never have achieved my goals.

ABSTRACT

The Wari empire emerged near the present day city of Ayacucho, Peru around AD 600 and collapsed approximately 400 years later. There is no doubt that Wari influence was widespread in the Andes; however, the extent to which the empire successfully integrated regional territories is not as well understood. This study examined the impact of the rise and fall of the Wari empire on the structure of interaction between populations hypothesized to have been within its sphere of influence. The relative frequencies of cranial non-metric traits were used to explore biological affinities among 17 populations that lived during and after the Wari empire. The samples include populations from regions with archaeological evidence of Wari influence. A basic premise of this study is that the economic, ideological, and political goals of the Wari created a cultural horizon that would have increased contact between regional populations that would in turn lead to gene flow and patterned differences in biological affinities between groups.

On a large scale results indicated that the Wari empire did not have a significant impact on gene flow in the central Andes. However, several suggestive patterns were observed when the data were examined on the smaller regional scale. The mechanisms by which Wari influence spread within and between regions is not easily understood and consistency in ideology could be mistaken for similarity in social action and interaction. Biological distance analyses of regional populations were a useful proxy for unraveling the complex pattern of social interactions required to transmit the consistent Wari ideology that characterized the Middle Horizon. Results of this study support hypotheses regarding a strong relationship between the Wari and Nasca, add new detail to the current understanding of interaction within the Nazca Valley during the height of the Wari empire, find little evidence of intensive interaction between the Wari and populations in the north-central highlands, and suggest that dualistic social organization documented by Spanish chroniclers truly has a deep history in the Andes. The findings of this study are illustrative of the multivariate and unpredictable nature of imperial expansion.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

Chapter I

Introduction

Deciphering the intricate relationships between ancient empires and the populations they administered from both the material record and skeletal biology have been extremely effective. This research uses a bioarchaeological perspective to examine population genetic variation that may have been consequent to ancient imperialism. Populations interacting directly and indirectly with the Wari empire[1], centered in the Ayacucho basin of modern day Peru, are addressed by this research. The Wari empire is widely considered to have been the first imperial level society in South America. They began their territorial expansion during the Middle Horizon (MH) around AD 600, and appear to have collapsed by AD 1100. Population genetic theory is the interpretive framework for understanding patterns in biological affinity among study samples as biological relationships should mirror the structure of social interactions between groups that the samples represent. This study further contextualizes population genetic structure in the Territorial-Hegemonic (Luttwak, 1976; Hassig, 1985) theoretical framework that considers incorporative strategies, territoriality, hegemony, and resistance.

Biological distance analyses based on frequencies of cranial non-metric traits were used to explore population genetic structure in the Peruvian Andes. Cranial non-metric traits were used because their expression is genetically mediated, they can be collected from fragmentary remains, the effects of cranial modification can be controlled for, and the data is reflective of genetic relationships but less destructive than DNA analyses. Populations spanning the MH through the Late Intermediate Period (LIP) (AD 1000-1400) were sampled from multiple geographic regions where evidence of Wari imperial influence was present. Diachronic

---

[1] "Wari Empire" is used to refer to the imperial body. "Wari" will be used in reference to the culture and the people that would have likely identified as a part of the culture.

comparisons were used explore what impact the Wari empire, and its subsequent collapse, had on the structure of social interaction, and therefore population genetic structure, in the Peruvian Andes. The following chapters in this dissertation explain the theoretical models employed in the study, statistical methodology, and discussion of the results in the context of the archaeological record.

1.1 Layout of the dissertation

In the second chapter social complexity theory with regard to empire is discussed. The word "empire" often evokes images of a powerful monolithic institution that exerts control over an expansive and homogenous domain. Similarly, "collapse" has been treated as a single moment in history where once there was a state and in the next instant nothing. This is likely influenced by the limitations of archaeological evidence which cannot offer temporal resolution fine enough to discern processes that took place over just a few generations. The literature abounds with concepts of empire; therefore, before moving to a discussion concerning theoretical models of empire and imperialism, the definition of empire used in this study is laid out. The discussion then turns to theoretical models of imperialism. There are many theoretical models of empire and imperialism that have fallen in and out of favor with anthropologists over time. Chapter Two discusses some of the theoretical models that have been applied to the Wari empire. Major criticisms of those models are reviewed and the Territorial-Hegemonic model is presented as that which best accommodates variability in imperial integration and the fluid nature of those relationships over time.

Chapter Two then turns to a brief review of the literature concerning the Wari empire. The rise and initial territorial expansion of the Wari is discussed. This study considers the Wari as an empire; however, not all scholars agree that the Wari truly reached this level of social complexity. Much of this controversy lies in disagreement about the extent to which the Wari incorporated regional territories. This debate is explained and the discussion is then turned to what is known about Wari imperial administration by region, and for particular sites in the central Andes. Schreiber's (1992) mosaic model is a metaphor specific to Wari administration. Many of the scenarios that Schreiber (1992, 2000, 2001) outlined could be observed in biological relationships as well as in the archaeological record.

Chapter Three outlines population genetic theory as it relates to biological distance analysis. The advantages and disadvantages of using cranial non-metric traits for biological distance analyses are then discussed. The expression of non-metric traits is dictated by an underlying genetic potential. The manifestation of these traits is the proxy for the gene pool for the population under study. The relationship of genetic and environmental influences on the expression of a non-metric trait is described by the Threshold Model. The importance of this model is explained with regard to distance measures that have been used with cranial non-metric traits. Mahalanobis distance is then discussed as the most appropriate statistic for this study.

The limitations of biological distance studies are also discussed in this chapter. Population genetic analyses can be broken down into two broad categories, model bound and model free. As a rule model bound analyses estimate some parameter, for example effective population size. The assumptions of model bound analyses are many and generally cannot be met with archaeologically derived samples. Model free analyses, like biological distance, are exploratory. They do not estimate parameters, but they do reveal patterns within and between populations. With an understanding that this study is model free and thus illuminates patterns in genetic variation within and between populations the results can be seated within the social theoretical framework. The patterns observed in the genetic relationships can be explained by a limited number of scenarios with regard to population genetic theory. These scenarios can then be compared to possible variations in social interactions outlined by the Mosaic model of Wari imperialism.

Chapter Four describes the samples used in this study. The samples are broken down by geographic region and chronology. Seventeen samples representing the Wari heartland, north-central highlands, south-central highlands, southern mid-valley, Nazca River valley, and central coast were considered in the study. When possible a sample from the MH during the apogee of the Wari empire, and a sample representing the LIP after the Wari collapse were included for each region. The archaeological site that the samples were derived from is described in this chapter. Evidence of Wari influence was also reviewed for each of the study samples. Being derived from archaeological collections there were many limitations with the samples. These are also discussed on a case by case basis in chapter four.

Chapter Five outlines the statistical methodology used in this study. The subsets of samples compared in the distance analyses, and the reasoning for the groupings is outlined here. As mentioned earlier a Mahalonobis distance was used to calculate the biological distances between study samples. Before biological distances were calculated individual traits were screened for Intraobserver error and correlation to variables including sex, age, and cranial modification. The calculation of F_{ST}, used to explore relative rates of gene flow, is also outlined in this chapter. Finally the calculation of correlations between biological distance matrices and geographic distance and chronological distance matrices was also discussed. Interpretations that can be drawn from the results of these calculations are explained for each statistic.

Chapter Six summarizes the results of each test described in chapter five. The results are presented according to the subsets of comparisons outlined in the previous chapter. Major patterns in the data and significant results that will be discussed further are highlighted in this chapter. Chapter Seven then offers explanations of the patterns identified in the results. This chapter discusses the impact that the Wari empire, and its collapse, had on the genetic relationships between sampled populations on a broad scale. The discussion then turns to interpretation of results on a regional scale. The results of this study regarding genetic structure of populations as it informs on the structure of social interactions during the MH and LIP generally fit with existing hypotheses based only on archaeological evidence. Implications for the results of the biological distance analyses are explored for samples dating to the MH. The discussion then turns to regional subsets. The dynamic of social interaction in the Wari heartland and changes over time are explored. The particular case of the Nasca and their relationship with the Wari and populations in the Ayacucho basin that predated the Wari empire are also considered in this chapter. Results for the south-central highlands groups are discussed in comparison to both the archaeological and ethnohistoric record. And finally the populations sampled from the north-central highlands are discussed in light of archaeological and linguistic evidence. While many important questions about the Wari, and more broadly the dynamics of ancient imperialism, were clarified by this study it is clear that there is much work yet to be done.

Chapter Eight summarizes the conclusions drawn from this study and proposes future directions of study. As with many bioarchaeological studies this research would be improved with larger samples, and more certainty regarding the chronology of those samples. It is also argued here that anthropologists should be incorporating more lines of evidence in their tests of ancient population interactions. Particularly genetic, skeletal biological, material culture, and spatial organization lines of evidence truly used together to test a hypothesis are more powerful than any one. Much work needs to be done in evolving the methodology and theory used to interpret past human interactions from the imperial body to the individual.

The overall objective of this dissertation is to explore theory particular to the process of developing social complexity in ancient empires and how population genetic studies can be interpreted in such a framework. Specifically, this study considers biological affinity between populations in the Peruvian central Andes that were likely impacted by the Wari empire. These biological relationships are explored using biological distance analysis based on cranial non-metric traits and understood within the context of population genetic theory. The dissertation begins with theoretical insights into ancient empires and how ancient imperial policies and practices can structure the population genetic structure of communities within an imperial realm.

Chapter II

Empires in the Archaeological Record

2.1 Empire defined

This chapter reviews definitions of empire as they have been applied to archaeological societies. The discussion then turns to different theoretical models of empire in prehistory. A past society could be considered an empire simply because that is how it defined itself (Sinopoli, 1994). While scholars often do not agree on the specifics, they do tend to accept some general commonalities of prehistoric empires. Empires are defined in this study as large heterogeneous states that encompass a diversity of cultures, ecological, and geographic zones. They are usually formed through some degree of military action either through actual coercion or the threat of force. Empires have a centralized capital (though not necessarily in the geographic center of the territory) that houses the authority figures. The capital is usually the largest city in the empire and may have monumental architecture or something else that makes it ‘special’ (Sinopoli, 1994). Scholars have agreed that the only predictable aspect of empires is that they will have internal variability based on their unique process of formation and territorial incorporation (Sinopoli, 1995). Where there is variation in integrative strategies employed by ancient empires, there is also a degree of consistency regarding imperial goals that lead to incorporation of new territory.

2.1.1 Common imperial goals

Of primary importance to an empire is the extraction of wealth from its territories. The extraction of wealth can take the form of subsistence crops, labor, animals, a multitude of valuable natural resources, and portable prestige goods (Sinopoli, 1995). A substantial body of literature is dedicated to the political economy of the state and various extractive strategies that have been used by past empires. Wealth finance versus staple finance political economic systems described by D’Altroy and Earle (1985) are perhaps the most often cited with regards to the extractive strategies of archaeological empires. Once an empire had access to goods and resources they may have sought to increase both production and exchange to reinforce an economic ideology consistent with unequal access to wealth (Brumfiel and Earle 1987). To model imperial control over interregional exchange of prestige goods in a wealth finance system Hirth (1996:224) suggests identifying nodes of control. These essentially equate to administrative centers in the archaeological record. These centers would have been placed strategically to best control the flow of trade and exert power over regional populations. Territorial expansion and emplacement of administrative centers would implicitly change the nature of interactions between regional populations.

Imperial expansion tends to happen quickly, and the retention of newly acquired territories depends upon many subsequent and ongoing processes of consolidation. This rapid expansion is a paradox to the archaeologist because current methodologies do not have enough precision to identify the sequence of events that may have happened in just a few generations. Archaeologically speaking, the end result of imperialism, a population consolidated under the domain of the empire, can look the same whether through coercion, a negotiated alliance, or some combination of the two strategies (Schreiber, 2001). Mann (1986 :1) described empire as, “multiple overlapping and intersecting socio-spatial networks.” Imperialism then is a process of negotiation operating on both an individual and collective scale, and on multiple socio-cultural levels over geographic space and through time (Glatz, 2009). Population genetic structure and material culture should reflect these continually mediated cultural, political, economic, and ideological relationships. This study focuses on the biological realm where patterns in genetic relationships were used to reveal “interactions”, or the lack thereof, between populations.

2.2 Theoretical Models of Empire

The traditional approach to studying past empires is through the identification of maximum geographical extent, chronological apex of political power, and the entirety of material remnants of the central polity in peripheral regions. However, this approach likely obscures crucial processes of establishment, negotiation, and definition of dominance relationships which would have been constantly shifting according to the changing interests of both the empire and communities under its administration (Schreiber, 2005). Acknowledging imperialism as a dynamic and fluid process leads to a more fruitful line of inquiry because even if scholars cannot agree on what an “empire” is, they can certainly acknowledge vestiges of the how, when, and why a complex society emerges, expands, and collapses (Morrison, 2001). Multiple theories of empire and imperialism have been constructed over time as a framework for understanding these processes. The following sections review some of the more recent models that have been applied to archaeological empires in South America.

2.2.1 The Core-Periphery Model

Wallerstein’s (1974) World System has come to be one of the models most commonly used by archaeologists to describe state and imperial relationships with provincial populations. The world system model was developed to describe the modern world market and consists of a core, semi-periphery, and periphery, each of which performs a specific class of functions. The core is the political and economic, if not geographic, center of the system. The core is the producer of prestige goods where the periphery is the source of raw materials and cheap labor.

The semi-periphery functions as an intermediary to promote the flow of finished goods, and raw materials and labor. Archaeological applications of this model often propose a political core exploiting peripheral communities through monopolistic control of an interregional trade network (Stein, 1998). Wallerstein was a Marxist scholar who believed that this system was not sustainable and would eventually lead to the revolt of the peripheral communities resulting in collapse of the empire. While the overall idea is an instructive rubric, it is perhaps not the best for understanding ancient empires operating on a smaller scale than the modern world market.

The Core-Periphery Model *sensu* Wallerstein (1974) has been critiqued by anthropologists as portraying peripheral groups as passive and reactive to the more complexly organized state or empire (Schortman and Urban, 1994; Lightfoot and Martinez, 1995; Stein, 2002). The core is thus interpreted as the sole impetus of change, be it political, economic, or ideological (Schortman and Urban, 1998). This view as structured by World Systems approach also emphasizes external impetus for change, and downplays the role of internal social, political, and economic change in regional communities (Stein, 2002). Schortman and Urban (1998) argue that instead of fitting these interactions into a relatively inflexible model like the Core-Periphery model, that they should be described in their own terms as cases of “culture contact.” Culture contact is described by Schortman (1989) as a prolonged case of direct interaction between groups that do not share a common identity. This is too ambiguous to be of much use in any real analytical sense (see Stein (2002:904-905) for a more detailed argument), and is more a critique of studies at that time than direction for future researchers to take. The point that this study takes from these critiques is that the cultural negotiations that take place in a process of imperialism over time are complex and mitigated by multiple social actors.

2.2.2 The Territorial-Hegemonic Model

The Territorial-Hegemonic model describes a continuum between direct control with heavy state intrusion (Territorial), and indirect control by the state (Hegemonic). Luttwak (1976) was one of the first to explicitly contrast territorial versus hegemonic empires in an attempt to describe the various strategies employed over time by the Romans to expand their empire. The model was then built upon by Hassig (1985) in his assessment of the Aztec empire with an emphasis on hegemonic strategies. D'Altroy (1992) also has used this model to describe Inka imperialism. To apply the Territorial-Hegemonic model it is necessary to understand the extremes of the spectrum, territorial versus hegemonic power.

Territorial Control

Territoriality necessitates more intensive contact between the state and regional populations (Sack, 1986). Territoriality is enforced and an imperial body would require a sophisticated and well-developed internal administrative framework to be successful at both attaining and retaining territory. The administrative framework maintains order within the political boundaries meaning that it can mobilize an army and direct the distribution of resources. Therefore territoriality can increase organizational efficiency, centralization, and span of control of the empire. However these gains are only possible to a point, and territoriality can also weaken an empire (Sack, 1986 :46). The effect of weakening an empire may be due to the inertia of territoriality. Sack (1986 :34) notes that territoriality engenders more territoriality. Essentially, the acquisition and incorporation of new territories by an empire necessarily leads to the addition of more territory. Eventually the territorial extent of an empire will extend further than what can effectively be controlled, leading to the possibility of a successful rebellion.

Territorial control is analogous to Eisenstadt's (1963, 1967) model of a bureaucratic empire with a well developed financial, political, military, and administrative bureaucracy. Bureaucratic empires undertake significant restructuring of conquered territories. In short territorial control is most concerned with the incorporation and direct domination of regions (Hassig, 1985). Mann (1977) even suggested that the order of territorial incorporation in such empires is first by military coercion, then administrative, and lastly economic. He was, however, referring to the rise of capitalism and the argument could be made that in the archaeological record one should not let this model obscure attention to the historical specificity of the empire under consideration.

With respect to ancient empires it is instructive to turn back to Sack's (1986) three essential elements of territoriality. In particular the second coordinate, communication of a boundary, would be difficult in a society without a form of writing because the boundary would have to be remembered. A social definition of territory means that to have access to land and resources one must be a member of the society that controls them (Sack, 1986). In the Andes there is a deep history of ancestor veneration. Generally, ancestors are thought to be tied to the land and resources (DeLeonardis and Lau, 2004). Mortuary monuments in the Andes, namely *chullpas* and *machays*, are usually situated quite prominently on the landscape which some have hypothesized may have communicated boundaries in societies that did not have writing (Isbell, 1997). The empire though, would have had to constantly negotiate alliances with regional groups if the maintenance of the physical boundary was in their control. This relationship is more characteristic of a hegemonic type of power.

Hegemonic Power

With the Hegemonic Power model, unlike with territorial control, there is no fixed political boundary. Infrastructure in such an empire is not as well developed, and regional polities remain largely autonomous. Eisenstadt (1963; 1967) would characterize this as a patrimonial empire where there is limited bureaucracy, and conquered territories experience little restructuring of their sociopolitical bodies. This can be adaptive where by utilizing a sociopolitical administrative structure that is already in place, the empire minimizes the costs of incorporating the group (Hassig, 1985). With hegemony there is a degree of political (ideological and economic) control that exceeds the territorial boundaries of the empire (Hassig, 1985). Hassig (1985: 93) identifies three characteristics of such an empire: 1) expansion of political dominance without direct territorial control, 2) a focus on the internal security of the empire by exercising influence on a limited range of activities within the provincial groups, and 3) the achievement of such influence by generally retaining rather than replacing local officials. By relying on local officials the empire could economize the use of their resources, co-opting local resources instead.

The minimization of imperial goals concerning regional populations would allow an empire to be maximally efficient in the sense of expenditure versus exploitation. Hegemonic strategies also allow for reliance on local resources for the maintenance of the empire. For example, local groups could provide security, or maintain borders in lieu of paying tribute. In this case an empire could have a zone of diplomatic control between the heartland and regions outside the boundaries of the empire. This zone would have insulated the heartland from direct threats and allowed the empire to extend their influence and acquire new territories more easily. In the context of this research the important aspect of hegemonic control in regions distant from the core is that as a rule, the empire would not need to maintain a physical presence on the frontier. If power could be maintained without coercion it would be unlikely that an empire would move large numbers of troops, or make attempts to colonize in regions far from the imperial heartland. There only needs to be the threat of force, not the actual exercise of force for an empire to maintain power (Tilley, 1991). In this way a standing army need not actually exist. Hassig (1985) in his examination of the Aztec empire notes that there was not always a standing army in existence, but there was a recognized military structure which allowed for the expedient mobilization of a military force. Consequently, elevated contact between regional populations would not be due directly to the presence of imperial administrators, but more likely due to increased interaction between immediate neighbors as the result of common ideology, identity, and economic goals.

2.3 The Wari

This research focuses on the Wari empire and populations that lived in the central Andes both during the height of their power and after their collapse. The Wari were centered in the Ayacucho basin in the south-central highlands of modern day Peru, and was the first empire in South America (Figure 2.1). The capital of the Wari empire, Huari[2], emerged at the end of the Early Intermediate Period (EIP) (200 BC- AD 600) out of the coalescence of existing Huarpa settlements in the valley (Schreiber, 2001). Huarpa ceramic style was first recognized and named by John Rowe, Donald Collier, and Gordon Willey (1950) when they visited the site of Huari in 1942. However, Lumbreras (1960) was the first to identify Huarpa as a distinct cultural group.

---

[2] "Wari" will be used in reference to the culture, and "Huari" will refer to the capital city of the Wari Empire in Ayacucho, Peru following Isbell and Schreiber (1978).

Some of the first studies of Peruvian ceramics dating to the MH cited similarities to those recovered from Tiwanaku and suggest that before the Inka there was a pan-Andean Tiahuanaco Horizon (Kroeber and Strong, 1924). However later Tello (1931; 1939) and Larco (1948) noticed differences between the Peruvian assemblages and Tiahuanaco ceramics significant enough to suggest a distinct origin, most likely centered at Huari. Rowe, Collier, and Willey (1950) formally investigated the site at Huari which was followed by excavations conducted by Bennett (1953). These initial investigations confirmed what Tello and Larco had initially suspected that Huari was the center of the culture that would later be known as Wari. Dorothy Menzel's (1964) comprehensive study of ceramic styles in the Ayacucho region identified a strong Nasca influence in Ayacucho prior to the MH. During the EIP there was a notable increase in number of Huarpa sites in the Ayacucho valley corresponding to population growth and an increasing dependence on agriculture (Ochatoma 2007). The intense interaction of the growing Huarpa population with the Nasca and Tiwanaku probably promoted an increase in social complexity that eventually led to the formation of the Wari as a state level society, and later an empire. However, this hypothesis is poorly supported by archaeological evidence and there clearly is much left to be discovered about the dynamic Huarpa culture that gave rise to the Wari (Ochatoma 2007).

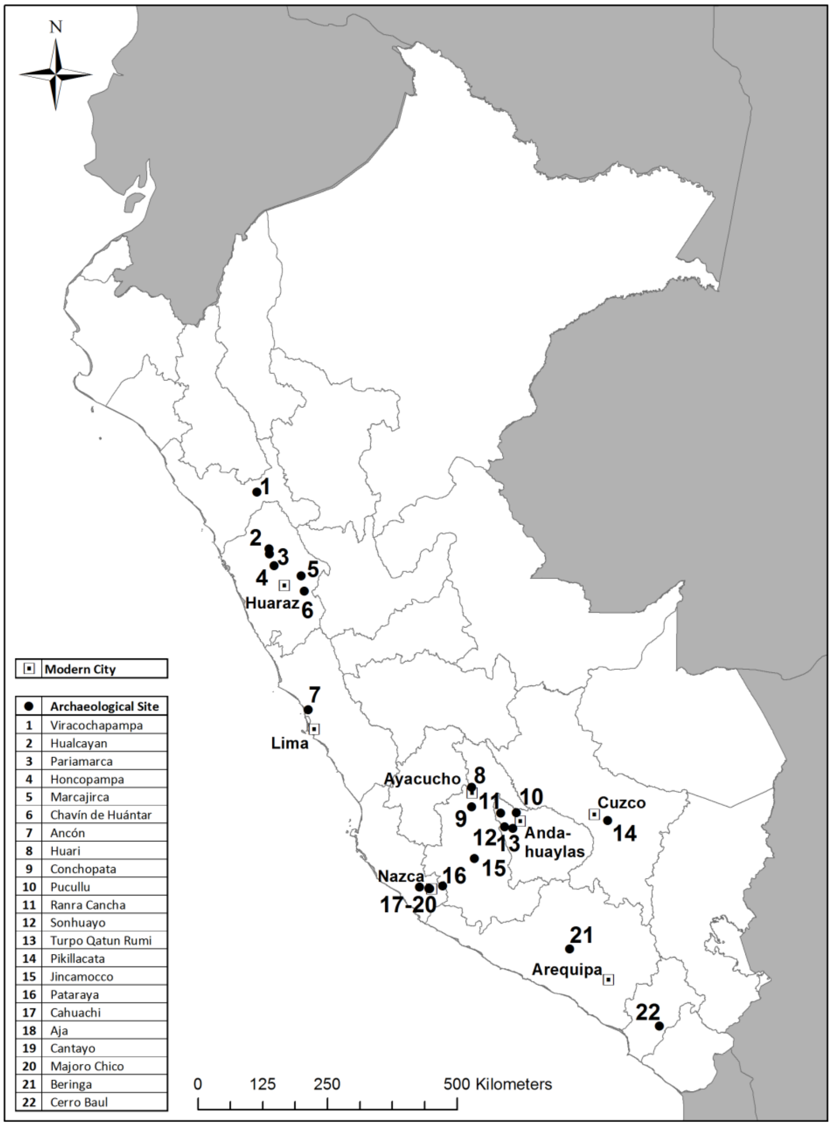


Figure 2.1. Map depicting archaeological sites mentioned in the text. (map created by Rebecca Bria)

The growth of Huari as a city and the expansion of the Wari empire out of the Ayacucho basin happened at about the same time. Huari was the largest urban center in the central Andes during the MH, covering an area of approximately 3km^2 situated on a mesa. Huari was defensively oriented, accessible only from the east, with high walls built around its perimeter (Isbell, 2004; Isbell et al., 1991; Isbell and Schreiber, 1978). Even within the city there were checkpoints and high walls around roads to control access to various sectors of the site (Isbell, 1991). Estimates vary, but Huari was home to no fewer than 10,000 people and likely had about 50,000 (possibly up to 70,000) residents at the height of its occupation (Isbell et al., 1991:51; Schreiber, 1992). The architecture at Huari demonstrates the finest examples of the imperial style with large rectangular patio groups and multistory structures. Ritual architecture including D-shaped structures and elaborate underground tombs are also found at Huari. Rigorous urban planning is evident at Huari with roads and sectors accommodating the gradual expansion of the city. Conformance with these architectural tenets is largely what archaeologists have used, in conjunction with ceramic styles, to identify Wari imperial presence outside of the Ayacucho region.

The site of Conchopata, located about 12 km from Huari, and is clearly an important secondary center early on in the heartland. Conchopata was discovered in 1942 by Julio Tello (Ochatoma, 2007). Lumbreras (1960) later realized the importance and complexity of this site through his excavations. The site demonstrated Wari influence by ca. AD 550 when it becomes an imperially sponsored community of potters (Isbell and Cook, 2002; Silverman and Isbell, 2002; Cook and Glowacki, 2003). The architecture is laid out in rectangular plaza groups and there are multiple D-shaped structures similar to those found at Huari (Isbell and Cook, 1991; Ochatoma, 2007). Evidence at Conchopata also suggests that feasting was an important activity at the site whereby elites may have demonstrated wealth and generosity in return for labor (Isbell and Cook, 1991). Intensification of consistency in mortuary ritual and grave goods, intensification of craft production, agriculture, and elite-sponsored feasting all point to Conchopata occupying a place of political, economic, and ideological importance in the Wari empire (Tung and Cook, 2007).

2.4 Wari regional presence

During the MH a number of smaller administrative centers were situated throughout the Wari heartland (Figure 2.2). Multiple administrative centers were built throughout the Andes likely situated on the landscape to most effectively incorporate local polities (Jennings and Craig, 2001). Many of these were locations of intensive agriculture, probably used to support the rapidly growing capital city's population (Isbell, 1977; Schreiber, 1992, 1999, 2001, 2005; McEwan, 1996). Administrative sites such as Pikillacta (McEwan, 1996, 2005), Jincamocco (Schreiber, 1991), and Cerro Baúl (Moseley et al., 1991; Williams, 2001) were present outside of the Ayacucho Basin by AD 600. By AD 700 Wari sites, as evidenced by architectural style and ceramic assemblages, are found as far north as Honcopampa and Viracochapampa (Isbell, 1989; Topic, 1991b). Lumbreras (1974b:162-163) noted that many Wari sites are situated along Inka roads. He suggested that the Inka probably improved upon, and added to a system of roads first built by the Wari.

Early research into Wari social complexity was done by Isbell and Schreiber (1978). They conducted a room shape analysis of Pikillacta, Jincamocco, and Viracochapampa exploring room-shape factor (room width divided by length) to test for significant differences in architectural programs [although for a critique see Scheps (1982)]. They first tested Viracochapampa, a probable Wari administrative center, against Marca Huamachuco which is a contemporaneous and locally built site. There was a significant difference between the two suggesting that Viracochapampa was not built according to the tenets of the local architectural program, and instead represents intrusion by the Wari empire over 700 km north of the capital city. Further analysis showed no significant difference in room-shape factor between

Viracochapampa, Pikillacta, and Jincamocco. This consistency in architecture is suggestive of an imperially administrated construction plan, and supported the notion of Wari as an empire.

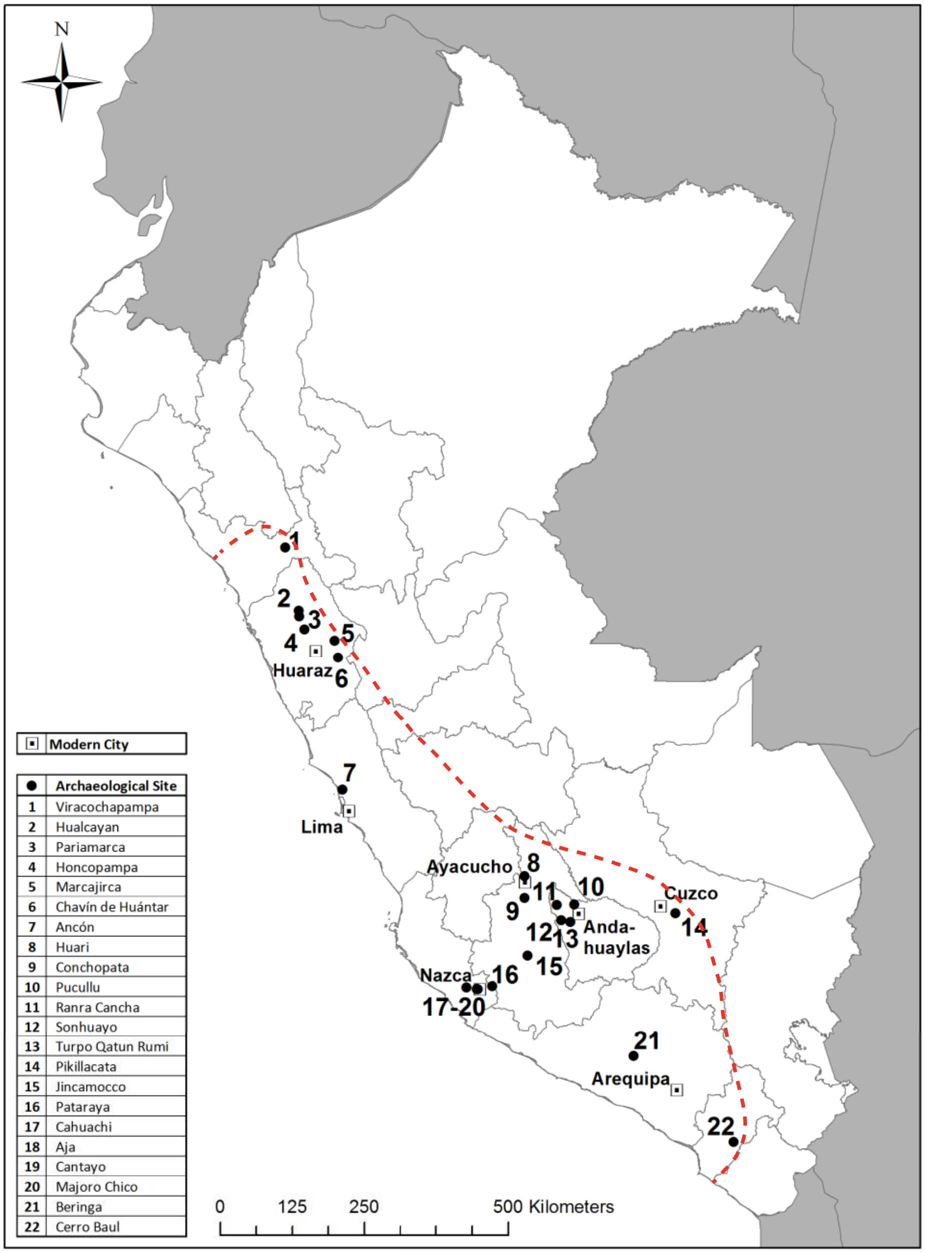


Figure 2.2. Hypothesized territorial extent of the Wari empire (red dashed line is a composite representation of the maximum boundaries previously suggested for the Wari empire).

Uniformity in ceramic style and architectural plans are good proxies for detecting imperial incorporation, but stronger evidence lies in obvious changes to settlement patterns which suggest a reorganization of economic and social activities geared towards channeling, or controlling resources and supporting a centralized administrative power. Examples of this type of settlement pattern shift coupled with intrusive Wari style ceramics and architecture are explicit at a number of sites that are well studied and have traditionally been used as the trademark administrative centers (Schreiber, 1987a; 1991).

Ázangaro was a regional administrative center located in the Huanta basin that has been argued as an important stronghold of the Wari empire (Schreiber, 1987a). In the later MH when the territorial extent of empire seemed to contract, resources were directed here to intensify agricultural production to support a burgeoning core population (Schreiber, 1987a). It may also have been an important ritual center tied to the calendar (Anders, 1986; 1991). Based on this interpretation Anders (1991) hypothesized that the Wari had no centralized power and were more consistent with a diffuse religious influence lacking real hierarchical relationships between the center and local populations.

Outside of the core area of Huari the closest two major administrative sites were Pikillacta and Jincamocco. Pikillacta is situated in the Lucre basin just east of Cuzco. It is the largest of the Wari administrative centers, and is about 250 km southeast of Huari (McEwan, 2005). Pikillacta has been the focus of anthropological inquiry since 1927, and was intensively excavated by Gordon McEwan from 1978-90 (McEwan, 2005). McEwan's working hypothesis was that one of the main functions of Pikillacta was the storage of ancestor mummies and other *huacas* (sacred objects) of subject populations. The Inka used this method to bolster their power in the Andes where there was a strong and ancient tradition of ancestor veneration. He suggests that Wari ancestor mummies may have also been kept at Pikillacta which would have served to reinforce a bond of fictive kinship between the Wari and their subjects. Indeed a cache of ten skulls were discovered during the 1982 field season at Pikillacta (Verano, 2005). Caches like these are not unique to Pikillacta, and have a long history in the Andes. Some of these are possibly related to ancestor veneration (as at Chavín (Burger, 1984)), ritual sacrifice (Verano et al., 1999), or as trophies such as in the case of trophy heads recovered from Conchopata (Tung, 2008) and Nasca (Brown et al., 1993; Forgey, 2006). Verano (2005) was able to study three of the skulls, but unable to locate the remaining seven. Further analysis on this sample could provide insight into whether these individuals were derived from the local population or foreigners, thus addressing the hypothesis that the skull cache was an attempt by Wari administrators to incorporate themselves as “kin” in the community.

Recently the site of Huaro was discovered about 15 km east of Pikillacta (Glowacki, 2002). Huaro was on the same scale as Pikillacta, and the current interpretation is that it may have housed the workers that built Pikillacta (Glowacki, 2001, 2002). This scale of infrastructure emplaced in and around Pikillacta suggests that the Wari had a keen interest in the region and its resources.

North of the modern city of Cuzco, and near the archaeological site of Vilcabamba, is the site of Espiritu Pampa. Ongoing excavations here recently uncovered the tomb of a high status Wari individual (Valdez, 2011). Vilcabamba is better known as the site of the last holdout of the Inka where Tupac Amarau was able to resist the Spanish until AD 1572 (Valdez, 2011). The discovery of a Wari mummy at Espiritu Pampa indicates they had a presence in the region long before the Inka. The discovery also expands the previously known territorial boundaries of the Wari empire.

Jincamocco was the other major Wari administrative center located in the Sondondo valley. By about AD 600 settlements in the valley shifted to lower altitudes coupled with major terrace construction suggestive of a shift in subsistence strategies with a new focus on maize cultivation (Schreiber, 1987b). Jincamocco began as a relatively simple Wari-style rectangular plaza structure, but was augmented with rectangular structures throughout the MH until the entire site covered about 15 ha (0.15 km^2) (Schreiber, 1987b). There were also three smaller sites near Jincamocco with Wari-style architecture. One of these appears to have been situated strategically along a road that runs through Jincamocco and probably connected the center with both Huari and the Nazca River valley (Schreiber, 1987a, 2005). The construction of an administrative center with satellite sites, intensification of maize agriculture, and a road through the Cahuarazo Valley during the MH suggests this region was under direct control by the Wari empire (Schreiber, 1987b).

Evidence for Wari imperial presence in the north and north-central highlands is less visible than in the south. However, sites like Viracochapampa, Honcopampa, and Pariamarca strongly suggest the Wari had some measure of territorial control in the region. Viracochapampa is located 700 km northwest of Huari and is usually cited as the northernmost clear example of Wari imperial presence (Isbell and Schreiber, 1978). Viracochapampa is within sight of Marca Humachuco, and it has been hypothesized that it was built to transfer the local ritual apparatus to a space under direct supervision of Wari administration (Topic, 1986; 1991). Topic's hypothesis was based on the fact that there are about the same number of niched halls at both sites and ritual items important to the local ruling lineages may have been transferred to Viracochapampa, similar to the Inka strategy of moving *huacas* to exercise power over local populations (Isbell, 2004). McEwan (2005) suggested this function for the Pikillacta site as well. In fact

Viracochapampa and Pikillacta are often compared on the basis of their architectural similarities (Isbell and Schreiber, 1978; Isbell, 2004; McEwan, 2005). Construction of Viracochapampa was never finished, and if the site was ever occupied it was only ephemeral (Topic, 1991). Topic (1991) argued that the Wari's program of co-opting local ritual objects to enforce their power failed. Ultimately, it does not appear that the Wari effectively incorporated the Huamachuco region into the empire.

Honcopampa was another site situated in the north-central highlands that appears to illustrate Wari imperial presence. Honcopampa was located about 550 km north of Huari in the Callejón de Huaylas. The site has been associated with the Wari largely based on architectural style. The site has rectangular patio groups, *chullpas*, and most notably D-shaped structures that are also seen at Huari and Conchopata (Isbell, 1991; Tschauner, 2003). Radiocarbon dates from carbon samples recovered inside patio room groups placed occupation at Honcopampa firmly in the MH (Isbell, 1991; Tschauner, 2003). In addition to the architectural features, Honcopampa was strategically located to control movement into and out of the valley. This site may have represented a Wari center that functioned to control the local population and the movement of trade through the Callejón de Huaylas (Isbell, 1991; Tschauner, 2003). Some have questioned the validity of Honcopampa as a Wari administrative center largely based on the construction techniques used (Isbell, 1991). The masonry techniques follow older northern highland traditions, and may be illustrative of local populations copying Wari styles in an effort to increase their own prestige. Given a loose adherence to Wari architectural cannons, Honcopampa is less universally accepted as a true Wari administrative center.

Pariamarca is another possible Wari settlement in the Callejón de Huaylas. Pariamarca has been suggested as an important Wari site on the basis of a large rectangular plaza structure identified in aerial photos (Jennings and Craig, 2001; Williams and Pineda, 1985). Until very recently no archaeological investigations had taken place on the ground at Pariamarca. In 2009 Rebecca Bria conducted an archaeological survey of the area and excavated exploratory units within the large plaza structure (Bria and Rivas Otaiza, 2010). The ceramic assemblage suggested an intensive occupation during the MH with many sherds decorated with Wari motifs (Bria and Rivas Otaiza, 2010). The location of the plaza next to a large terraced hill with elaborate Chavin-style masonry and canals throughout may follow a similar pattern to Viracochapampa where the Wari incorporated locally recognized places and objects of power to legitimate their own power. As of this time the lack of intensive investigations at this site preclude the ability to draw any hard conclusions about the nature of Wari presence, if any, at Pariamarca.

2.4.1 Territorial expansion and the mosaic model of Wari imperialism

The Wari appear to have been centered in the central Andean highlands. However, there are strong correlations between Wari and Nasca styles suggesting that the populations in the Ayacucho basin have always had strong relationships with the Nasca. Notably, Nasca underwent a cultural upheaval in the beginning of the MH corresponding to the Wari expansion (Schreiber, 2001). As mentioned earlier, Wari administrative centers appear in the Nazca valley by AD 750. Pataraya, an example of one of these centers, was a colonial outpost placed in the valley to exert territorial control over the region (Edwards, 2010) (see Figure 2.2). Pataraya is evidence that the Wari had imperial interests in intensifying production of goods, and exercising control over the movement of both goods and people in the valley.

As research focused on the Wari has progressed it has been apparent that the empire did extend all the way to coastal Peru (see Figure 2.2). Wari-style mummy bundles have been recovered from Huaca Pucllana in Lima. In Ancón, about 40km north of Lima, Wari-style ceramics were also recovered from the MH cemetery. Slovak's (2007) work demonstrated that human remains in Ancón, buried in a style consistent with a high status Wari individual, had Sr signatures consistent with the Ayacucho basin. This study is discussed in more detail later, but certainly lends support to the argument that the Wari were a territorially expansive empire.

The southern limit of the Wari empire is defined by the site of Cerro Baúl and extends to the northern Atacama Desert (see Figure 2.2). Cerro Baúl was a Wari administrative and ceremonial center located in the Moquegua Valley about 600 km south of Huari. The site was situated on top of a large hill for which the site is named. It is also at the southern extent of the Wari empire on the border shared with the Tiwanaku (Williams, 2001). The site was occupied contemporaneously with two other Tiwanaku sites in the valley, Chen Chen and Omo (Williams 2001). Cerro Baúl remained occupied until the collapse of both the Wari and Tiwanaku at the end of the MH.

Largely mitigated by physical geography, Andean polities generally did not attempt to control contiguous territories as would be suggested by a Core-Periphery model, and questions remain as to the formulation and functioning of the imperial administration (McEwan 2005). With respect to the degree of territorial incorporation the Wari achieved in distant regions scholars tend to fall into one of two camps. Some see the Wari as a powerful empire with direct control exercised in provincial areas, while others interpret the Wari as having an indirect influence on a number of independent regional polities. Schreiber (1992) argues for a hybrid of these two polar interpretations. She posits a "mosaic" model of imperial incorporation in which the Wari exercised flexibility with their tactics based on each individual situation. She argued that variables such as pre-existing social complexity, physical environment, available resources, population density, and strategic importance dictated the incorporative approach utilized by the Wari.

The paradox for studying empires like the Wari is that infrastructure may only have been built in regions where there was not highly developed political centralization (Schreiber, 1992). If there had benn no existing infrastructure then imperial investment would be needed if the Wari desired to incorporate and exploit the resources of a region. Conversely, if there had been pre-existing political centralization in the region then the Wari could co-opt that structure for their needs. By gaining acceptance of their ideology the Wari can expand their power beyond the territorial boundaries of the existing state in a hegemonic manner. Perhaps at first local authorities may have co-opted Wari ideology enforcing unequal power relationships to reinforce their own standing in the community. As Earle (1997:149) points out,

> "Ideology is a system of beliefs and ideas presented publicly in ceremonies and other occasions. It is created and manipulated strategically by social segments, most importantly the ruling elite, to establish and maintain positions of social power."

Mann (1986) suggested that many forms of power greatly exceed the physical borders of an empire and facilitate its territorial expansion. Emulation makes possible the interaction and eventual inclusion of a group into the empire. In other words, artifacts that appear to modern archaeologists simply as local copies of imperial goods may have been far more significant with regard to the actual relationship with the empire. The downfall for archaeologists is that due to this phenomenon, some of the most important Wari sites may be interpreted as only exhibiting an indirect Wari influence rather than full incorporation in the empire.

Like most early empires, it has been argued that the Wari expansion out of the Ayacucho basin was militaristic and began very quickly. Tung (2012) argued that both archaeological and osteological evidence suggest the warrior elite either occupied many of the high level political positions, or closely coordinated with political elites ensuring a savvy integration of military and political power. Thus, military leaders likely played a big role in building and shaping state institutions. Controlling regions far from the capital exclusively by military might, as is characterized by a Territorial power, would be very costly to the empire and certainly was not the only strategy employed; ritual authority and economic dominance also helped the Wari to establish and maintain control (Tung, 2012).

Patricia Knobloch (2010) has explored the complex landscape for Wari populations and those they sought to integrate in the empire through ceramic iconography as one physical representation of human activity. Of interest to this study she identified “faces” that may represent individuals, social group, or perhaps an anthropomorphic representation of an idea or process that is not yet recognized. For example in Figure 2.3 a sample of the figures presented by Knobloch (2010) illustrates the complexity of Wari imperialism. There are high status individuals, possible provincial administrators, warriors, and enemies or prisoners. Individual (b) in Figure 2.3 is especially interesting in that these characters appear to administer agricultural production and distribution. The Wari likely developed a very sophisticated imperial administrative body to necessitate such specialized positions. This further suggests that Wari imperialism was planned in detail and customized dependant on the purpose for incorporation (agricultural intensification, extraction of prestige goods or other material resources, or subsuming a rival group). As previous studies have shown, the Wari empire used a mixed strategy of militarism, ritualism, and economic and technological dominance.

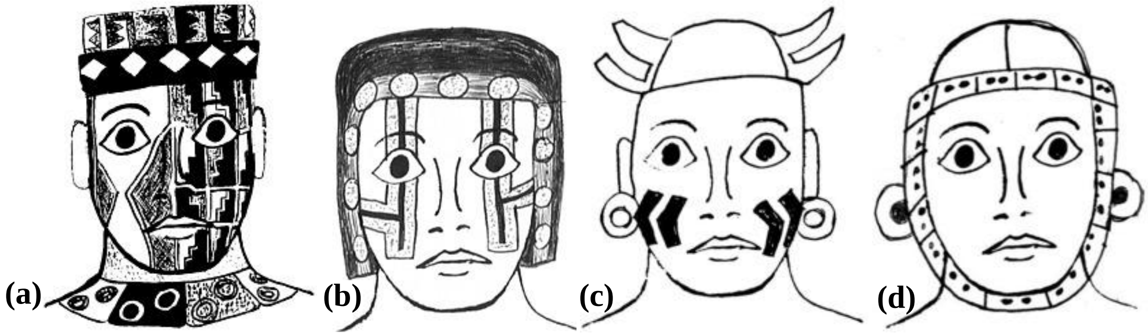


Figure 2.3. Faces depicted on Wari ceramics distributed throughout the Wari empire as illustrated by Knobloch (2010). The faces represent high status individuals from Huari that may have been a hunter or warrior (a), a possible administrator over agricultural activities (b), a warrior with a trophy head found at Conchopata (c), and a prisoner or representative of a rival group (d).

2.4.2 Opposition to the concept of Wari as an Empire

Whereas the Inka left clear archaeological indicators of their imperial activities, the history of the Wari has been less easily interpreted. Historical records recount Inka myths of ancient conquerors that some have interpreted as a memory of the Wari (Duvoils, 1973 cited in Silverblatt, 1987). The notion of Wari as an empire was first proposed by John Rowe (1956). Dorothy Menzel's (1964, 1969) important work on ceramic seriation in the MH further led credence to the argument that Wari was a powerful secular state. Lumbreras (1969) also suggested that the Wari were the first true state, or a pristine state *sensu* Fried (1960), in South America.

However, since Rowe (1956) many have challenged the idea that Wari was an empire (see Donnan and Mackey, 1978:213; Conrad, 1981; Czwarno et al., 1989; Shady Solis, 1989; Shimada, 1990; Topic 1991a, 1991b). Opposition to Wari as an empire stems particularly from Andeanists working in northern regions who see little evidence for direct control of these polities during the MH (Isbell and McEwan 1991; Shady Solis 1989; Topic 1991a, 1991b). Shady and Ruiz (1979) attributed the presence of Wari artifacts outside of Ayacucho as simply due to trade. Anders (1991) also argued, from much closer to the Wari heartland, that the Wari may have been a religious cult rather than a state or imperial level society.

Schreiber (2000) has summarized three categorizations of the Wari that have resulted from various interpretations of the material record. She argued that direct political control (Conchopata), economic interaction (Nasca), and Wari as a religious movement (Ázangaro) are all interpretations that could be supported by archaeological evidence, but does not suggest that Wari should be expected to fall into one of these categories uniformly across the Andes. For a site-by-site basis, Table 2.1 summarizes traits that would be expected in each of the three characterizations of Wari.

Although the nature of Wari influence in regions of Peru remains contested, recent archaeological research supports the interpretation of Wari as an empire with an expansive sphere of ideological, political, and economic influence (Lumbreras 1974a; Isbell and Cook 1987, 2002; Schreiber 1987a, 1987b, 1991, 1992, 2001, 2005; Brewster-Wray 1989; McEwan 1991, 2005; Cook 1992, 2001; Jennings and Craig 2001; Cook and Glowacki 2003; Glowacki and Malpass 2003; Tung 2003, 2008; 2012; Tung and Cook 2005; Jennings 2006; Edwards 2010). It appears that the Wari employed a wealth finance economic system in regions geographically distant from Huari to extract and exchange portable prestige goods like ceramics, obsidian, textiles, and metal objects (Burger et al. 2000; Isbell 1997; Jennings and Craig 2001; Nash and Williams 2004).

Table 2.1. Three classes of possible Wari interaction in regional communities (after Schreiber 2000:443).

	Category of Interaction		
	Political Control	**Economic Interaction**	**Religious Movement**
Presence of Wari artifacts	**X**[*]	**X**	**X**
Presence of Wari traits:			
Roads	**X**	**X**	**o**
D-shaped structures		**o**[†]	**X**
Tombs and burials		**o**	**X**
Offerings		**o**	**X**
Agricultural traits (terracing)	**X**	**X**	**o**
Presence of a Wari site (following architectural cannons)	**X**	**o**	**o**
Changes in settlement patterns:			
Relocation of productive zones	**X**	**X**	**o**
Authority (hierarchy) reorganized or centralized	**X**	**o**	**o**

[*] Trait will be present
[†] Trait is likely to, but may not be present

2.4.3 Collapse of the Wari Empire

Around AD 1000 to AD 1100 the Wari capital at Huari was largely abandoned and it seemed the empire had collapsed (Schreiber, 2005). The undoubtedly complex interaction of events that led to the collapse is at present not well understood. Research on this subject is also ongoing (Castillo, 2000; La Lone, 2000; McEwan, 1996; Schreiber 2000, 2001; Williams, 2001). Some have cited a prolonged drought as the root cause of the collapse of both Tiwanaku and Wari (Binford et al., 1997; Thompson et al., 2000; Williams, 2001). Drought may have been a factor; however, recently Tung (2008) and Kurin (2012) found that populations in the former Wari imperial heartland and Chanka populations around Andahuaylas, respectively experienced heightened violence consistent with raiding and/or warfare that might be expected during a time of political and economic instability. This evidence of political fragmentation, consistent with imperial collapse, was not correlated with the drought. While the drought may have been a contributing cause to the demise of the Wari it is unlikely it was the sole cause.

The contraction of the Wari empire likely did not happen concurrently in all regions. For example Schreiber (2000, 2001) has noted that the Wari abandon the Nazca River valley before AD 1000. Being highland-centered, the Wari may have abandoned their investments in regions distant from the capital due to the high cost of maintaining them. Collapse certainly is a process much like territorial expansion. Like expansion, the Wari collapse may have happened quickly enough that in the archaeological record it appears almost instantaneous. While the exact causes of the collapse of the Wari is not in the purview of this dissertation, the effects of imperial decline on population structure in the central Andes should be detectable.

2.5 Wari imperialism and biological distance analysis

If the Wari integrated a large territory under their administration and exercised hegemonic power outside of those territorial boundaries, then changes in the nature of social interaction should be reflected in biological affinities among populations in the central Andes. If Wari imperialism did significantly affect the structure of social interaction on a large scale by intensifying contact then populations dating to the MH should have closer biological relationships than those dating to the LIP. Regional populations where direct Wari administration is evident in the archaeological record should have a close biological affinity to populations from the Wari heartland.

Chapter III

Theoretical Background: Population Genetics and Non-Metric Traits

This chapter will discuss the theoretical basis for the use of cranial non-metric traits in the analysis of Andean population history related to the rise and fall of the Wari empire. This study is essentially one of human migration due directly or indirectly to imperialism (Lasker and Mascie-Taylor, 1988:1). Kamp and Yoffee (1980:99) stated that social groups integrate and split for a myriad of political and historical reasons. Biological distance analyses reveal only evidence of the integrations and splits, but not the causes. In this regard, the results of this study cannot demonstrate why or how exactly the alliances between regional populations and the Wari empire were negotiated, how the placement of administrative centers maintained imperial control of a region, or why military coercion was used in some cases. However, the consequences of these actions can be read in the population genetic history of Andean populations that lived during and after the Wari empire. Increased migration whether on a small regional scale or over large geographical areas due to trade or conquest and colonization, should result in increased gene flow. This would result in increased genetic homogeneity among these populations, and should be detectable through inherited traits in the skeleton. Given what is known (and in many cases not known) about Wari imperialism during the MH, evidence of gene flow would be helpful in understanding the scale of Wari influence and patterns of colonization in the ancient Andes.

3.1 Quantitative Genetic Theory

To evaluate the exchange of genes between populations, or gene flow, it is assumed that the skeletal traits are under a significant degree of genetic control. Variation must be also be present in the expression of the trait. The phenotypic variation (σ_P^2) of a quantitative trait can be expressed as,

$$\sigma_P^2 = \sigma_G^2 + \sigma_E^2 , \qquad 3.1$$

where σ_G^2 is the genetic variance and σ_E^2 is the environmental variance. The phenotypic variance then is always greater than or equal to the genetic variance (Falconer, 1989:125). Equation 3.1 can be expanded to consider multiple traits,

$$P = G + E, \qquad 3.2$$

where P, G, and E are phenotypic, genetic, and environmental covariance matrices respectively. The environmental effects on trait expression are difficult both to identify and quantify. However, due to the genetic coordinate in the expression of skeletal traits (both metric and non-metric) they can be used as a proxy to model microevolution if the environmental effects are randomly distributed over time and space (Cheverud and Buikstra, 1981a, 1981b; Cheverud, 1988). Indeed recent studies of phenotypic vs. genetic distances have found correlation between aforementioned variance-covariance matrices suggesting that phenotypic trait data can be as effective as molecular data in understanding population history (for example see Ricau,t et al. 2010).

3.2 Threshold Model

The relationship of genetic variance to the expression of non-metric traits must be identified before any statistical models can be applied to their relative frequency within and among populations. In this study non-metric traits are considered using the Threshold Model. Grüneberg (1952, 1963) described skeletal non-metric traits as “quasi-continuous” in their expression. It follows that non-metric traits are polygenic, where the expression of a trait is due to a combination of inheritance and environmental pressures (Cheverud and Buikstra, 1981a; Falconer, 1989). However, unlike many polygenic traits that have a continuum of expression, non-metric skeletal traits are expressed in a few discrete forms, thus quasi-continuous. Cheverud and Buikstra (1981a:44) apply the Threshold Model where one or more thresholds act on a continuously distributed liability. When the additive genetic and environmental effects surpass the threshold the trait is expressed.

Falconer (1989) can be credited with refining this model. He found that comparing populations based on straight frequencies was not informative because differences existed in the variances in trait frequencies. Therefore, he suggested that the incidences of traits needed to be converted to mean liabilities where it is assumed that the liabilities are normally distributed. Then the, “unit of liability is its standard deviation, σ” (Falconer, 1989:302). Figure 3.1 illustrates an example trait liability in two populations. In Population A the trait incidence is small, 3%. In Population B the trait incidence is much larger at 33%. The liability for the trait in each of these populations is 1.88 and 0.44 respectively. The difference in liability of trait expression between these populations is 1.22 standard deviations. It is these liabilities, rather than the frequency of expression, that is used to calculate biological affinity between populations. It should be noted that not all measures of biological distance use the Threshold Model (for example Smith’s Mean Measure of Divergence and Balakrishman and Sanghvi’s B^2 discussed later in this chapter).

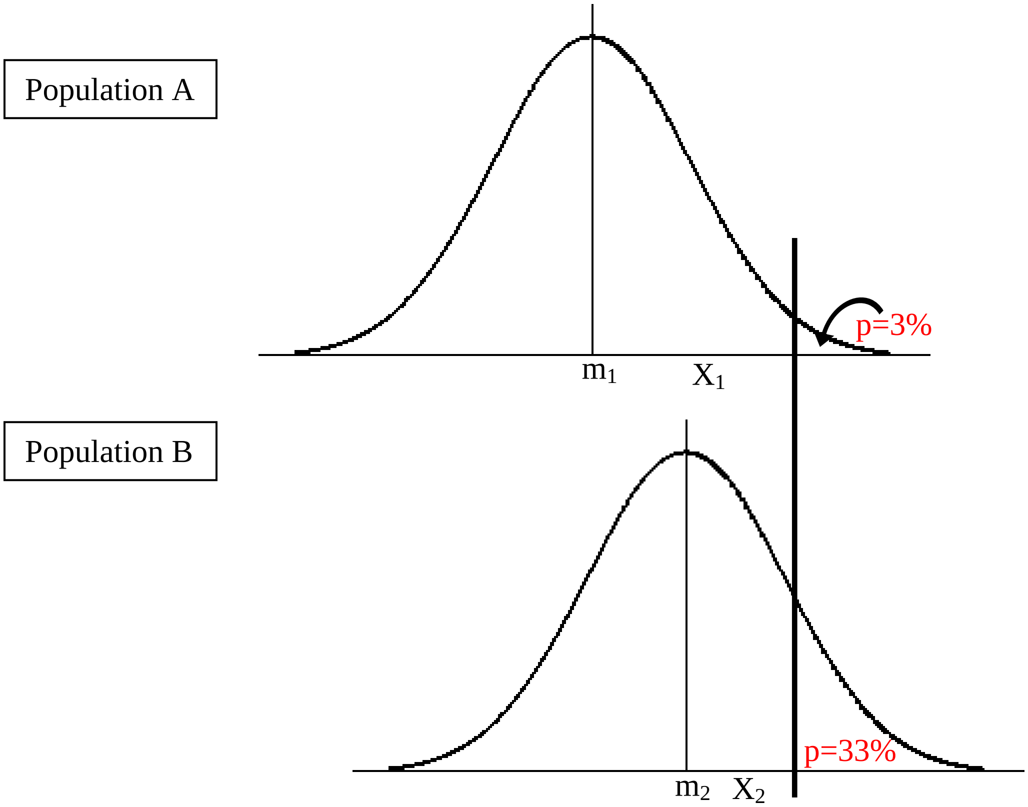


Figure 3.1. Threshold Model for two populations (after Falconer, 1989:301).

3.3 Heritability of Non-Metric Traits

As alluded to earlier in this chapter, for biological distance studies based on non-metric skeletal traits to be valid there must be a significant genetic coordinate to the expression of these traits. Heritability (h^2) is the additive genetic variance divided by the phenotypic variance,

$$h^2 = \frac{\sigma_G^2}{\sigma_P^2}, \qquad 3.3$$

which essentially quantifies the genetic contribution to the expression of the trait. This is heritability in the *narrow sense* as it addresses the expression of a phenotype as determined by the genes transmitted from the parents (Falconer, 1989). Few studies have addressed the heritability of cranial non-metric traits due to a lack of suitably pedigreed collections and the difficulty in manipulating categorical data. However, there have been studies that do specifically address the heritability of these traits (Berry and Berry, 1967; Berry, 1968; Berry, 1975; Cheverud and Buikstra, 1981a; Sjøvold, 1984; Carson, 2006). Due to the lack of suitable samples only two of these have addressed heritability in human samples (Sjøvold, 1984; Carson, 2006). Sjøvold (1984) analyzed a pedigreed skeletal sample from Hallstatt, Austria and found h^2 values ranging from 0.0 to 0.954 for the cranial non-metric traits he considered. He calculated heritability of non-metric traits by using a dichotomous scoring system (0=absent, 1=present) and regressing offspring on parents (Sjøvold, 1984). More recently, Carson (2006) examined the same population used by Sjøvold. She calculated heritabilities using a maximum-likelihood variance coordinates analysis on traits scored both dichotomously and using a multilevel system (Carson, 2006). Using this approach she found uniformly low h^2 values for the 36 traits she considered. Of note, Carson (2006) also found that h^2 values were higher when the dichotomous scoring system was used. Clearly, the findings of Sjøvold (1984) and Carson (2006) are problematic for this study. What remains unresolved is the question of the incongruence of low heritabilities for cranial non-metric traits, yet their significant correlation with genetic data in the context of biological distance studies. In a recent study of the heritability of human cranial dimensions considering the cranium in sub-divided regions Martínez-Abadías et al. (2009) found that their **G** and **P** matrices were correlated. Many biological distance studies undertaken since Cheverud’s (1988) work assumed that genotypic and phenotypic distance matrices are both similar and proportional. However, Martínez-Abadías and colleague’s (2009) analysis suggested that genotypic and phenotypic correlation matrices are similar and probably reflect the same genetic patterns, however they are neither identical nor necessarily proportional. It is useful now to turn to a discussion of how biological affinity between groups, or biological distance, is calculated using skeletally derived data.

3.4 Measures of Biological Distance

3.4.1 C.A.B. Smith's Mean Measure of Divergence (MMD)

The MMD is a distance measure that converts non-metric trait frequencies to a numerical value such that the more similar two groups are, the smaller the number is. Smith's formula was developed for Grewal (1962) to explore the biological divergence (due to accumulated mutations) that developed across generations of laboratory mice using skeletal non-metric traits. To this end, MMD can also be used to estimate the biological distance between two or more groups. Smith's MMD as described by Grewal (1962), and later clarified by Harris and Sjøvold (2004), is:

$$MMD = \frac{{}_{k=1}^{r}(\theta_{ik}-\theta_{jk})^2}{r} - \frac{1}{n_i} + \frac{1}{n_j} \ , \tag{3.4}$$

where the difference between samples *i* and *j* for the arcsine-transformed frequencies of trait *k* is calculated and squared so that positive and negative values do not cancel one another. The sum of the differences is divided by the number of traits used in the equation, *r*, to generate the average difference between samples *i* and *j*. A correction term,$(\frac{1}{n_i} + \frac{1}{n_j})$, is then subtracted from the average to correct for sampling fluctuations. Since Grewal (1962) the MMD has been used extensively with osteological and dental traits to explore biological relationships within and among populations (Berry and Berry, 1972; Berry, 1974; Buikstra, 1976; Donlon, 2000; Edgar, 2007; Greene, 1982; Hallgrímsson et al., 2004; Hanihara et al., 2003; Irish and Turner, 1990; Irish, 1997, 1998a, 1998b, 2010; Ossenberg et al., 2006; Sutter and Verano, 2007). Through its extensive use some limitations have been identified and improved upon (Harris and Sjøvold, 2004). The corrected formula, published by Harris and Sjøvold (2004) is:

$$\text{MMD} = \frac{{}_{k=1}^{r}\,(\theta_{ik} - \theta_{jk})^2 - \overbrace{(\frac{1}{n_{ik}+\frac{1}{2}} + \frac{1}{n_{jk}+\frac{1}{2}})}}{r} \qquad 3.5$$

The correction term used in Formula 3.4 results in an overestimate of the true variance between samples as noted by Green and Suchey (1976) and Green et al. (1979). Essentially very high (>0.95) and very low (<0.10) trait frequencies affected the variance. A new correction term, highlighted with a bracket in Formula 3.5, has been suggested following Freeman and Tukey (1950). In Equation 3.4 it is assumed that all samples are complete and sample sizes are identical. Since this is rarely the case, the correction formula needed to be more robust to unequal sample sizes and missing data.

The statistical significance of MMD values can be determined by comparing it to its standard deviation. The standard deviation is calculated:

$$\text{SD(MMD)} = \overline{\frac{2 \quad \frac{1}{n_{ik}+\frac{1}{2}} + \frac{1}{n_{jk}+\frac{1}{2}} \;{}^{2}}{r^2}} \qquad 3.6$$

If the value is greater than two times its standard deviation the null hypothesis (the samples are identical) is rejected at the p = 0.025 level (Harris and Sjøvold, 2004). It is important to note that failure to reject the null hypothesis could also be due to small sample sizes which would also inflate the variance.

Using the corrected derivation of Smith's MMD, recent studies have generated biological distance matrices that correlate with Mahalanobis D^2 matrices (Irish, 2010; Nikita et al., 2012;

Schillaci et al., 2009). However, even with an improved correction term limitations still exist with the MMD. Because the MMD is not a Euclidean distance it does not account for trait correlation. Since many cranial non-metric traits are significantly correlated (Cheverud, 1979), Smith's MMD is not appropriate for this study.

3.4.2 Balakrishnan and Sanghvi's B^2

Balakrishnan and Sanghvi's B^2 (1968; Sanghvi and Balakrishnan, 1972) was one of the first Euclidean distance measure used to deal with categorical data such as cranial non-metric traits. Distances are calculated by figuring variance with a dispersion matrix:

$$B^2 = \sum_{i=1}^{r} \frac{(p_{1i}-p_{2i})^2}{V_{\iota}}, \tag{3.7}$$

where p_{li} is the i^{th} trait in the l^{th} sample and V_{ι} is the weighted variance-covariance (dispersion) matrix (Balakrishnan and Sanghvi 1968). The weighted variance-covariance matrix takes into account correlation of traits over the distance matrix that the MMD does not. Sanghvi and Balakrishnan (1972) did show that the B^2 matrices correlated with those derived using the MMD.

3.4.3 Mahalanobis D^2 Distance Matrix

The Euclidean distance measure used in most recent studies is the Mahalanobis D^2. The generalized D^2 statistic was first published by Mahalanobis (1936) as a measure of divergence between two populations based on continuous data. The Mahalanobis D^2 was extended to use with non-metric traits by Konigsberg (1990; see also Williams-Blangero and Blangero, 1989). Categorical data, such as cranial non-metric traits, can be analyzed for biological distance by using a tetrachoric correlation matrix rather than the dispersion matrix utilized in Balakrishnan and Sanghvi's B^2. The tetrachoric correlation coefficient is appropriate when traits are scored dichotomously, but have an underlying continuous distribution. The tetrachoric correlation is the statistical measure of variance in this study since cranial non-metric trait data is categorical. The Threshold Model assumes that all trait liabilities have a variance of 1.0, and therefore a variance-covariance matrix cannot be calculate These correlations are calculated within each group, then pooled using sample size to find the weighted average correlation (Konigsberg, 1990:60). The formula used by Konigsberg (1990), and in this study is:

$$D_{ij}^{2} = \; z_i - \; z_j \;' \boldsymbol{T}^{-1} \; z_i - \; z_j \; , \tag{3.8}$$

where z_i is the z-score for a trait in population i, and z_i is the z-score for the same trait in population j. $\mathbf{T}^{-1}$ is the inverse of the pooled within-group tetrachoric correlation matrix between all traits. The resulting distances are conservative in that they represent the minimum possible distance between groups (Blangero and Williams-Blangero, 1989). Like all distance measures described in this chapter the Mahalanobis D^2 is sensitive to small sample sizes in that sample size affects calculation of the tetrachoric correlations (Konigsberg et al., 1993). A benefit of the Mahalanobis D^2 distance is that the significance of the individual distances can be assessed with an F-test (Droessler, 1981; Konigsberg et al., 1993).

3.5 Wright's F_{ST}

The F-statistic, or inbreeding coefficient, was described by Sewall Wright (1951). F_{ST} is defined as the average inbreeding of a subpopulation relative to the whole population (Falconer 1989). In biological distance studies F_{ST} is a measure of the biological differentiation of subpopulations. In other words a relatively small F_{ST} value for subpopulations within a study indicates that those subpopulations were experiencing significant gene flow thus increasing heterogeneity within groups and homogeneity between groups.

F_{ST} as derived from phenotypic data is an estimation of the real, or genetic, F_{ST}. If it is assumed that phenotypic and genetic variance-covariance matrices are proportional and the effective population sizes (N_e) are equal across groups then the minimum F_{ST} (phenotypic) is proportional to the real F_{ST} (genetic) if the trait heritabilities are moderate to high (Konigsberg and Ousley 1995). Relethford et al. (1997) provide a method for calculating F_{ST} based on phenotypic data. The C matrix is first calculated from the distance matrix:

$$\mathrm{C} = - \;\; I - lw' \;\; D^2(I - lw')/2, \qquad 3.9$$

where *w* is equal to a column vector of the proportion of N_e, *I* is the identity matrix with the same dimensions as the distance matrix, and *l* is a vector of 1's equal in length to the number of subpopulations. Once the C matrix has been derived minimum F_{ST} can be calculated:

$$F_{ST} = \frac{w' diag[C]}{2t + w' diag[C]}, \qquad 3.10$$

where *t* is the number of traits. If the effective population size is assumed to be equal for all samples in the study then *w* is a column vector with each element equal to one over the number of samples. Under these assumptions F_{ST} estimates provide a measure of within-group heterogeneity that biological distance does not explicitly offer. This strengthens interpretations of population histories by giving quantitative estimates to the evolutionary processes of gene flow and genetic drift.

Caution is warranted concerning the calculation of F_{ST} with respect to disparate and small sample sizes. In this case the effects of genetic drift (isolation and founder's effect) can influence the F_{ST} value making its interpretation questionable (Jorde, 1980). It is also noted that recent studies have identified effects of natural selection that significantly alter patterns of between-population variation (Roseman 2004; Roseman and Weaver 2004). Given that the samples for this study are restricted to the Andes, the effects of environment on the expression of non-metric traits should be negligible.

3.6 Model-Free vs. Model-Bound Methodology

Relethford and Lees (1982) identified two basic approaches to using quantitative traits in understanding population histories; model-free and model-bound. Model-bound approaches include the estimation of some population parameter such as the proportion of admixture, or the amount of genetic similarity between individuals (kinship coefficient). Because these are direct estimates of rates or proportions that inform on population structure more assumptions must be made about the populations that samples are derived from (Relethford and Lees, 1982). In studies of archaeological populations like this one, many of the assumptions necessary for model-bound methods cannot be made. In particular model-bound methods treat nongenetic influences on population structure as inconsequential because they either do not exist, or are randomly distributed across populations (Relethford and Lees, 1982). In light of these assumptions it is better in this study to use model-free methods.

The benefit of using model-free methods is that they assess relative degree and pattern of among-group variation to understand general relationships between populations, “but not their exact form” (Relethford and Lees, 1982:116). The analysis to detect patterns is performed “free” of any genetic model, but from these patterns the processes of gene flow and genetic drift may be detected (Jantz, 1973). Relethford and Lees (1982) identify two classes of model-free studies, differentiation and comparative. Differentiation studies, like discriminant analysis, identify the extent of variation among groups, but not the pattern. Comparative studies attempt to determine the degree of correlation between two or more distance (similarity) matrices. The goal of these analyses is then to compare the pattern of among-group variation with other biological, cultural, or historical variables (Relethford and Lees, 1982:121). Studies of biological distance, including this one, fall into the class of model-free comparative studies. Here the pattern of among-group similarities is compared to biological, geographical, and cultural variables to understand population histories.

Chapter IV

Study Samples

4.1 Sampling strategy

The sampling strategy for this study is partially based on Sinopoli's (2001) call to explore variation in imperial organization by collecting data from a number of sites representing an extensive geographical range. To recognize changes in degree and patterning of gene flow associated with Wari imperialism the sampling strategy was to have material derived from the MH (during the Wari empire) and LIP (post collapse). The samples also represent most of the skeletal material that is currently available within the known sphere of Wari influence during the MH. Ideally these samples would encompass both the MH and LIP within a site, but presently this is not feasible so samples were collected by region.

There were a total of 450 crania scored. These samples were compared across and within geographical regions to explore patterns in gene flow and genetic isolation consequent to changing relationships during and after the Wari cultural horizon. The samples were broken down into subsets by geographical regions and chronology (Table 4.1). Highland samples are those where the corresponding archaeological site is located above 2,000 meters above sea level (masl). The highland samples include those in the Wari heartland (Conchopata and Ayacucho), north-central highlands (Hualcayan and Marcajirca), and the south-central highlands (Turpo Qatun Rumi, Mina Puka Machay, Sonhuayo, Pucullu, and Ranra Cancha). Mid-valley sites are defined in this study as those that are in river valleys below 2,000 masl, but not within 25 km of the coast. These include the Beringa site and a group of sites in the Nazca River valley (Cahuachi, Cantayo, Aja, and Majoro Chico). There is limited archaeological evidence of Wari presence on the coast except for areas around the present day city of Lima, Peru. The Ancón site is located directly on the coast to the north of Lima. The MH and LIP coordinates of the Ancón site make up the entirety of the coastal samples in this study.

Table 4.1. Geographic region and chronology of study samples.

Region	Sub-Region	Site	n	Radiocarbon 2-sigma range (AD)◊	Chronology‡	Citation
Highlands	Wari Heartland	Conchopata	22	685 - 900	MH	Ketterman (2002)
				690 - 1000	MH	
		Ayacucho (Huari)	17	Late Intermediate Period†	LIP	Ochatoma (pers.comm. 2009)
	North-Central Highlands	Hualcayan	24	Middle Horizon†	MH	Bria (2012)
		Marcajirca	35	1250-1430	LIP	Ibarra Asencios (2003)
				1028-1208	LIP	
				1208-1408	LIP	
				1548-1748*	LH	
	South-Central Highlands	Turpo Qatun Rumi	12	890-995	MH	Kurin (2012)
		Sonhuayo	65	1155-1250	LIP	
				1155-1230	LIP	
				1205-1290	LIP	
		Mina Puka Machay	26	1160-1260	LIP	
		Pucullu	18	1170-1270	LIP	
		Ranra Cancha	33	1160-1260	LIP	
Mid-Valley	Southern Mid-Valley	Beringa	10	540-762	MH	Tung (2007)
				622-767	MH	
				640-744	MH	
				651-771	MH	
				689-879	MH	
		Beringa	9	1024-1187	LIP	Tung (2007)
				1044-1278	LIP	
	Nazca River Valley	Aja	9	Middle Horizon†	MH	Kroeber et al. (1998)
		Cahuachi	18	Middle Horizon†	MH	
		Cantayo	12	Middle Horizon†	MH	
		Majoro Chico	23	Middle Horizon†	MH	
Coastal	Central Coast	Ancón	62	Middle Horizon†	MH	Menzel (1977)
		Ancón	55	Middle Horizon to Late Intermediate Period†	LIP	Menzel (1977)

◊ The general time period is given when a radiocarbon date is not available
‡ MH – Middle Horizon, LIP – Late Intermediate Period, LH-Late Horizon
† Relative date based on ceramic style and other artifacts
* This date was obtained from an intrusive burial.

4.2 Study samples

4.2.1 Wari Heartland (Conchopata and Huari)

Conchopata (CON_MH)

Conchopata, located 2685 masl, was a Wari administrative site during the MH that has been extensively excavated (Ochatoma, 2007) (Figures 4.1 and 4.2). The Conchopata skeletal collection was selected for this study because it represents a population that was clearly under Wari imperial control and is located in close proximity to the capital of Huari. This sample should be an accurate reflection of the genetic structure of the populations living in and around the capital during the height of the Wari empire.

Figure 4.1. Location of sites in the Wari Heartland. (note “Cachi” refers to Sonhuayo and Mina Puka Machay)

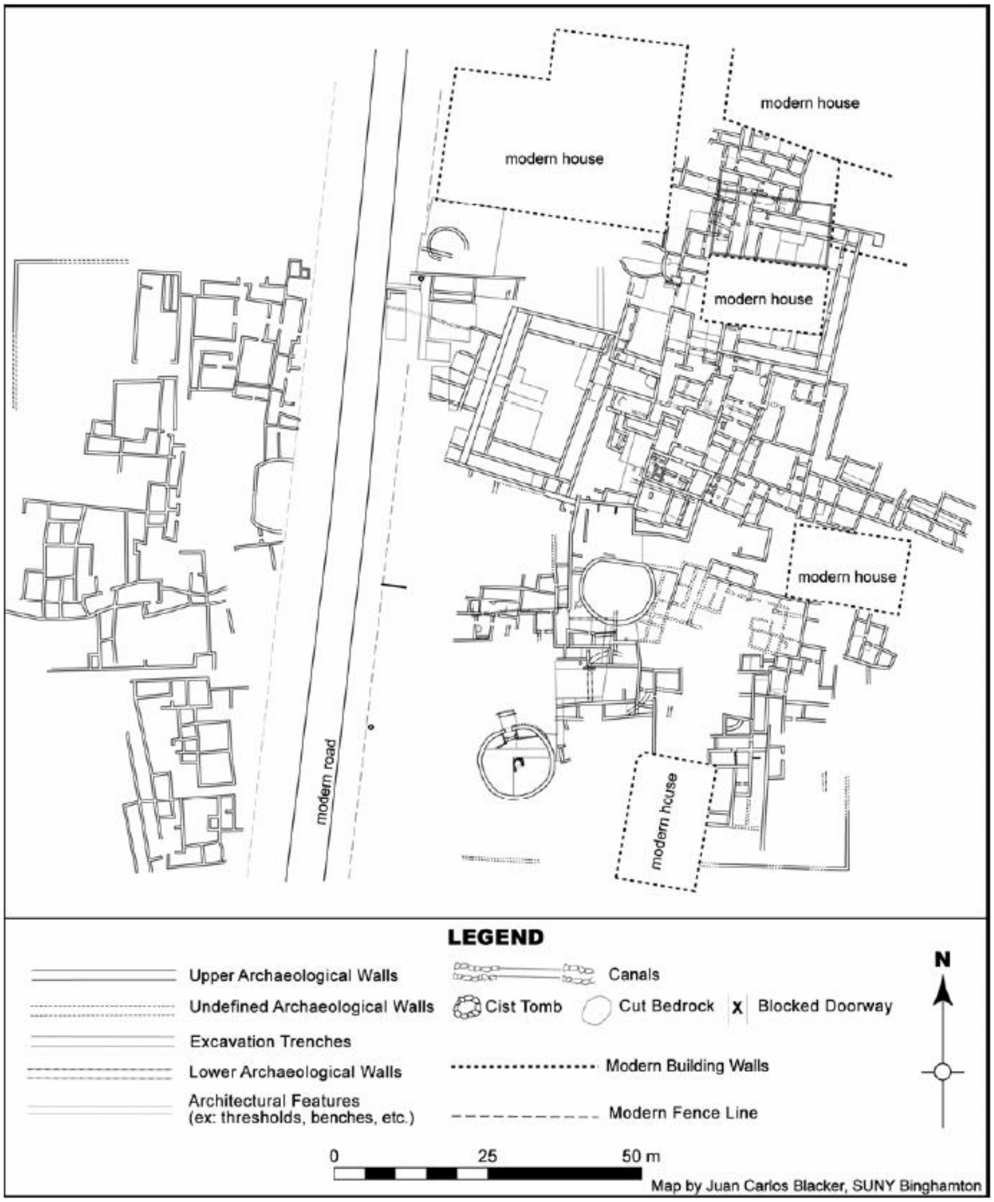


Figure 4.2. Plan map of the Conchopata site from Tung (2003:34). Sample used in this study was recovered from the architecture on the east side of the modern road.

The Conchopata sample was also included in the study due to the availability of extensive background information. In her dissertation Tiffiny Tung (2003) described the demographic and health profiles of the Conchopata population. The majority of the skeletal sample from Conchopata dates to the MH (AD 685-1000) (Ketterman, 2002) with a Minimum Number of

Individuals (MNI) of 242, of which 124 are adults (Tung, 2003). It is important to consider that the sex ratio for the Conchopata is significantly deviated from 50/50 with females making up 62% of the individuals that could be accurately sexed (Tung, 2003). Though the MNI for the entire skeletal is large, the number of individuals included in this analysis is significantly smaller (n=22). This is mostly due to preservation issues. Similar to the larger sample, approximately 54% of the individuals included in this sample were female.

Since Tung's (2003; see also Tung, 2007, 2008b) initial work on the Conchopata remains, extensive Sr isotopic analyses (Knudson and Tung, 2007; Tung and Knudson, 2008, 2010) and ancient DNA (aDNA) analysis (Kemp et al., 2009) have been conducted. The results of these analyses provide a robust framework for the interpretation of the biological distance results from this study. Data from the Conchopata collection were collected at the Universidad Nacional San Cristóbal de Huamanga in Ayacucho, Peru.

Ayacucho (AYA_LIP)

The sample designated Ayacucho is from a collection of remains housed at the Universidad Nacional San Cristóbal de Huamanga in Ayacucho, Peru. The sample comprised of crania representing post-collapse (LIP) populations living in and around (n=17) the site of Huari located approximately eight kilometers north of Ayacucho at about 2700 masl (Figure 4.1). The crania from Huari are from the Vegachoyoc Moqo and Monqachayoq sectors excavated by Enrique Bragayrac, and Francisco Solano respectively (Figures 4.3 and 4.4). Because attention has been focused on MH Wari groups, not much skeletal material dating to the LIP is available for study. This is compounded by the fact that Ayacucho has been the center of modern warfare and violence due to the Shining Path (Sendero Luminoso) movement during the 1980's through the 1990's. During this time of violence many archaeological assemblages were lost including skeletal collections from Huari. While there is skeletal material available from the Ayacucho basin dating to the LIP, this sample represents most of the nearly complete crania with provenience information.

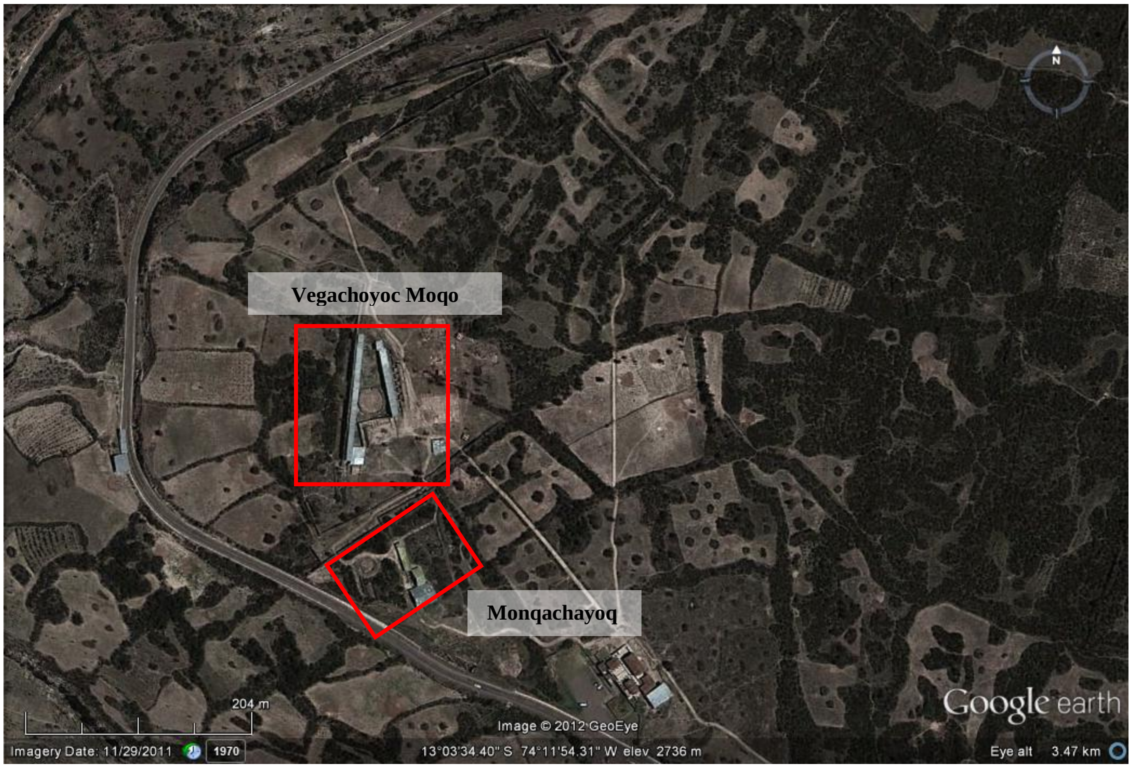


Figure 4.3. The eastern side of Huari.

Figure 4.4. Wall at eastern extent of the Vegachoyoc Moqo sector where remains were recovered.

4.2.2 North-central Highlands (Hualcayan and Marcajirca)

Hualcayan (HUA_MH)

Hualcayan is located on the western side of the Cordillera Blanca in the northern extent of the Callejón de Huaylas (Figure 4.5). The cemetery (Sector C) is situated on the mountainside above and to the south of the ritual (Sector A) and habitation (Sector B) zones (Figure 4.6). The crania included in the study were recovered during the 2011 field season from two adjacent tomb contexts. The machay tombs, designated Operation 3 and Operation 8, are located on the west face of a large terraced mountainside (Figures 4.6 and 4.7). Unfortunately, they are situated along a heavily traveled footpath and have been extensively looted. Despite the highly disturbed contexts, much of the material recovered was in an excellent state of preservation.

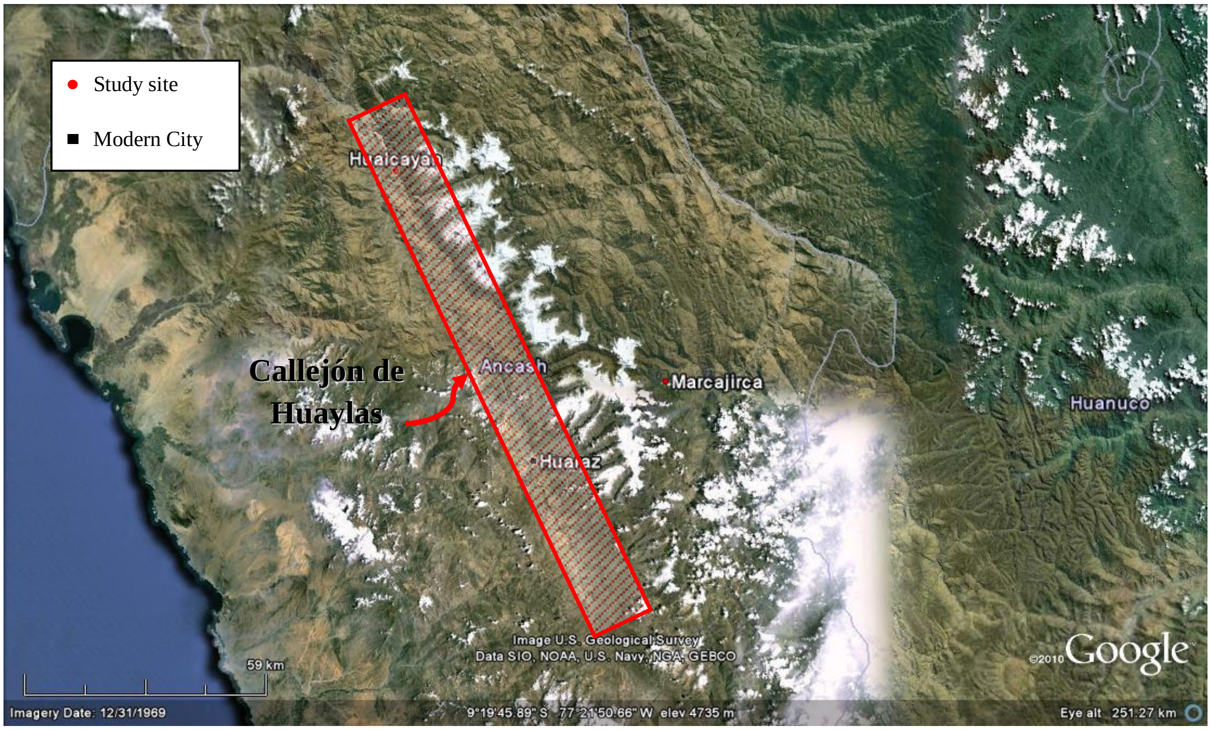


Figure 4.5. Sites in the North-central Highlands group.

The remains from Hualcayan have been dated to the MH based on artifacts associated with them (Pink and Bria, 2012; Bria, 2012; Witt et al., 2012). Many sherds of the local MH style were recovered during excavations. Additionally, Wari-style sherds were found in context with the crania comprising this sample (Figure 4.8). Sherds consistent with Early Horizon, EIP, and LIP styles were also recovered, but in very small quantities. This could indicate that they date much earlier than the MH. However given that Sectors A and B were occupied through these time periods, it is reasonable that these materials could have been placed as heirlooms, or simply picked up around the site and placed in the tomb (Pink and Bria, 2012). As there are not radiocarbon dates available for the tombs yet, the artifact assemblage supports a MH chronology. This sample is relatively small (n=24) it is one of the very few skeletal collections available for study from the north-central highlands.

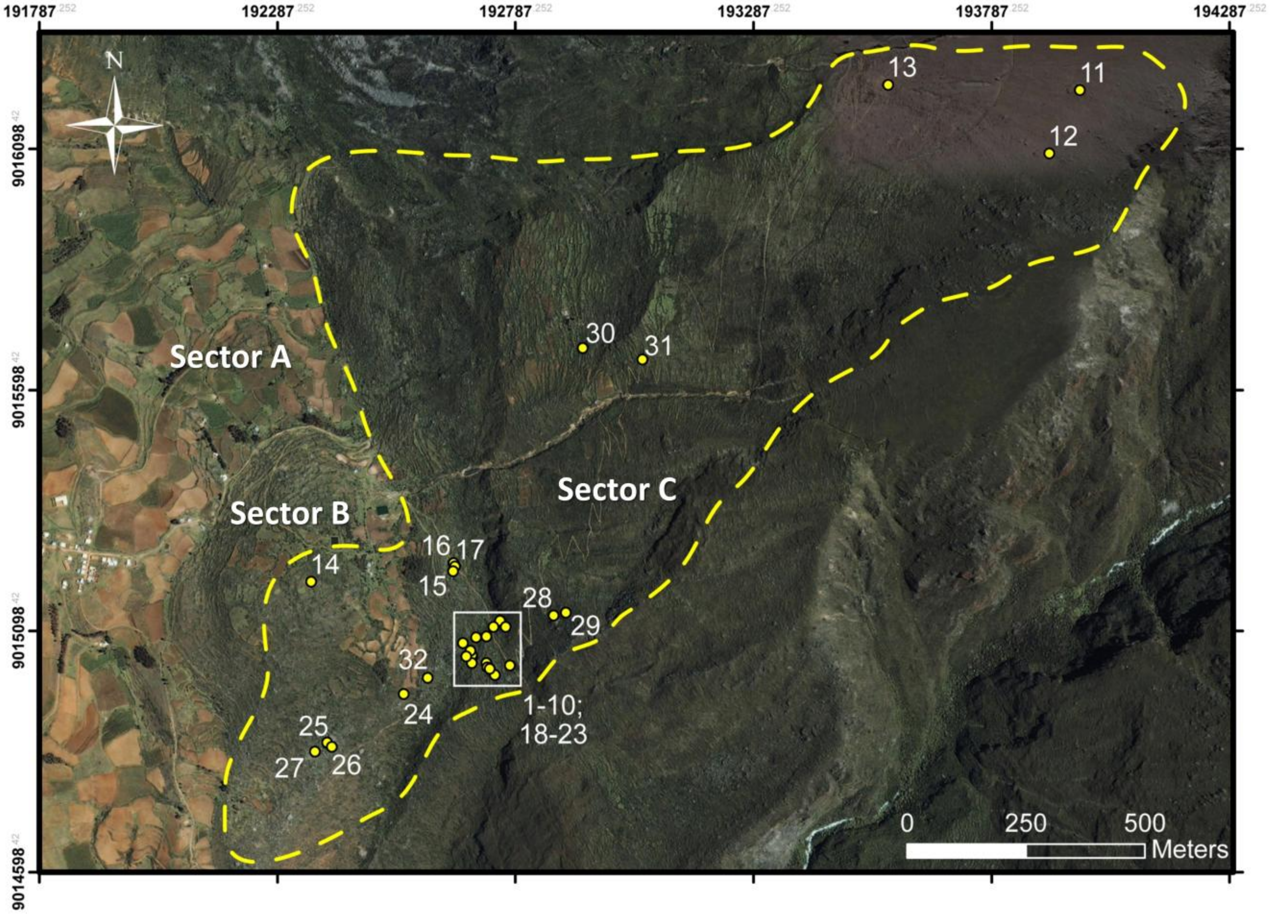


Figure 4.6. Map of tomb locations (highlighted in yellow) at Hualcayan, Sector C

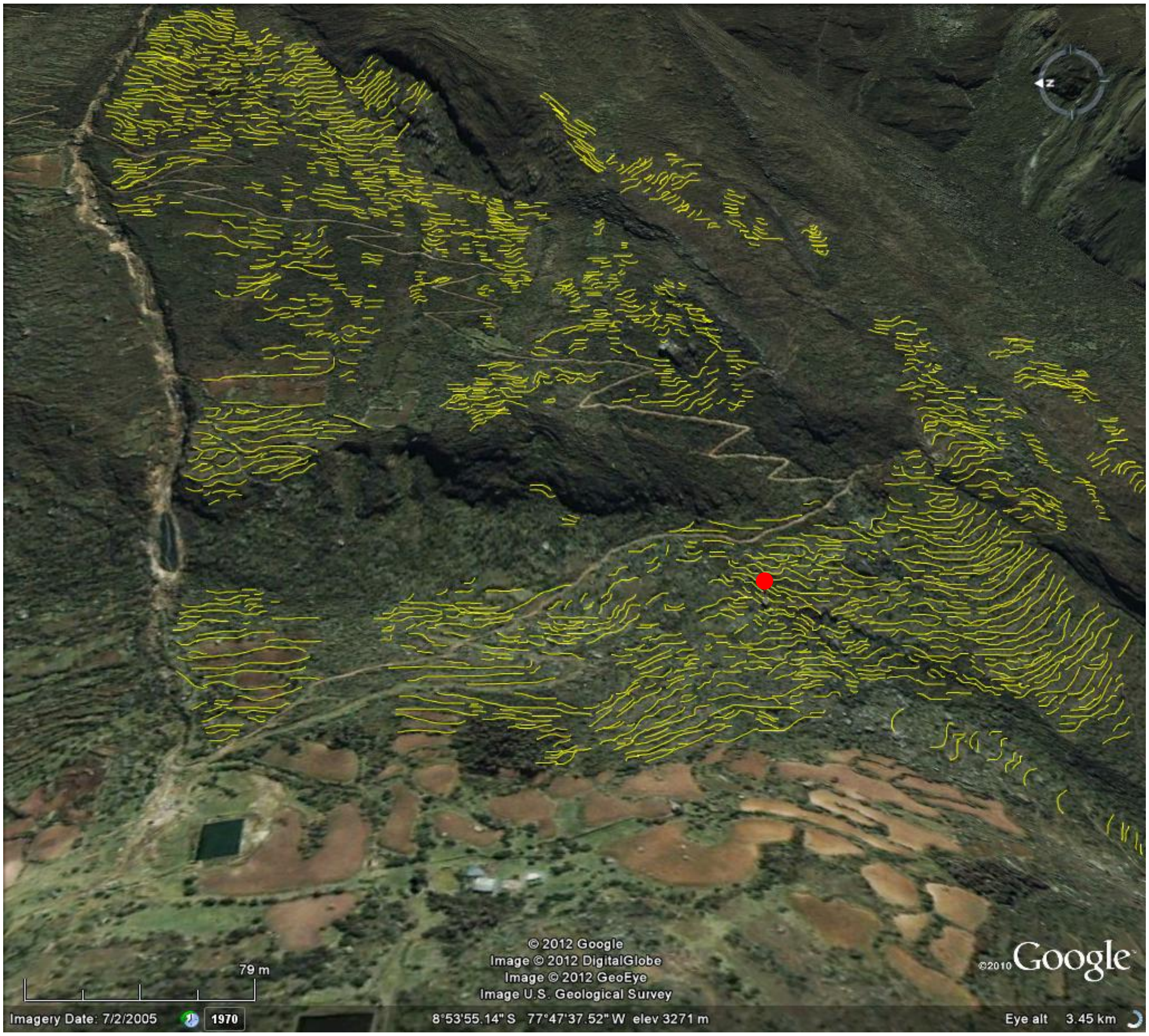


Figure 4.7. View to the east of sector C . Terracing is highlighted in yellow and Operations 3 and 8 are indicated with a red dot.

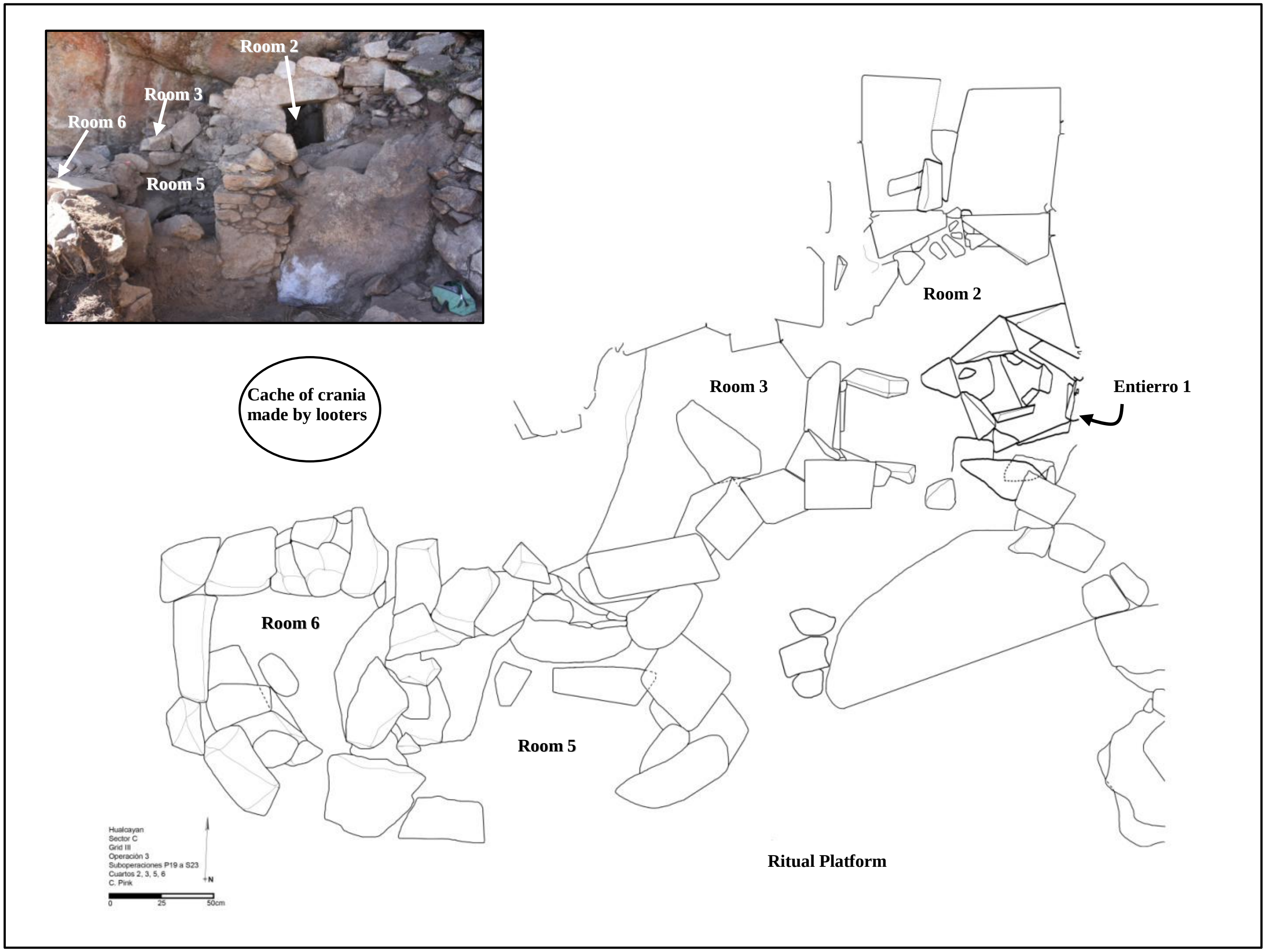


Figure 4.8. Plan map of Operation 3 with photograph of the southern face (inset).

Figure 4.9. Wari-style sherds from Operation 3 at Hualcayan (top) and a vessel from Huari with the same chevron design (bottom).

Marcajirca (MAR_LIP)

The Marcajirca site is located at 3,800 masl in the north-central highlands of Peru near the modern city of Huari with occupation dating to the LIP (AD 1000-1476) (Figure 4.5). The site is located on a high ridge-top in the Cordillera Blanca in the north-central highlands of Peru. Marcajirca is comprised of a sector of mostly of residential structures concentrated at the southern extent of the site, and mortuary structures (*chullpas* and *machays*) that increase in concentration to the north (Figures 4.9 and 4.10). No evidence of Wari presence has been reflected in the material record (Ibarra Asencios, 2003). A lack of Wari-style artifacts at Marcajirca is not unexpected since it post-dates the collapse of the empire. Consistent with many LIP sites, Marcajirca is positioned on a ridge-top that is more easily defended. The threat of violence to those who lived at Marcajirca is further confirmed by a high frequency of cranial trauma observed during data collection for this study (Figure 4.10). It is likely that populations living in this region during the MH would have resided at a lower elevation. However, even archaeological sites in the immediate vicinity of Marcajirca do not have strong evidence of contact with the Wari during the MH (Ibarra Asencios personal communication 2008).

This sample consists of 35 individuals with a 3:1 ratio of males to females. The mortuary contexts at Marcajirca are extremely disturbed and still frequently visited by the modern inhabitants of Huari. The unequal distribution of males and females in the Marcajirca sample may be due to funerary practices with respect to sex, or post-depositional disturbance. Though there has been significant alteration to the site, the Marcajirca sample is important to this study because it is one of the few skeletal collections from this region dating to the LIP available for study.

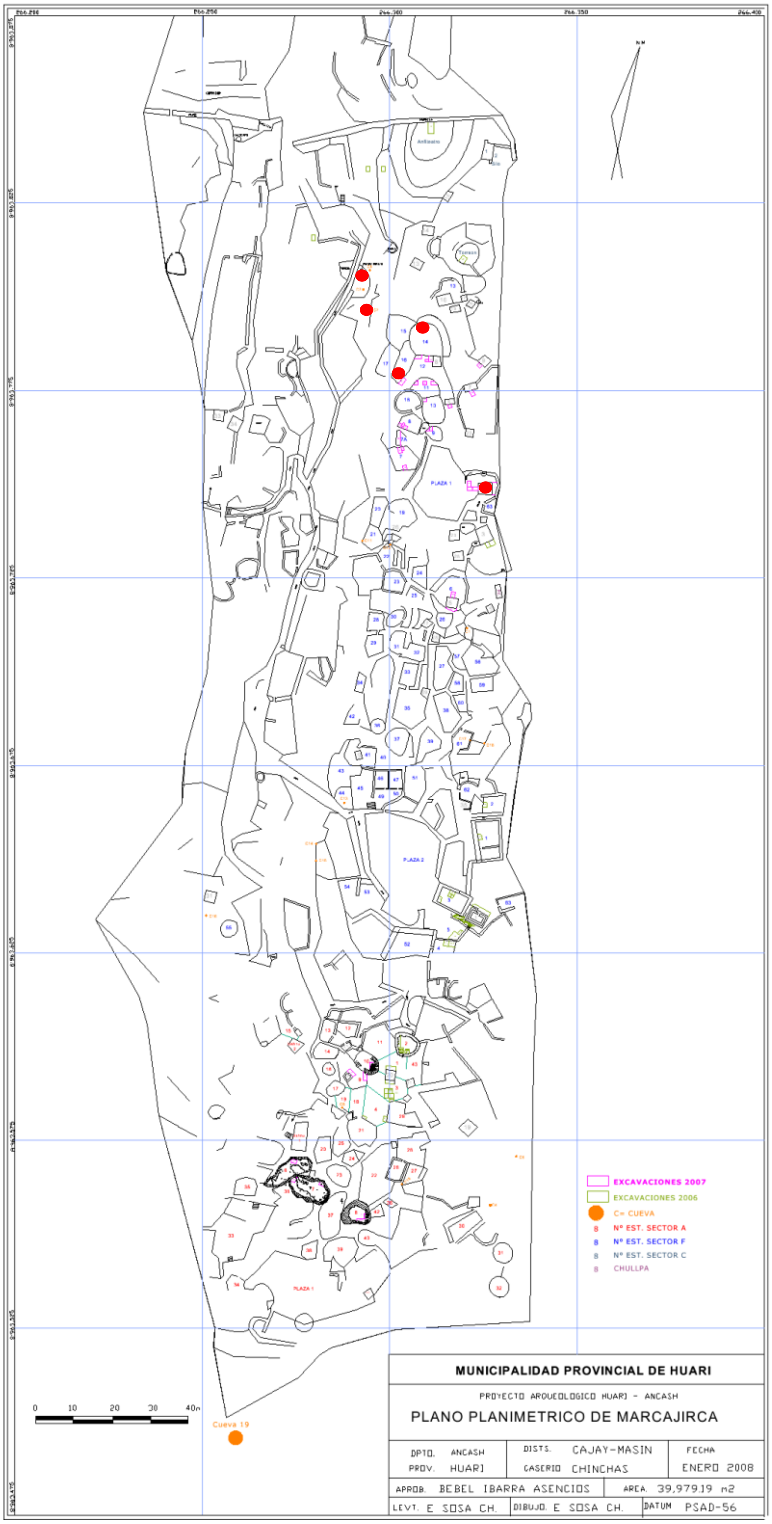


Figure 4.10. Plan map of the Marcajirca site with sample locations highlighted with red dots. Map courtesy of Bebel Ibarra Asencios (Pink and Ibarra Asencios, 2009).

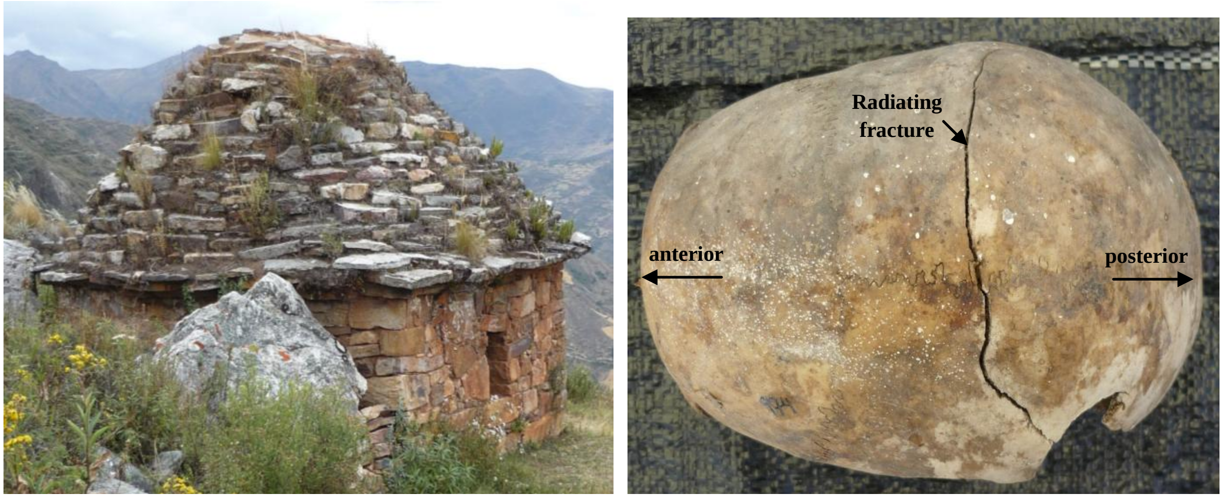


Figure 4.11. Representative chullpa tomb at Marcajirca (left), and superior view of a cranium with perimortem blunt force trauma from the study sample (right).

4.2.3 South-central Highlands (The Andahuaylas group)

The group of samples representative of the south-central Peruvian highlands are all located in close proximity to the modern city of Andahuaylas (Figure 4.12). These sites are connected by Wari roads and situated in the center of a triangle whose points are defined by Huari to the north, Jincamocco to the southwest, and Pikillacta to the east (Figures 4.12 and 4.13). Chronology, based on radiocarbon dates, and relative geographic proximity were used as the basis for grouping the samples.

Turpo Qatun Rumi (TUR_MH)

Turpo Qatun Rumi (Turpo) is represents the MH in this group. Radiocarbon dates situate squarely in the MH (Table 4.1). Furthermore, the ceramics recovered in context with the remains have clear Wari stylistic influence (Figure 4.14) (Kurin, 2012). During the MH the valley in which Turpo is located was used for intensive maize agriculture (Kurin, 2012). Given its location along a Wari road, Turpo may have functioned as an important weigh station; however, following the collapse of the Wari empire Turpo was abandoned (Kurin, 2012). Though there is a MNI of 40 at Turpo, only 12 crania were preserved well enough to be included in this study.

Figure 4.12. Location of the south-central highlands sample group (map courtesy Kurin, 2012). Study sites are highlighted in red.

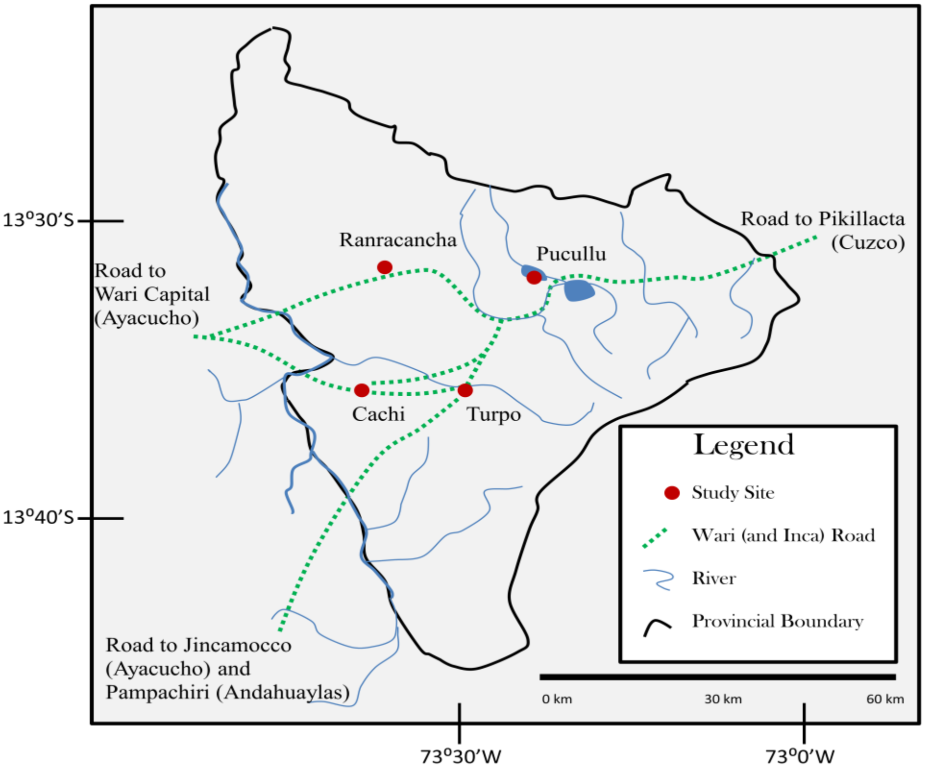


Figure 4.13. Map of south-central highlands sample group depicting Wari roads (map courtesy Kurin, 2012). Study sites are highlighted in red.

Figure 4.14. Wari-style sherd recovered in association with remains at Turpo (photograph courtesy of D. Kurin).

Mina Puka Machay (MPM_LIP)

Mina Puka Machay (MPM) is a small *machay* style tomb located in close proximity to a salt mine (Figures 4.15 and 4.16). Mina Puka Machay is relatively dated based on associations of LIP style ceramics with the remains. The sample from this tomb is relatively small (n=26), and is situated in close proximity to a salt mine which may have impacted mortuary practice. The salt from this mine was transported up to 100 km away; and even with increased violence in the region it seems that trade was maintained after the collapse of the Wari empire (Kurin, 2012).

Figure 4.15. The entrance to Mina Puka Machay before excavation. Note the piles of bones made by looters outside the cave entrance (Photograph courtesy of D. Kurin).

Sonhuayo (SON_MH)

Sonhuayo is also part of the group labeled “Cachi” in Figures 4.12 and 4.13 along with MPM. Unlike the other tomb contexts (MPM), Sonhuayo functioned as a hilltop fortress (Kurin, 2012) (Figure 4.16). Sonhuayo was excavated in eastern and western sectors and the burial contexts were identified as loci of human interments and offering assemblages (Kurin 2012). Radiocarbon dates place the Sonhuayo sample in the LIP (Table 4.1) (Kurin, 2012). This is consistent with the fortified nature of the settlement that is characteristic of LIP sites. Sonhuayo is also the largest of the south-central highlands sites (n=65).

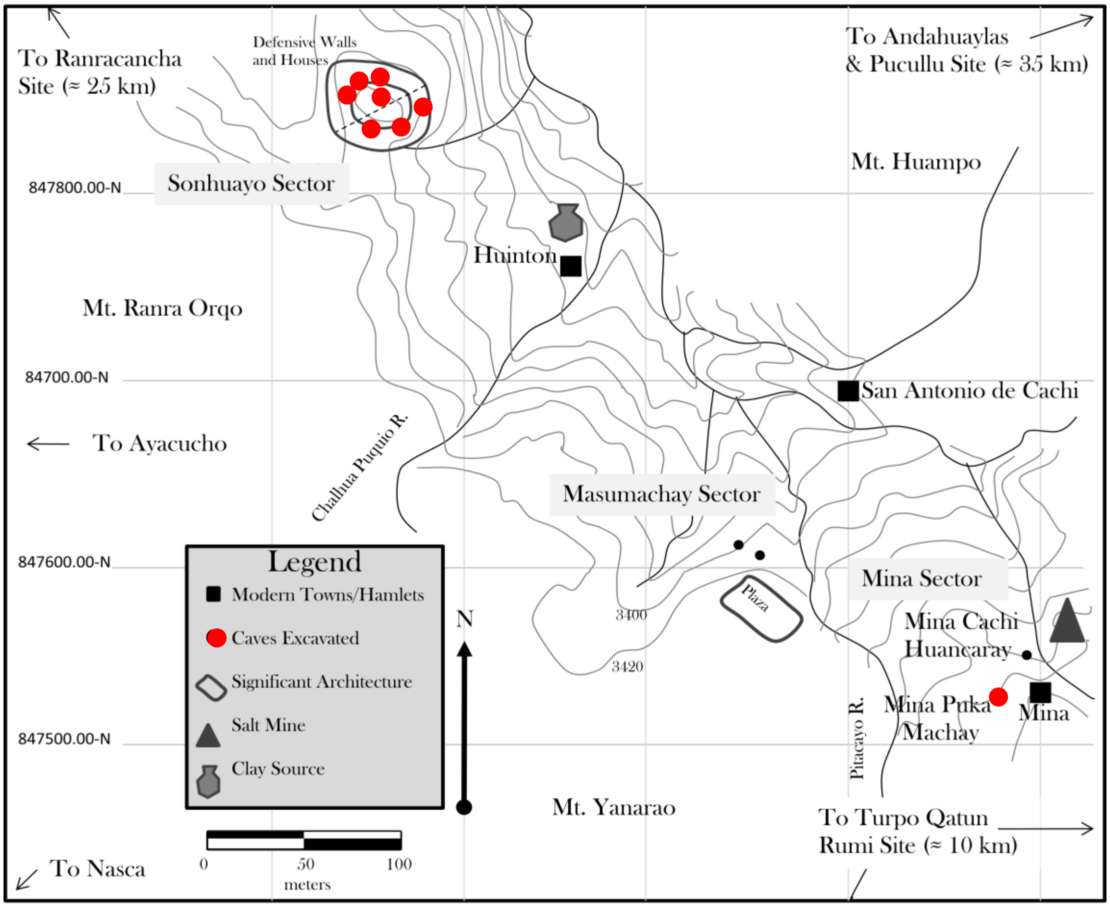


Figure 4.16. Map of sites denoted “Cachi” in Figures 4.12 and 4.13 (adapted from Kurin, 2012).

Pucullu (PUC_LIP) and Ranra Cancha (RCC_LIP)

Pucullu is an isolated mortuary context located on a steep hill. The lack of associated architecture makes it difficult to say much about the population that utilized this tomb other than that they probably practice agropastoralism much like other groups in the same valley (Kurin, 2012). Ranra Cancha is located about 25 km to the west of Pucullu along a Wari road (Figure 4.13). Both sites are dated to the LIP on the basis of Chanka style ceramics recovered in association with the human remains (Kurin, 2012). The habitation sites associated with Pucullu (n=18) and Ranra Cancha (n=33) have not been excavated so little can be said directly about the daily life of the living populations that these skeletal samples are derived from. However, there is ethnohistorical evidence about the social structure of people living at the sites that comprise the south-central highlands samples for this study.

The Encomienda de Andahuaylas written by Diego Maldonado in 1539 described the economy of the region of Andahuaylas as it pertained to the Spanish mostly concerning taxation. It also described some aspects of social organization stating that groups living at Pucullu and Ranra Cancha made up one half of a moiety system and the Cachi groups made up the other half (cited in Kurin (2012) [translated by Busto Duthurburu 1962; Lockhart 1977:221-223; Puente Brunke 1992]). In light of the ethnohistoric data, the south-central highland samples will be compared separate from the other Andean regional samples. Strontium isotope analysis has also been done on a sample of individuals from the sites in the south-central highlands region used for this study. Preliminary results suggest that the remains recovered from these sites represent the local population (Lofaro and Kurin, 2012; Lofaro personal communication June 2012). Though archaeological evidence about the habitation sites associated with the tombs the south-central highlands groups were recovered from is scant, there is a substantial amount of ethnohistorical and skeletal biological information to draw on in the interpretation of the biological distance results of this study.

4.2.4 Mid-valley Samples (Beringa)

Figure 4.17. Map of the mid-valley sites.

Figure 4.18. Map of Nazca River valley sites.

Beringa (BER_MH and BER_LIP)

Beringa is located in the upper Majes valley (Figures 4.17 and 4.19). Wari cultural material including ceramics and textiles were recovered from Beringa and radiocarbon dates place the occupation during the MH and into the early LIP (AD 595-1163) (Tung, 2007). The ceramics at Beringa do not imply Wari intrusion, but rather a strong influence from Ayacucho (Owen, 2007). The skeletal evidence also suggests that Wari migrants were unlikely at Beringa, as there are no crania modified in a form consistent with that found in Ayacucho (Tung and Owen, 2006: 447). As with Conchopata, the Beringa skeletal population has been analyzed for Sr isotopes (Knudson and Tung, 2011). Strontium isotope information coupled with demographic and health profiles for the collection (Tung, 2007), and a detailed analysis of the ceramics and other archaeological material also add strength to the interpretation of results from this study (Owen, 2007).

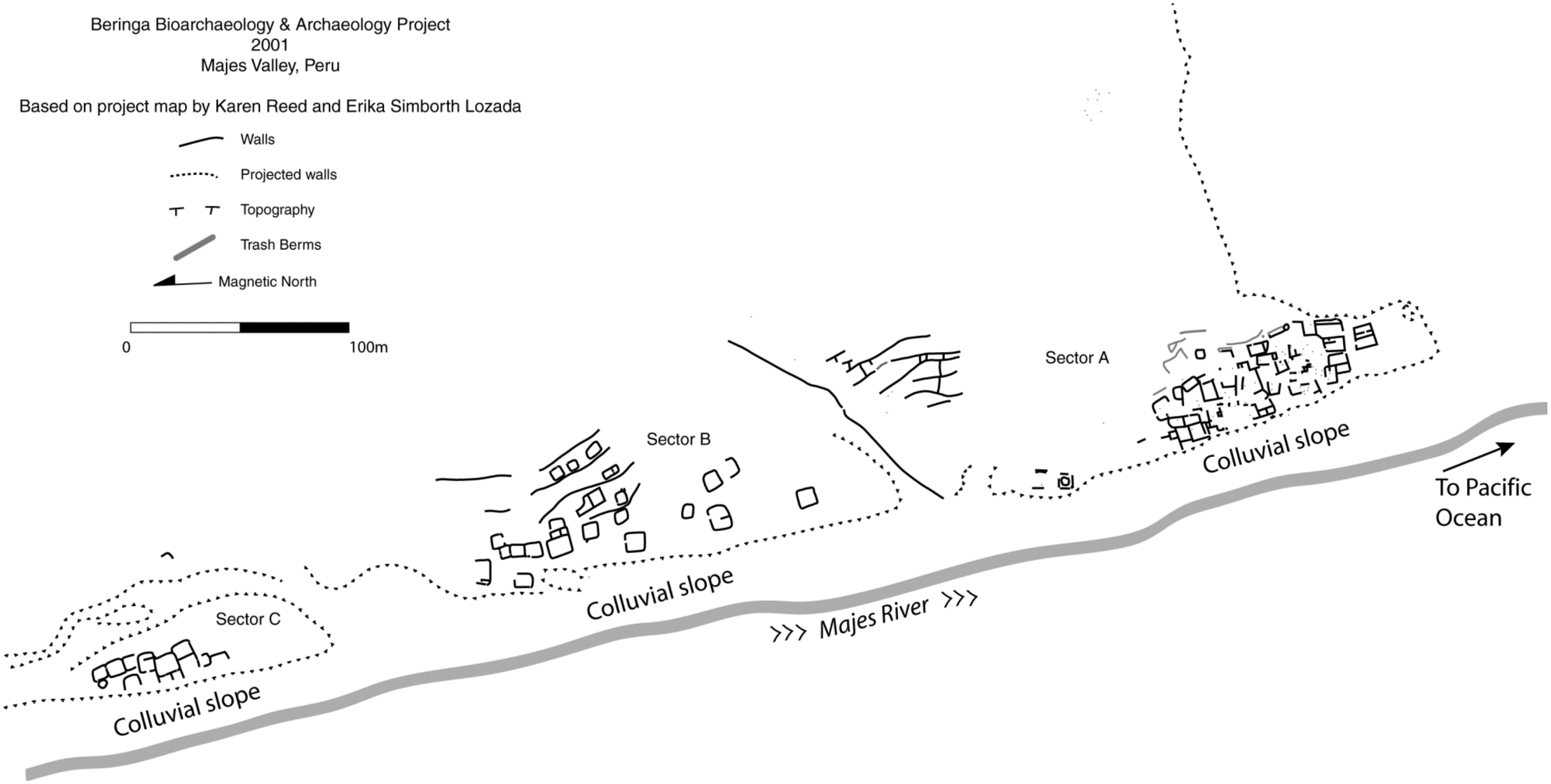


Figure 4.19. Site map for the Beringa site reproduced from Tung (2007) with author's permission. Samples for this study were recovered from Sector A.

4.2.5 Nazca[3] River Valley

There is archaeological evidence of contact between populations in the Nazca River drainage and those in the Ayacucho basin since long before the rise of the Wari Empire (Menzel, 1964; Schreiber, 1992; Conlee, 2010). The samples from this region are derived from the Kroeber Collection housed at the Chicago Field Museum of Natural History. Alfred Kroeber visited Peru during the 1925 Marshall Field Expedition. Based on his observations Kroeber decided to return to the Nazca River valley the next year to conduct excavations and further surface collections. The samples included in this study do not have any radiocarbon dates associated with them, but have been relatively dated based on architectural styles at the sites and associated artifacts. In many cases (Cahuachi, Aja, Cantayo, Majoro Chico) the site has architectural features that are early Nasca in style corresponding to the EIP, but the cemeteries continue to be used into the MH and LIP (Forgey, 2006). For example, Cahuachi is largely uninhabited by the MH however the cemetery continues to be used through the MH (Kroeber and Collier, 1998; Forgey, 2006). Though the chronology is established using relative methods, and sometimes poorly documented, the Nazca River Valley sites are important to include in this study due to the strong relationship that existed between these populations and those in the Ayacucho Basin mentioned above. Additionally, there are few large Nasca skeletal collections that are available for analysis. Given these limitations it is felt that the Nasca samples should be included despite some uncertainty in the chronology. Since the chronology is unclear in some cases, collapsing of samples was avoided when possible. Brief site descriptions and explanations of sample constitution follow below.

---

[3] Nazca is used in this study to refer to the geographical feature of the Nazca River. Nasca is the term used to refer to the culture.

Cahuachi (CAH_MH)

Cahuachi is the second largest known Nasca site (Forgey, 2006) and makes up a large proportion of the Nasca samples (n=18) (Figures 4.18 and 4.20). At its height during the EIP Cahuachi was used as a ceremonial center (Silverman, 1993; Strong, 1957). Though the site was largely unoccupied after the EIP, burials at the site span the EIP through the LIP (Kroeber and Collier, 1998). Burials from the later periods (MH and LIP) were generally located at the base of mounds or in large open areas and dated based on mortuary offerings (Kroeber and Collier, 1998; Forgey, 2006). The Cahuachi sub-sample is comprised only of crania that were recovered at that site.

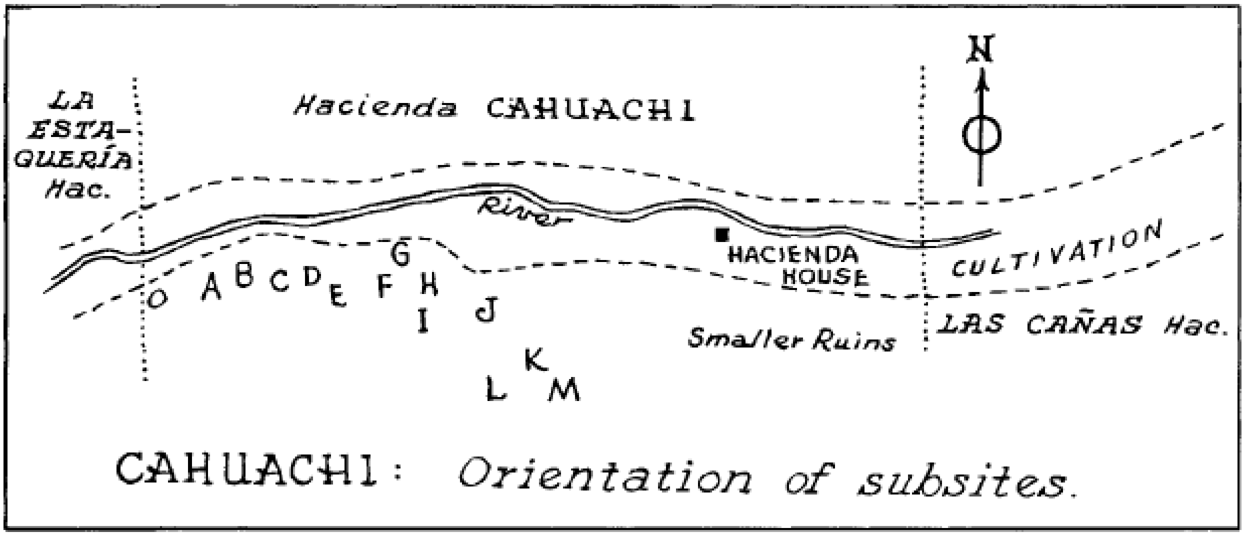


Figure 4.20. Map of the Cahuachi site (reproduced from Williams et al., 2001).

Cantayo (CAN_MH)

Cantayo covers an area of approximately 4 km on the sides of the Nazca River valley just east of the confluence with the Aja River (Forgey, 2006). Kroeber and Julio Tello, who joined him after the Marshall Expedition, felt that Cantayo was probably constructed early, during the EIP (Forgey, 2006). Carmicheal (1998) also concluded that the site was early based on the artifact assemblages. There have been no radiocarbon dates of the material from Cantayo and given the fact that many cemeteries were used long after the use of the site was discontinued this sample is retained in the study. It is worth noting that the Cantayo sub-sample is relatively small with 11 crania, and does not include individuals from any other site.

Aja (AJA_MH)

The Aja subsample is named for the Aja site located on the north bank just west of the confluence of the Aja and Tierras Blancos Rivers. The sub-sample includes crania from the Aja site (n=6), Las Cañas (n=1), Pangaravi East (n=1), and Agua Santa (n=1). Given their proximity and the relatively small overall sample size, crania from these four sites were collapsed into one sub-sample.

Majoro Chico **(MAJ_MH)**

Majoro Chico itself is a relatively small site with coordinates relatively dated from the EIP through the LIP (Figure 4.21). Similar to the Aja sub-sample, Majoro Chico represents six sites collapsed into one sub-sample. In addition to the crania from Majoro Chico (n=11) crania from Soisongo (n=5), Ocongalla (n=3), Paredones (n=1), La Huayrona (n=2), La Estaqueria (n=1) were collapsed into the sub-sample based on close geographic proximity (within 10 km) and reasonably consistent chronology.

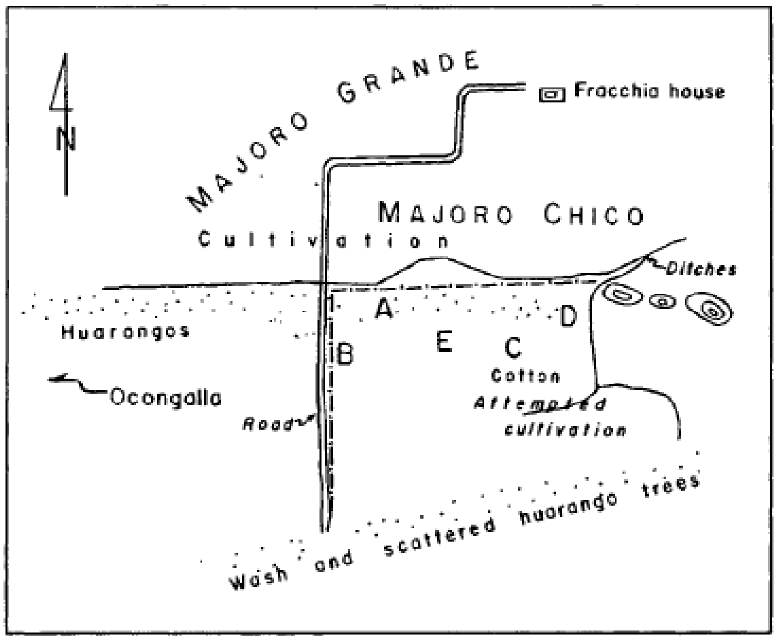


Figure 4.21. Map of the Majoro Chico site (reproduced from Williams et al., 2001).

It is important to note that some of the crania sampled in the Nasca group were trophy heads. The geographic origin of trophy heads are often questioned since they could be war trophies fashioned from the heads of far away enemies as much as they could be made from local ancestors. Knudson et al. (2009) conducted Sr isotope analysis on the trophy heads in the Kroeber collection and found them to be most likely derived of the local population. Since these crania are probably derived of the local population, and sample sizes are already relatively small, the data collected from trophy heads was retained in this study.

4.2.6 Central coast (Ancón)

Ancón (ANC_MH and ANC_LIP)

Ancón is situated on the coast approximately 40km north of Lima. The site has been extensively excavated with a focus on the mortuary complex (Ravines, 1977, 1981; Slovak, 2007; Slovak et al., 2009) (Figure 4.22). Human remains have been recovered from the lower sector of the Necropolis dating to the MH on the basis of ceramic style (Figure 4.23). During the MH the zone of habitation and mortuary practices shifted appreciably becoming associated with Wari material culture (Menzel, 1977; Uhle, 1968[1912]). Slovak (2007; Slovak et al., 2009) identified a nonlocal individual through Sr analysis interpreted as a possible Wari migrant. During July-August 2009 skeletal data was collected from 62 individuals at the Museo Nacional de Antropología, Arqueología, e Historia del Peru (MNAAHP). For comparative purposes, the same individuals sampled for Slovak's study were scored for this study when possible, and additional specimens were added to this study. No radiometric dates are available for the Ancón material sampled in this study so crania were dated to the MH based on the style of mortuary offerings (see Figure 4.23). So as not to over-sample higher status individuals, some crania were scored from graves that had little or no offerings, but were in close enough proximity to other MH burials to reasonably believe that they also dated to the MH.

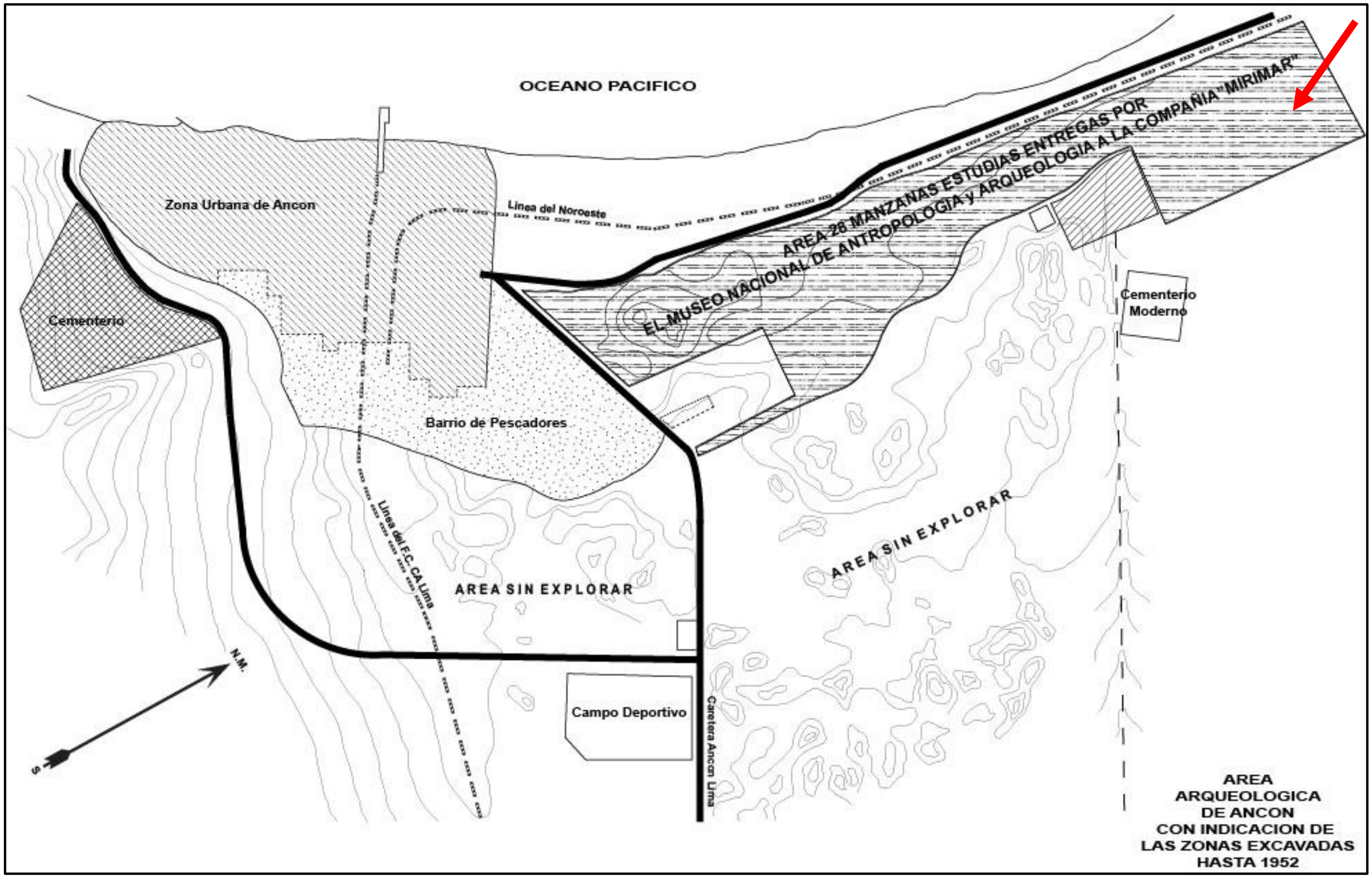
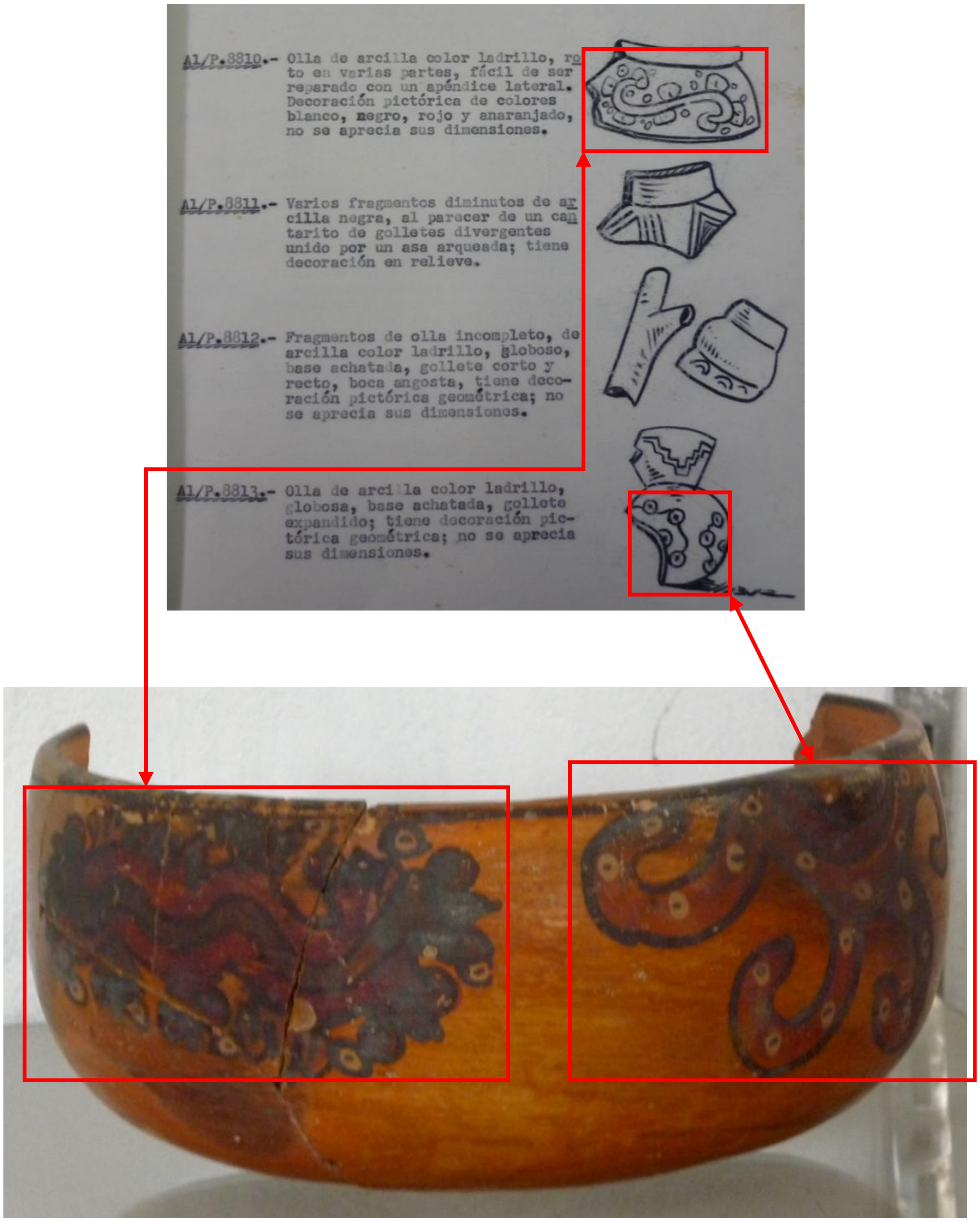


Figure 4.22. Plan map of the Ancón site adapted from Ravines (1977). Specimens used in this study were recovered from the "MIRIMAR" sector highlighted by a red arrow.



Al/P.8810.- Olla de arcilla color ladrillo, roto en varias partes, fácil de ser reparado con un apéndice lateral. Decoración pictórica de colores blanco, negro, rojo y anaranjado, no se aprecia sus dimensiones.

Al/P.8811.- Varios fragmentos diminutos de arcilla negra, al parecer de un cantarito de golletes divergentes unido por un asa arqueada; tiene decoración en relieve.

Al/P.8812.- Fragmentos de olla incompleto, de arcilla color ladrillo, globoso, base achatada, gollete corto y recto, boca angosta, tiene decoración pictórica geométrica; no se aprecia sus dimensiones.

Al/P.8813.- Olla de arcilla color ladrillo, globosa, base achatada, gollete expandido; tiene decoración pictórica geométrica; no se aprecia sus dimensiones.

Figure 4.23. Example from MNAAHP museum accession records for Ancón (above), and an example of Wari-style ceramic decoration from the Conchopata collection at the Universidad Nacional San Cristóbal de Huamanga in Ayacucho, Peru (bottom). Stylistic consistencies are highlighted with red boxes.

A sample of crania from Ancón (n=55) dating to the LIP after the Wari collapse housed at the Chicago Field Museum of Natural History was also scored for non-metric traits. This material was collected by George Dorsey in 1892 (Dorsey, 1895). Based on associated mortuary offerings Dorothy Menzel (1977) analyzed the ceramics from this collection and dated it broadly to the MH through the LIP (AD 600-1450). Some of this material was scored previously by Konigsberg (see Konigsberg et al., 1993). However, those data were not used for this study and the material was rescored to minimized inter-observer error. It is also acknowledged that there may be some chronological overlap between this and the Ancón sample collected at the MNAAHP.

Chapter V

Methods

5.1 Cranial non-metric trait data

Cranial non-metric traits were used to model population genetic relationships among sample populations. These traits were used because they are observable even when remains are poorly preserved which is often the case with archaeological samples. Analyses of cranial non-metric traits are non-destructive, inexpensive, and provide a good proxy for genetic relationships among populations. Thirty-six traits were observed (Table 5.1). In an effort to capture data concerning the range of expression the traits were scored using a multi-coordinate system after Buikstra and Ubelaker (1994) and Hauser and DeStefano (1989) (see Appendix A for the scoring rubric). For more manageable statistical analysis observations were collapsed into a dichotomous system of present (Score=1) and absent (Score=0). Traits that were unobservable were scored nine. For traits that are expressed bilaterally if only one side was observable, that score was used. If both sides were observable, the score for one side was randomly selected to avoid bias due to asymmetry or differential preservation (after Konigsberg et al., 1993).

Non-metric traits were also selected because the effects of cranial modification on trait frequency are more easily controlled for with categorical data than with metric traits. The practice of artificial cranial modification was prevalent in the prehistoric Andes and was frequently observed in this study (Figure 5.1). Konigsberg and colleagues (1993) have shown that cranial modification affects the relative frequency of few traits, and the overall effect on biological distance calculations is not significant (see also Cheverud et al., 1992; Rhode and Arriaza, 2006; Pomeroy et al., 2010). Data regarding cranial modification was collected so that its effects on trait expression could be evaluated. For the archaeological samples considered in this study non-metric traits allow for maximum data recovery and control of confounding variables like cranial modification. For these reasons cranial non-metric traits was determined to be the best type of data for elucidating biological relationships among the study populations.

Table 5.1. Non-metric traits observed in the study.

1. Metopic suture	19. Inca bone
2. Supraorbital notch	20. Condylar canal
3. Supraorbital foramen	21. Divided hypoglossal canal
4. Infraorbital suture	22. Flexure of superior sagittal sulcus right
5. Multiple infraorbital foramina	23. Foramen ovale incomplete
6. Zygomatico-facial foramina	24. Foramen spinosum incomplete
7. Parietal foramen	25. Pterygo-spinous bridge
8. Epiteric bone	26. Pterygo-alar bridge
9. Coronal ossicle	27. Tympanic dehiscence
10. Bregmatic bone	28. Auditory exostosis
11. Sagittal ossicle	29. Mastoid foramen
12. Apical bone	30. Double condylar facet
13. Lambdoid ossicle	31. Bridging of jugular foramen
14. Asterionic bone	32. Pharyngeal tubercle
15. Ossicle in occipito-mastoid suture	33. Palatine torus
16. Parietal notch bone	34. Mental foramen
17. Divided parietal bone	35. Mandibular torus
18. Os japonicum	36. Mylohyoid bridge

Figure 5.1. Specimens exhibiting varying types and degrees of cranial modification. Specimens from the Ayacucho LIP (left and are middle) and Conchopata MH (right) samples.

5.2 Intraobserver error

The data were screened for intraobserver error using a Pearson Chi-square test of independence. The data used for this test were a subset of the Ancón MH sample (n=20). The chi-square tests the null hypothesis that two categorical variables from the same population are independent of each other. A significant p-value (α≤0.05) indicates that there is *not* interdependence between the first and second trial scores. Therefore, traits that had significant p-values were retained for further analysis and those with non-significant p-values would be removed from further analysis due to intraobserver error. The calculation of the Pearson Chi-square statistic was done with NCSS statistical software (Hintze, 2007).

In the preliminary analysis three mandibular traits, multiple mental foramen (#34), presence of a mandibular torus (#35), and mylohyoid bridging (#36), were removed because very few mandibles could be associated with a cranium. Traits including divided parietal bone (#17), foramen ovale incomplete (#23), foramen spinosum incomplete (#24), and presence of a pharyngeal tubercle (#32) were removed from analysis for zero variation after the scores were collapsed. After the initial data screening procedures the traits were then tested for correlation with demographic and environmental variables.

5.3 *Cranial non-metric trait correlations with age , sex, and cranial modification*

The expression of non-metric traits can be correlated with the age and sex of the individual (see discussion in Chapter 3). An additional concern in this study was the effect of cranial modification on the expression of traits. Those traits that are affected by these variables were not included in the analysis. The effect of age, sex, and cranial modification on the expression of the reduced list of thirty cranial non-metric traits was assessed using a series of logistic regression analyses following Konigsberg (1987). This logit can be expressed as equation 5.1 and is abbreviated as the logit model in equation 5.2:

$$log\left[\frac{P(t=1)}{1-P(t=1)}\right] = \alpha + \beta x \qquad 5.1$$

$$logit[P \quad t = 1 \quad] = \alpha + \beta_1(sex) + \beta_2(age) + \beta_3(mod) \qquad 5.2$$

where P(t=1)/1-P(t=1) is the odds that an individual will express a certain trait. In equation 5.2 α is the constant and the beta weights are regressed on age, sex, and cranial modification (Konigsberg, 1987). The statistical software package NCSS was used to calculate the parameter scores and p-values for the effects of age, sex, cranial modification, and all possible interactions of these variables on trait expression. Since a large number of comparisons were made the significance level for the removal of traits from the analysis was adjusted using the Šidák correction which is similar to, but more sensitive than the Bonferroni correction.

$$\alpha = 1 - (1 - \bar{\alpha})^{1/n} \qquad 5.3$$

The trait with the smallest number of comparisons (n=199) and $\bar{\alpha}$ equal to 0.05 were used to calculate α for trait correlations as described in Equation 5.3. Any trait found to be significantly correlated ($\alpha \leq 0.001$) to a variable, or variable interactions, was excluded from the biological distance analysis.

5.4 Biological Distance Calculation

To estimate biological distances between samples a modification of the Mahalanobis D^2 was used to accommodate discrete traits following Konigsberg and colleagues (1993:38-39; see also Bedrick et al., 2000). The individual Mahalanobis D^2 values were calculated using individual trait threshold values and a pooled within-group tetrachoric correlation matrix. The threshold values were calculated using a logistic regression approach. Age, sex, and cranial modification effects were assumed to be homogenous across samples

The tetrachoric correlations for pairs of traits were computed for all possible combinations within each sample and then pooled incorporating sample size to determine the weighted average correlations. The weighted average correlations were combined to form the pooled tetrachoric correlation matrix. The threshold values and tetrachoric correlation matrix were computed using *ThreshD*, an R package written by Dr. Lyle Konigsberg. The individual distances are then calculated with the D2.matrix by the following equation:

$$d_{ij}^2 = \ z_i - z_j \ {}' \, T^{-1}(z_i - z_j), \qquad 5.4$$

where $(z_i - z_j)$ is a column vector of differences between threshold values for trait *z* sites *i* and *j* and T is a matrix of pooled within-group tetrachoric correlations between traits. The distance values then represent the minimum possible distances between groups assuming full heritability of the traits (Williams-Blangero and Blangero, 1990; Konigsberg, 1990).

This analysis was performed on several subsets of the total sample (Table 5.2). A distance matrix that included all samples in the study was calculated. This was repeated for a subset of MH samples and LIP samples. The distance matrix for the south-central highlands region (Andahuaylas) was also calculated for all samples and for only the LIP samples.

Table 5.2. Summary of sample groupings or the biological distance calculations.

Sample Groupings	**n**
All Samples	450
All Middle Horizon Samples	192
All Late Intermediate Period Samples	258
All Andahuaylas Samples	154
Andahuaylas Late Intermediate Period Samples	142

5.5 F_{ST}

The relative quantity of differentiation between groups in the sample subsets is useful to understand changes in population genetic structure over time. Wright's F_{ST} can be derived from the distance matrices and is a conservative measure of the minimum amount of microdifferentiation between groups. Konigsberg (2006:278-9) provides a method to transform the $\mathbf{D}^2$ matrix of biological distances to an **R** matrix following Relethford and Blangero (1990; Relethford, 1994; Relethford et al., 1997). A Principal Coordinates Analysis (PCA) of the **R** matrices was done and the samples plotted by the first two and first three principal coordinates for a graphical illustration of biological distances. F_{ST} values were then calculated as the average distance to the centroid derived from the PCA plots. Since the F_{ST} is the amount of micodifferentiation between groups, a larger value would be interpreted as representing increased heterogeneity between groups possibly as the result of genetic isolation or Founder's Effect. A small F_{ST} value would indicate less differentiation between groups consistent with a higher level of gene flow. These interpretations are dependent on the effective populations being equal, and were interpreted in light of this assumption.

5.6 Spatial and Temporal Effects on Biological Distance and Matrix Comparisons

The goal of the biological distance analysis is to detect patterns of gene flow. As gene flow increases the genetic, and therefore biological distances should decrease. Geographical and temporal proximity will also have an effect on the biological distance values. Isolation by time when controlling for geographic distance, will serve to decrease the genetic distances which will be reflected in smaller biological distances (Konigsberg, 1990). Mantel matrix permutation tests have been the preferred methods in the recent anthropological literature for examining the correlation between spatial, temporal, and biological distances (Mantel, 1967; Smouse et al., 1986; Manly, 1986, 1997; Oden and Sokal, 1992; Smouse and Long, 1992; González Jose et al., 2002).

Mantel (1967) first proposed a two-matrix comparison where the products of all off-diagonal combinations are summed. For this comparison if the matrices are correlated the Z-value will be large:

$$Z = \sum_{i=1}^{n} \sum_{j=1}^{n} A_{ij}B_{ij}, \qquad 5.5$$

The matrix elements can be standardized to calculate the product-moment correlation coefficient:

$$r = \frac{stdA_{ij}stdB_{ij}}{n-1}, \qquad 5.6$$

Dow and Cheverud (1985; see also Manly, 1986; Smouse et al., 1986) extended the Mantel (1967) test to deal with multiple matrices referred to as a Partial Mantel Test. Manly's (1986) approach is based on multiple regression and is calculated by:

$$A_{ij} = \beta_0 + \beta_1 B_{ij} + \beta_2 C_{ij} + \epsilon_{ij}, \qquad 5.7$$

where β_1 measures the relationship of **A** and **B** after following the effects of **C**, β_2 measures the relationship of **A** and **C** after allowing for the effects of **B**, and $\in$ is an independent error. The permutation aspect of the test results from the reordering of the elements of A (biological distances) and calculating the correlation coefficient. This study follows the approach of Smouse et al. (1986) where a series of residuals ($\mathbf{A'}$ and $\mathbf{B'}$) are derived by regressing the two matrices (**A** and **B**) on a third matrix (**C**). Thus, the statistic tests the relationship of **A** and **B** conditional on **C**. In this study all two-way and three-way comparisons of biological, geographic, and temporal distances are done. The correlation coefficients and p-values for full and partial correlations were calculated from 999 random permutations of the distance matrices. The analysis was done in R using the *vegan* package (functions mantel and mantel.partial) following Smouse et al. (1986) (Oksanen et al., 2012).

5.7 Geographic and temporal distance matrices

Three matrices were constructed to evaluate correlation between biological, spatial, and temporal distances (Tables 5.3 and 5.4). For the geographic distance between samples two matrices were compared to the biological distance matrix. To understand the relative spatial relationships between sites point-to-point linear distances can be used. However, people do not tend to move about the landscape in a linear manner, especially in terrain as difficult to traverse as the Andes. As such a matrix of linear distances and a matrix of distances along rivers and archaeologically documented roads were used (Table 5.3, Figures 5.2 and 5.3). The road and river distance matrix was calculated by approximating well known ancient roads, documented in Hyslop (1984) that may have been used by these populations and the shortest river distance between the roads (Figure 5.3).

Table 5.3. Table of geographic distances in kilometers. The upper triangle values are linear distances and the lower triangle values are road and river distances.

	CON_MH	**AYA_LIP**	**HUA_MH**	**MAR_LIP**	**TUR_MH**	**SON_LIP**	**MPM_LIP**	**PUC_LIP**	**RCC_LIP**	**BER_MH**	**BER_LIP**	**CAH_MH**	**CAN_MH**	**AJA_MH**	**MAJ_MH**	**ANC_MH**	**ANC_LIP**
CON_MH	0.0	10.6	614	534	104	90.7	90.7	92.4	66.9	364	364	210	204	203	204	356	356
AYA_LIP	18	0.0	608	526	110	97.6	97.6	96	73.4	356	356	219	213	213	214	354	354
HUA_MH	817	563	0.0	81.3	716	704	704	700	679	966	966	715	724	725	723	326	326
MAR_LIP	697	715	123	0.0	636	624	624	597	624	887	887	643	651	652	652	265	265
TUR_MH	138	153	950	835	0.0	16.3	16.3	30.9	37.6	258	258	213	198	199	200	458	458
SON_LIP	153	168	965	850	15	0.0	0.0	35.3	27.5	268	268	201	188	189	189	442	442
MPM_LIP	153	168	965	850	15	0.0	0.0	35.3	27.5	268	268	201	188	189	189	442	442
PUC_LIP	160	178	875	860	25	40	40	0.0	30.1	282	282	235	222	222	223	449	449
RCC_LIP	173	188	985	870	35	55	55	35	0.0	294	294	212	200	200	201	423	423
BER_MH	485	505	1273	1223	332	347	347	404	379	0.0	0.0	313	295	296	296	684	684
BER_LIP	485	505	1273	1223	332	347	347	404	379	0.0	0.0	313	295	296	296	684	684
CAH_MH	383	401	886	836	236	221	221	261	252	387	387	0.0	19.3	18.2	18	401	401
CAN_MH	364	382	908	855	217	202	202	242	233	406	406	22	0.0	1.0	1.0	414	414
AJA_MH	363	381	906	856	216	201	201	241	232	407	407	20	1	0.0	0.98	413	413
MAJ_MH	364	382	905	855	217	202	202	242	233	406	406	19	2	1	0.0	413	413
ANC_MH	464	482	478	428	552	567	567	527	562	795	795	408	430	428	427	0.0	0.0
ANC_LIP	464	482	478	428	552	567	567	527	562	795	795	408	430	428	427	0	0.0

Not all samples used in this study have radiometric dates. Ancón, Ayacucho, and the Nazca River valley samples are all relatively dated based on artifact associations. Given this limitation, a simple design matrix of relative chronology was used to compare to the biological distance matrices (Table 5.4). In the temporal distance matrix pairs of samples that both dated to the same time period were given a zero, signifying there was no, or a very small, temporal distance. Those pairs that dated to different time periods were given a one.

Table 5.4. Design matrix of temporal distances between samples.

	CON_MH	**AYA_LIP**	**HUA_MH**	**MAR_LIP**	**TUR_MH**	**SON_LIP**	**MPM_LIP**	**PUC_LIP**	**RCC_LIP**	**BER_MH**	**BER_LIP**	**CAH_MH**	**CAN_MH**	**AJA_MH**	**MAJ_MH**	**ANC_MH**	**ANC_LIP**
CON_MH	0																
AYA_LIP	1	0															
HUA_MH	0	1	0														
MAR_LIP	1	0	1	0													
TUR_MH	0	1	0	1	0												
SON_LIP	1	0	1	0	1	0											
MPM_LIP	1	0	1	0	1	0	0										
PUC_LIP	1	0	1	0	1	0	0	0									
RCC_LIP	1	0	1	0	1	0	0	0	0								
BER_MH	0	1	0	1	0	1	1	1	1	0							
BER_LIP	1	0	1	0	1	0	0	0	0	0	0						
CAH_MH	0	1	0	1	0	1	1	1	1	0	1	0					
CAN_MH	0	1	0	1	0	1	1	1	1	0	1	0	0				
AJA_MH	0	1	0	1	0	1	1	1	1	0	1	0	0	0			
MAJ_MH	0	1	0	1	0	1	1	1	1	0	1	0	0	0	0		
ANC_MH	0	1	0	1	0	1	1	1	1	0	1	0	0	0	0	0	
ANC_LIP	1	0	1	0	1	0	0	0	0	1	0	1	1	1	1	1	0

Figure 5.2. Map depicting the linear distances between sites from which the study samples were derived (note that "Chachi" refers to SON_LIP and MPM_LIP).

Figure 5.3. Map depicting the road and river distances between sites from which the study samples were derived (note that "Chachi" refers to SON_LIP and MPM_LIP).

Chapter VI

Results

6.1 Data Screening Results

The following chapter summarizes the results of the analyses outlined in Chapter Four. Initially all traits were tested for intraobserver error to ensure the observations were consistent between specimens and samples. Table 6.1 illustrates the result of a Pearson chi-squared test of homogeneity of trait scores for a subset of twenty specimens from the Ancón MH (ANC_MH) sample over two trials. A significant p-value ($\alpha \leq 0.05$) indicated that the two trials were not independent, or alternatively that the observations are associated. All of the traits had a significant p-value. Therefore no traits were excluded from further analysis on the basis of intraobserver error.

Several traits including presence of a bregmatic bone (#10), divided parietal bone (#17), incomplete foramen ovale (#23), incomplete foramen spinosum (#24), and presence of a pharyngeal tubercle (#32) were removed due to zero variation across samples after the scores were collapsed to the binary system. The mandibular traits, multiple mental foramen (#34), presence of a mandibular torus (#35), and mylohyoid bridging (#36 and #37), were removed from further analysis because very few mandibles could be reliably associated with crania for the study sample. The reduced set of traits was tested for correlation between expression and the age and sex of the individual by logistic regression. The expression of a trait was also tested for correlation with cranial modification. All traits that were significantly correlated ($\alpha \leq 0.001$) with age, sex, or cranial modification were removed from the analysis (Table 6.2). Correlations between trait expression and the interaction between age, sex, and cranial modification were also tested with logistic regression (Table 6.3). Any traits that were significantly correlated with variable interactions were removed from the analysis. After the data screening procedures were completed, a reduced set of nine traits were found to be useful for the biological distance analysis (Table 6.4).

Table 6.1. Results of Intraobserver Error Pearson chi-squared test.

Trait	***df***	**p-value**
1. Metopic suture	1	<0.0001
2. Supraorbital notch	1	<0.0001
3. Supraorbital foramen	1	<0.0001
4. Infraorbital suture	1	<0.0001
5. Multiple infraorbital foramina	1	<0.0001
6. Zygomatico-facial foramina	1	<0.0001
7. Parietal foramen	1	<0.0001
8. Epiteric bone	1	<0.0001
9. Coronal ossicle	1	0.0001
11. Sagittal ossicle	1	0.0001
12. Apical bone	1	0.0002
13. Lambdoid ossicle	1	<0.0001
14. Asterionic bone	1	<0.0001
15. Ossicle in occipito-mastoid suture	1	<0.0001
16. Parietal notch bone	1	<0.0001
18. Os japonicum	1	0.0021
19. Inca bone	1	<0.0001
20. Condylar canal	1	<0.0001
21. Divided hypoglossal canal	1	0.0017
22. Flexure of superior sagittal sulcus right	1	0.0003
25. Pterygo-spinous bridge	1	0.0001
26. Pterygo-alar bridge	1	0.0003
27. Tympanic dihiscence	1	<0.0001
28. Auditory exostosis	1	<0.0001
29. Mastoid foramen	1	<0.0001
30. Double (occipital) condylar facet	1	<0.0001
31. Bridging of jugular foramen	1	<0.0001
33. Palatine torus	1	<0.0001
34. Multiple mental foramen	1	<0.0001
35. Mandibular torus	1	<0.0001
36. Mylohyoid bridge	1	<0.0001
37. Degree of mylohyoid bridge	1	<0.0001

Table 6.2. Trait correlations with age, sex, and cranial modification.

Trait	**Age**		**Sex**		**Modification**	
	N	**p-value**	**N**	**p-value**	**N**	**p-value**
1. Metopic suture	357	0.6317	407	0.8751	516	0.0091
2. Supraorbital notch	356	0.4199	406	0.8494	506	0.4471
3. Supraorbital foramen	356	0.3115	406	0.9688	506	0.6251
4. Infraorbital suture	318	0.0358	342	**0.0002***	413	0.4597
5. Mult. Infraorbital foramina	319	0.3563	341	0.9950	412	0.2578
6. Zygomatico-facial foramina	332	0.1575	355	0.7205	437	0.8033
7. Parietal foramen	319	0.2771	364	0.8604	464	0.0125
8. Epiteric bone	303	0.1092	353	0.0415	425	0.0326
9. Coronal ossicle	327	0.3865	380	0.1620	478	0.0456
11. Sagittal ossicle	325	0.9331	381	0.6892	486	0.6813
12. Apical bone	311	0.3565	361	0.0767	454	0.1076
13. Lambdoid ossicle	313	0.4110	369	0.8407	461	0.2882
14. Asterionic bone	293	0.4722	348	0.7810	423	0.1335
15. Ossicle in occipito-mastoid suture	287	0.0042	344	0.0339	414	0.1178
16. Parietal notch bone	301	0.3179	360	0.7005	436	0.0003
18. Os japonicum	302	0.1023	334	0.2356	403	0.0535
19. Inca bone	321	0.5199	367	0.2711	467	0.7149
20. Condylar canal	293	0.1171	340	0.1684	416	0.6215
21. Divided hypoglossal canal	296	0.1465	344	0.0830	414	0.8602
22. Flexure of superior sagittal sulcus right	311	0.6226	356	0.5191	451	0.4283
25. Pterygo-spinous bridge	312	0.3774	361	0.0164	438	0.7112
26. Pterygo-alar bridge	321	0.8507	367	0.7713	447	0.3001
27. Tympanic dehiscence	343	0.7975	391	**0.0008***	493	0.9187
28. Auditory exostosis	343	0.2770	395	<**0.0001***	500	0.5204
29. Mastoid foramen	340	0.4324	392	**0.0001***	496	0.1174
30. Double condylar facet	282	0.1119	324	0.8533	391	0.1587
31. Bridging of jugular foramen	252	0.1918	303	0.9078	357	0.0197
33. Palatine torus	306	0.0017	328	0.2119	392	0.5956

***** Significant at $\alpha \leq 0.001$

Table 6.3. Trait correlations with variable interactions.

Trait	n	Age*Mod	Age*Sex	Sex*Mod	Age*Sex*Mod
		p-value	**p-value**	**p-value**	**p-value**
1. Metopic suture	269	0.8118	**0.0336***	0.8810	0.2783
2. Supraorbital notch	270	0.5847	0.8761	0.8801	0.7624
3. Supraorbital foramen	270	0.8471	0.7250	0.7788	0.9717
4. Infraorbital suture	240	0.1026	0.2207	0.0371	0.2934
5. Mult. Infraorbital foramina	247	0.6483	0.9440	0.9559	0.8885
6. Zygomatico-facial foramina	247	0.6483	0.9440	0.9559	0.8885
7. Parietal foramen	241	0.5965	0.1904	0.6393	0.8234
8. Epiteric bone	238	0.9610	0.9760	0.8040	0.9912
9. Coronal ossicle	250	0.9928	0.8404	0.9989	0.5165
11. Sagittal ossicle	249	0.9871	0.9267	0.9231	0.9285
12. Apical bone	241	0.8880	0.7920	0.0088	0.1666
13. Lambdoid ossicle	241	0.0168	0.0452	0.0759	0.2859
14. Asterionic bone	230	1.0000	0.0579	0.9993	0.9994
15. Ossicle in occipito-mastoid suture	226	0.7261	0.4321	0.8723	0.7771
16. Parietal notch bone	237	0.6062	0.4389	0.4346	0.1180
18. Os japonicum	229	0.3845	0.9961	0.9993	0.1456
19. Inca bone	243	0.9198	0.9367	0.0323	0.1492
20. Condylar canal	227	0.7863	0.6578	0.5291	0.5598
21. Divided hypoglossal canal	233	0.5428	0.2064	0.4935	0.0146
22. Flexure of superior sagittal sulcus right	237	0.9733	0.6438	0.4705	0.7547
25. Pterygo-spinous bridge	240	0.9705	1.0000	0.9307	0.9628
26. Pterygo-alar bridge	246	1.0000	0.0792	0.9474	0.3882
27. Tympanic dehiscence	258	0.2638	0.2962	0.4464	0.0366
28. Auditory exostosis	258	0.9303	0.9927	0.7752	0.9806
29. Mastoid foramen	257	0.7604	0.8005	0.8617	0.8253
30. Double condylar facet	222	0.9946	0.9517	0.9998	0.9533
31. Bridging of jugular foramen	199	0.8620	0.4278	0.9996	0.8641
33. Palatine torus	232	0.7486	0.4553	0.2927	0.6815

***** Significant at α≤0.001

Table 6.4. Final traits used in analysis.

Final Trait List
1. Metopic suture
2. Supraorbital notch
3. Supraorbital foramen
5. Mult. Infraorbital foramina
6. Zygomatico-facial foramina
7. Parietal foramen
8. Epiteric bone
9. Coronal ossicle
11. Sagittal ossicle
12. Apical bone
13. Lambdoid ossicle
14. Asterionic bone
15. Ossicle in occipito-mastoid suture
18. Os japonicum
19. Inca bone
20. Condylar canal
21. Divided hypoglossal canal
22. Flexure of superior sagittal sulcus right
25. Pterygo-spinous bridge
26. Pterygo-alar bridge
30. Double condylar facet
31. Bridging of jugular foramen
33. Palatine torus

6.2 Biological Distance Analysis

Once the final trait list was determined, all specimens that had more than 12 unobservable traits (score=9) were eliminated from the sample. The total sample size was 450 individuals, and the breakdown of sub-samples is summarized in Table 6.5. One of the goals of this project was to explore the effects of cultural horizons on both regional and interregional gene flow. Accordingly, the samples were grouped chronologically belonging to either the MH or LIP for the biological distance analysis. Table 6.6 summarizes the sample groupings.

Table 6.5. Summary of sample sizes.

Sample	Time Period	Sample Label	n
Conchopata	Middle Horizon	CON_MH	22
Ayacucho Basin	Late Intermediate Period	AYA_LIP	17
Hualcayan	Middle Horizon	HUA_MH	24
Marca Jirca	Late Intermediate Period	MAR_LIP	35
Turpo Qatun Rumi	Middle Horizon	TUR_MH	12
Sonhuayo	Late Intermediate Period	SON_LIP	65
Mina Puka Machay	Late Intermediate Period	MPM_LIP	26
Puccullu	Late Intermediate Period	PUC_LIP	18
Ranra Cancha	Late Intermediate Period	RCC_LIP	33
Beringa	Middle Horizon	BER_MH	10
Beringa	Late Intermediate Period	BER_LIP	9
Cahuachi	Middle Horizon	CAH_MH	18
Cantayo	Middle Horizon	CAN_MH	12
Aja	Middle Horizon	AJA_MH	9
Majoro Chico	Middle Horizon	MAJ_MH	23
Ancón	Middle Horizon	ANC_MH	62
Ancón	Late Intermediate Period	ANC_LIP	55
Total			**450**

Table 6.6. Sample groupings for biological distance analysis.

Sample Groupings	n
All Samples	450
All Samples (AJA_MH and BER_LIP excluded)†	432
All Middle Horizon Samples	192
All Middle Horizon Samples (AJA_MH excluded)†	183
All Late Intermediate Period Samples	258
All Late Intermediate Period Samples (BER_LIP excluded)†	249
All Andahuaylas Samples	154
Andahuaylas Late Intermediate Period Samples	142

† The AJA_MH and BER_LIP samples were excluded in some analyses because they were outliers.

6.2.1 Trait Threshold Values, Tetrachoric Correlation matrices, and Mahalanobis D^2 matrices

The individual trait threshold values used to calculate the Mahalanobis D^2 matrices for all sample groupings are summarized in Table 6.7. The within-group pooled tetrachoric correlation matrices used in the calculation of the Mahalanobis D^2 matrices are summarized in Tables 6.8 to

6.15. The Mahalanobis D^2 matrices derived from the individual trait threshold values and pooled within-group tetrachoric correlation matrices are illustrated in Tables 6.16 to 6.23. To visualize the biological distances more easily each R matrix was decomposed by Principal Coordinates Analysis. The loadings on the first two principal coordinates were plotted in two-dimensional scatterplots. Three-dimensional scatterplots were also plotted for the first three principal coordinates. The relative biological distances for each of the sample groupings are summarized individually in the following sections.

Table 6.7. Threshold values for all samples.

	T1	**T2**	**T3**	**T5**	**T6**	**T7**	**T8**	**T9**	**T11**	**T12**	**T13**
CON_MH	-1.3352	0.0597	-0.0597	-1.7688	1.6449	0.9674	-1.3830	-1.1868	-1.8895	-0.6745	0.3360
AYA_LIP	-0.9289	0.3774	0.0738	-1.7688	1.5011	-0.2533	-0.7916	-1.1503	-1.8339	-1.7317	0.6745
HUA_MH	-2.0368	0.5119	0.1642	-0.9289	0.7215	-0.0545	-2.0368	-1.3830	-1.6906	-0.7810	-0.3912
MAR_LIP	-1.3676	0.6522	-0.0358	-0.3661	1.8339	-0.3186	-1.3180	-2.1539	-1.3002	-1.1503	-0.2691
TUR_MH	-1.7317	0.6745	-0.4307	-0.7647	1.5932	0.4307	-1.5341	-1.7317	-1.7317	-1.6906	-0.3488
SON_LIP	-0.8075	0.2035	0.0000	-1.1750	1.5446	-0.0205	-1.3002	-1.0100	-1.6759	-0.6621	0.3601
MPM_LIP	-1.1750	0.5119	-0.5119	-1.1868	1.9145	0.7363	-2.0368	-1.0201	-2.0699	-1.7507	-0.0502
PUC_LIP	-0.9674	0.7647	-0.9674	-1.2206	1.2206	0.2230	-1.5932	-1.5932	-1.5647	-1.5647	-0.0738
RCC_LIP	-0.5157	0.6745	-0.6745	-0.7916	2.1002	0.4888	-1.3180	-1.1689	-2.1661	-1.5341	-0.1142
BER_MH	-1.5932	0.7647	0.1397	-1.5341	1.1503	1.1503	-1.2206	-1.2206	-1.5341	-1.1503	-0.3186
BER_LIP	-1.5932	0.4307	0.0000	-1.8627	1.1868	0.3774	-1.8027	-1.5932	-1.8895	-1.5647	-0.3774
CAH_MH	-1.7317	0.6046	-0.9085	-1.3352	1.3352	0.4307	-1.7317	-1.7317	-1.7317	-1.7317	-0.2104
CAN_MH	-2.0191	0.5119	-0.2759	-0.7124	1.3352	0.0545	-1.8895	-1.7117	-2.0191	-0.9085	-0.2299
AJA_MH	-1.6449	-0.4307	-0.1397	-0.7647	1.6449	-0.5244	-1.6449	-1.6449	-1.6449	-1.6449	0.0000
MAJ_MH	-1.5932	-0.7647	-0.4307	-1.5932	1.5932	-1.0676	-0.4307	-1.5932	-1.5932	-1.5341	0.3186
ANC_MH	-2.1412	0.5059	-0.5059	-0.6745	2.1213	0.5588	-1.1503	-2.0928	-1.6449	-0.5386	0.3993
ANC_LIP	-2.3619	0.4475	-0.3007	-1.3352	1.1394	0.2822	-1.7862	-1.6023	-1.7945	-0.6046	-0.0684

Table 6.7 continued. Threshold values for all samples.

	T14	T15	T18	T19	T20	T21	T22	T25	T26	T30	T31	T33
CON_MH	-0.7647	-1.4652	-1.9145	-1.5932	0.6336	-1.0968	0.3853	-1.6449	-1.1503	-1.9808	-0.9674	-0.9289
AYA_LIP	-1.4261	-1.4652	-1.8339	-1.3830	1.3830	-0.7363	1.0201	-1.5341	-1.1503	-1.7688	-1.6449	0.5024
HUA_MH	-2.0191	-1.3597	-1.5647	-2.0368	1.3352	-1.3352	0.5659	-1.6906	-1.3352	-1.9600	-1.6449	1.1503
MAR_LIP	-1.1503	-1.9022	-1.5011	-1.3352	0.4888	-0.7764	0.9085	-1.3517	-1.1868	-2.0537	-1.1689	1.0444
TUR_MH	-0.8416	-1.1503	-1.2816	-1.6906	0.5244	-1.6449	0.8416	-1.6449	-1.3352	-1.5341	-1.3830	0.5659
SON_LIP	-1.6759	-1.2206	-2.2949	-1.8486	0.6193	-0.9915	0.4152	-1.6759	-2.1539	-1.7599	-2.0928	0.3885
MPM_LIP	-1.7117	-1.1243	-1.8627	-1.3830	0.4728	-1.0968	0.6745	-1.7507	-1.1750	-1.9600	-0.9085	0.5414
PUC_LIP	-0.9674	-1.9145	-1.5932	-1.5647	0.4307	-0.7215	0.6745	-1.9145	-1.9145	-1.5932	-1.5932	0.6745
RCC_LIP	-1.8764	-0.7991	-1.7117	-1.3352	0.1573	-1.3002	0.8649	-1.5497	-1.3352	-1.8186	-1.3002	0.7916
BER_MH	-1.1503	-0.4307	-1.5341	-1.5341	0.5659	-0.4307	1.1503	-1.5341	-1.1503	-0.9674	-1.3830	-0.5659
BER_LIP	-1.1503	-0.8871	-1.8895	-1.8895	1.5647	-0.4888	0.7916	-1.1868	-1.8627	-1.8627	-1.8027	-0.8416
CAH_MH	-1.7317	-0.4307	-1.6449	-1.3830	0.9085	-0.9085	1.3830	-1.7317	-0.6745	-1.5932	-1.5932	-0.9085
CAN_MH	-1.3092	-1.0364	-2.0004	-1.3597	1.9145	-1.1868	0.7124	-1.9145	-1.5932	-1.8895	-1.8027	-0.1992
AJA_MH	-0.8416	-0.4307	-1.5932	-1.6449	1.6449	0.0000	0.8416	-1.2206	-1.5932	-1.6449	-1.5932	0.3186
MAJ_MH	-1.5932	-0.4307	-1.2206	-0.6745	1.2206	-0.4307	0.1800	-1.5932	-1.2206	-1.5932	-1.2206	1.2206
ANC_MH	-1.2314	-1.1281	-1.4835	-1.2016	0.8296	-0.7835	0.4917	-2.1347	-1.2909	-1.8413	-2.0699	-1.5011
ANC_LIP	-1.3352	-1.3352	-2.3619	-2.0928	1.1394	-0.4307	0.5024	-1.7862	-1.4461	-1.7862	-2.0699	0.0000

Table 6.8. Tetrachoric correlation matrix for all samples.

	T1	T2	T3	T5	T6	T7	T8	T9	T11	T12	T13
T1	1.0000										
T2	-0.1242	1.0000									
T3	0.1171	-0.7497	1.0000								
T5	0.0502	-0.0273	0.0960	1.0000							
T6	-0.1916	0.0632	-0.0950	-0.1380	1.0000						
T7	-0.0767	-0.0295	-0.0281	-0.0543	0.0519	1.0000					
T8	0.1837	-0.0655	0.0855	0.2272	-0.2841	-0.0048	1.0000				
T9	0.1876	-0.1395	0.0875	0.1258	-0.2897	0.0084	0.2178	1.0000			
T11	0.1627	-0.0079	-0.0106	0.1229	-0.2777	0.0722	0.2586	0.3426	1.0000		
T12	0.1562	-0.0842	0.0539	-0.0161	-0.1464	-0.0910	0.2135	0.3512	0.2673	1.0000	
T13	0.1405	0.1028	-0.0295	-0.0275	-0.0555	-0.0257	0.1102	0.1447	0.0955	0.3329	1.0000
T14	0.1202	-0.0027	0.0071	0.2060	-0.2339	-0.0482	0.2328	0.3755	0.2012	0.3006	-0.0194
T15	0.0909	0.0093	-0.0029	0.0527	-0.2590	-0.0411	0.1604	0.2503	0.1927	0.1505	-0.0344
T18	0.0824	-0.0467	0.0789	0.0611	-0.1923	-0.0069	0.1078	0.1866	0.1448	0.1957	-0.0456
T19	0.1646	-0.0274	-0.0398	0.1956	-0.3782	-0.0073	0.2915	0.2974	0.2521	0.1355	0.0622
T20	-0.1470	0.0194	-0.0167	-0.0037	0.1908	-0.1018	-0.0052	-0.1217	-0.1364	-0.0317	0.0870
T21	0.2588	-0.0952	0.0284	0.1235	-0.1470	-0.0194	0.0987	0.1494	0.1376	0.0930	0.0633
T22	-0.0244	-0.0917	0.1149	0.0238	0.1432	-0.0689	-0.1818	-0.1422	0.0203	-0.1402	0.0493
T25	0.2253	-0.0731	0.0175	0.2515	-0.3648	-0.0667	0.2286	0.3110	0.2811	0.1644	-0.0229
T26	0.1884	-0.0591	-0.0065	0.2701	-0.3028	0.0249	0.2775	0.3057	0.2745	0.1391	-0.0345
T30	0.1804	-0.1692	0.0086	0.1824	-0.2598	-0.0656	0.3071	0.2903	0.3088	0.1341	-0.1098
T31	0.0850	-0.0649	0.0512	0.3451	-0.3924	-0.0264	0.3249	0.3209	0.3998	0.2546	-0.0535
T33	-0.0278	-0.0754	0.0645	-0.0056	-0.0521	0.0054	0.0689	0.0443	0.0164	-0.1300	0.0488

Table 6.8 continued. Tetrachoric correlation matrix for all samples.

	T14	**T15**	**T18**	**T19**	**T20**	**T21**	**T22**	**T25**	**T26**	**T30**	**T31**	**T33**
T14	1.0000											
T15	0.3721	1.0000										
T18	0.1490	0.1587	1.0000									
T19	0.3192	0.1864	0.1045	1.0000								
T20	-0.0931	-0.1633	-0.0478	-0.2443	1.0000							
T21	0.2257	0.0586	0.0710	0.2172	-0.1190	1.0000						
T22	-0.0687	-0.1951	-0.0476	-0.1276	-0.0319	-0.0480	1.0000					
T25	0.3262	0.3286	0.2121	0.3256	-0.2064	0.2318	-0.2606	1.0000				
T26	0.3382	0.2430	0.1245	0.4517	-0.1139	0.0773	-0.1451	0.3521	1.0000			
T30	0.2907	0.1332	0.1572	0.2857	-0.1067	0.0595	-0.1402	0.3558	0.2336	1.0000		
T31	0.3907	0.3663	0.2781	0.3616	-0.2841	0.1822	-0.2386	0.5049	0.2768	0.4398	1.0000	
T33	-0.1391	-0.0178	-0.0872	0.1144	-0.0727	-0.0141	0.1172	-0.0282	-0.1120	0.0608	-0.0543	1.0000

Table 6.9. Tetrachoric correlation matrix for all samples (AJA_MH and BER_LIP excluded).

	T1	**T2**	**T3**	**T5**	**T6**	**T7**	**T8**	**T9**	**T11**	**T12**	**T13**
T1	1.0000										
T2	-0.1296	1.0000									
T3	0.1221	-0.7701	1.0000								
T5	0.0525	-0.0285	0.1005	1.0000							
T6	-0.2002	0.0511	-0.0993	-0.1441	1.0000						
T7	-0.0796	-0.0451	-0.0350	-0.0565	0.0539	1.0000					
T8	0.1923	-0.0539	0.0915	0.2385	-0.2817	0.0034	1.0000				
T9	0.1958	-0.1357	0.0932	0.1318	-0.2877	0.0228	0.2280	1.0000			
T11	0.1694	-0.0082	-0.0111	0.1285	-0.2900	0.0749	0.2702	0.3570	1.0000		
T12	0.1623	-0.0734	0.0560	-0.0168	-0.1392	-0.0820	0.2075	0.3511	0.2773	1.0000	
T13	0.1460	0.1156	-0.0408	-0.0287	-0.0556	-0.0246	0.1051	0.1467	0.0991	0.3423	1.0000
T14	0.1254	0.0119	0.0074	0.2157	-0.2309	-0.0375	0.2434	0.3919	0.2096	0.2985	-0.0242
T15	0.0952	-0.0113	-0.0092	0.0554	-0.2674	-0.0361	0.1725	0.2561	0.2014	0.1528	-0.0194
T18	0.0863	-0.0602	0.0763	0.0642	-0.2010	-0.0211	0.1064	0.1958	0.1515	0.2044	-0.0476
T19	0.1710	-0.0285	-0.0464	0.2040	-0.3940	-0.0119	0.2926	0.3093	0.2616	0.1408	0.0696
T20	-0.1531	0.0242	-0.0143	-0.0039	0.1991	-0.1053	0.0078	-0.1202	-0.1418	-0.0262	0.0952
T21	0.2688	-0.0902	0.0397	0.1290	-0.1529	-0.0328	0.0800	0.1508	0.1428	0.0919	0.0634
T22	-0.0253	-0.1071	0.1221	0.0248	0.1352	-0.0859	-0.1812	-0.1330	0.0210	-0.1456	0.0525
T25	0.2349	-0.0763	0.0182	0.2630	-0.3813	-0.0691	0.2390	0.3245	0.2927	0.1709	-0.0238
T26	0.1963	-0.0635	-0.0086	0.2824	-0.3162	0.0136	0.2690	0.3046	0.2857	0.1322	-0.0339
T30	0.1878	-0.1654	0.0138	0.1909	-0.2707	-0.0678	0.3092	0.2915	0.3210	0.1394	-0.1189
T31	0.0887	-0.0796	0.0467	0.3621	-0.4102	-0.0273	0.3327	0.3350	0.4163	0.2651	-0.0512
T33	-0.0291	-0.0691	0.0835	-0.0059	-0.0544	0.0200	0.0715	0.0390	0.0172	-0.1408	0.0438

Table 6.9 continued. Tetrachoric correlation matrix for all samples (AJA_MH and BER_LIP excluded).

	T14	T15	T18	T19	T20	T21	T22	T25	T26	T30	T31	T33
T14	1.0000											
T15	0.3846	1.0000										
T18	0.1563	0.1600	1.0000									
T19	0.3324	0.1999	0.1091	1.0000								
T20	-0.0903	-0.1613	-0.0306	-0.2453	1.0000							
T21	0.2303	0.0717	0.0674	0.2252	-0.1115	1.0000						
T22	-0.0561	-0.1959	-0.0497	-0.1298	-0.0421	-0.0523	1.0000					
T25	0.3400	0.3435	0.2221	0.3383	-0.2148	0.2412	-0.2705	1.0000				
T26	0.3399	0.2438	0.1115	0.4606	-0.1011	0.0743	-0.1357	0.3669	1.0000			
T30	0.2921	0.1390	0.1645	0.2969	-0.1063	0.0572	-0.1454	0.3710	0.2434	1.0000		
T31	0.4078	0.3756	0.2703	0.3668	-0.2775	0.1835	-0.2456	0.5271	0.2699	0.4602	1.0000	
T33	-0.1509	-0.0096	-0.0915	0.1192	-0.0907	-0.0171	0.1273	-0.0294	-0.0978	0.0538	-0.0346	1.0000

Table 6.10. Tetrachoric correlation matrix for all Middle Horizon samples.

	T1	**T2**	**T3**	**T5**	**T6**	**T7**	**T8**	**T9**	**T11**	**T12**	**T13**
T1	1.0000										
T2	-0.1306	1.0000									
T3	0.1102	-0.7796	1.0000								
T5	0.0000	-0.0921	0.1440	1.0000							
T6	-0.1308	0.1368	-0.0528	-0.2112	1.0000						
T7	-0.1205	-0.1421	-0.1046	0.0570	0.1690	1.0000					
T8	0.0391	0.0924	-0.1230	0.1838	-0.2645	0.0472	1.0000				
T9	0.1360	-0.2589	0.1136	0.1589	-0.5206	-0.1253	0.1653	1.0000			
T11	0.2198	0.0453	-0.0873	0.1171	-0.2717	0.0638	0.1429	0.2873	1.0000		
T12	0.0732	-0.0562	0.0524	0.0369	-0.1928	0.1039	0.1236	0.2773	0.1964	1.0000	
T13	-0.0320	0.0873	-0.0345	0.0636	0.0609	-0.0749	0.0458	-0.0001	0.0240	0.3910	1.0000
T14	0.0247	-0.0614	0.0043	0.0026	-0.3696	-0.0152	0.0595	0.3622	0.0605	0.2224	0.0092
T15	0.0457	0.0392	0.0056	0.0050	-0.3618	-0.0744	0.0287	0.3879	0.1127	0.1488	0.0328
T18	0.0000	0.0029	0.0718	0.0439	-0.2489	0.0300	-0.0045	0.2687	0.1733	0.1694	-0.1569
T19	0.2378	0.0385	-0.0103	0.0669	-0.3925	0.0272	0.1306	0.2941	0.0361	-0.0533	0.0033
T20	-0.2321	0.1267	0.0851	0.1427	0.2884	-0.1194	-0.0204	-0.2991	-0.0502	-0.1928	-0.0419
T21	0.2388	-0.2165	0.0182	0.0659	-0.2460	-0.1246	-0.0835	0.3246	0.0423	0.1130	0.0828
T22	-0.0498	0.0303	0.0781	-0.1650	0.2131	-0.1106	-0.2070	-0.2209	0.0473	-0.0808	0.0870
T25	0.3759	-0.0681	0.0306	0.1932	-0.4081	-0.1023	0.1794	0.4462	0.3465	0.1838	0.0197
T26	0.2371	-0.0351	-0.1014	0.2107	-0.3541	-0.0258	0.2265	0.4105	0.2310	0.1141	0.1111
T30	0.2692	-0.1051	-0.0328	0.1204	-0.2760	0.0192	0.2293	0.2784	0.2784	0.0889	-0.0480
T31	0.0000	-0.1009	0.0442	0.1721	-0.4053	-0.0834	0.2017	0.4214	0.3733	0.1614	-0.0198
T33	0.0999	-0.1809	0.1814	0.1069	-0.3093	0.0164	0.0562	0.3003	0.0309	0.0036	0.1713

Table 6.10 continued. Tetrachoric correlation matrix for all Middle Horizon samples.

	T14	**T15**	**T18**	**T19**	**T20**	**T21**	**T22**	**T25**	**T26**	**T30**	**T31**	**T33**
T14	1.0000											
T15	0.3133	1.0000										
T18	0.2441	0.1605	1.0000									
T19	0.1304	0.0561	0.0020	1.0000								
T20	-0.0639	-0.1197	-0.0359	-0.1700	1.0000							
T21	-0.0090	-0.1027	-0.0082	0.1200	-0.0387	1.0000						
T22	-0.1539	-0.3380	-0.0018	-0.0685	0.0001	-0.2169	1.0000					
T25	0.2379	0.3368	0.3198	0.1788	-0.2787	0.2331	-0.1653	1.0000				
T26	0.2423	0.2325	0.0819	0.4027	-0.0785	0.1852	-0.2869	0.2750	1.0000			
T30	0.1260	0.0819	0.1475	0.0889	-0.1468	0.0261	-0.0819	0.3035	0.3087	1.0000		
T31	0.2274	0.2726	0.3354	0.1754	-0.2237	0.1272	-0.1176	0.4595	0.3044	0.3009	1.0000	
T33	0.0249	0.0176	0.0047	0.3735	-0.3159	-0.0063	0.1591	0.2117	0.0098	0.1794	0.1620	1.0000

Table 6.11. Tetrachoric correlation matrix for all Middle Horizon samples (AJA_MH excluded).

	T1	T2	T3	T5	T6	T7	T8	T9	T11	T12	T13
T1	1.0000										
T2	-0.1372	1.0000									
T3	0.1157	-0.8001	1.0000								
T5	0.0000	-0.0968	0.1514	1.0000							
T6	-0.1371	0.1091	-0.0553	-0.2210	1.0000						
T7	-0.1261	-0.1681	-0.1186	0.0597	0.1765	1.0000					
T8	0.0414	0.1249	-0.1254	0.1946	-0.2395	0.0882	1.0000				
T9	0.1432	-0.2487	0.1241	0.1675	-0.5110	-0.0974	0.1755	1.0000			
T11	0.2300	0.0475	-0.0914	0.1227	-0.2840	0.0668	0.1508	0.3012	1.0000		
T12	0.0766	-0.0253	0.0548	0.0387	-0.1707	0.1370	0.0916	0.2563	0.2047	1.0000	
T13	-0.0335	0.1006	-0.0553	0.0667	0.0688	-0.0733	0.0377	-0.0097	0.0250	0.4005	1.0000
T14	0.0259	-0.0275	0.0046	0.0027	-0.3542	0.0153	0.0629	0.3811	0.0634	0.1972	-0.0005
T15	0.0485	0.0309	-0.0098	0.0053	-0.3717	-0.0560	0.0144	0.3962	0.1189	0.1463	0.0407
T18	0.0000	0.0031	0.0755	0.0464	-0.2601	0.0314	-0.0048	0.2834	0.1815	0.1774	-0.1644
T19	0.2486	0.0403	-0.0108	0.0700	-0.4099	0.0284	0.1377	0.3083	0.0377	-0.0558	0.0035
T20	-0.2419	0.1167	0.0823	0.1497	0.3000	-0.1239	-0.0039	-0.2964	-0.0521	-0.1854	-0.0226
T21	0.2474	-0.2138	0.0189	0.0686	-0.2541	-0.1285	-0.0990	0.3261	0.0436	0.1063	0.0941
T22	-0.0522	-0.0024	0.0819	-0.1730	0.1916	-0.1446	-0.1788	-0.1964	0.0494	-0.0848	0.1008
T25	0.3948	-0.0716	0.0322	0.2028	-0.4278	-0.1070	0.1898	0.4700	0.3625	0.1923	0.0207
T26	0.2485	-0.0166	-0.0969	0.2210	-0.3704	-0.0270	0.1999	0.3951	0.2414	0.0886	0.1110
T30	0.2791	-0.0845	-0.0232	0.1256	-0.2852	0.0198	0.2111	0.2635	0.2876	0.0924	-0.0612
T31	0.0000	-0.1057	0.0463	0.1810	-0.4226	-0.0868	0.2117	0.4416	0.3883	0.1691	-0.0208
T33	0.1044	-0.1933	0.2118	0.1119	-0.3218	0.0172	0.0403	0.2974	0.0324	-0.0084	0.1617

Table 6.11 continued. Tetrachoric correlation matrix for all Middle Horizon samples (AJA_MH excluded).

	T14	**T15**	**T18**	**T19**	**T20**	**T21**	**T22**	**T25**	**T26**	**T30**	**T31**	**T33**
T14	1.0000											
T15	0.3199	1.0000										
T18	0.2570	0.1703	1.0000									
T19	0.1371	0.0592	0.0021	1.0000								
T20	-0.0496	-0.1181	-0.0377	-0.1775	1.0000							
T21	-0.0213	-0.1072	-0.0085	0.1245	-0.0254	1.0000						
T22	-0.1238	-0.3463	-0.0019	-0.0718	-0.0161	-0.2142	1.0000					
T25	0.2495	0.3561	0.3359	0.1869	-0.2902	0.2426	-0.1733	1.0000				
T26	0.2211	0.2347	0.0859	0.4204	-0.0817	0.1924	-0.2686	0.2889	1.0000			
T30	0.1035	0.0855	0.1537	0.0923	-0.1414	0.0162	-0.0851	0.3162	0.3211	1.0000		
T31	0.2383	0.2858	0.3532	0.1838	-0.2346	0.1333	-0.1234	0.4817	0.3192	0.3159	1.0000	
T33	0.0128	0.0235	0.0049	0.3888	-0.3171	-0.0277	0.1783	0.2209	0.0103	0.1641	0.1692	1.0000

Table 6.12. Tetrachoric correlation matrix for all Late Intermediate Period samples.

	T1	**T2**	**T3**	**T5**	**T6**	**T7**	**T8**	**T9**	**T11**	**T12**	**T13**
T1	1.0000										
T2	-0.1194	1.0000									
T3	0.1223	-0.7274	1.0000								
T5	0.0881	0.0212	0.0602	1.0000							
T6	-0.2392	0.0061	-0.1277	-0.0846	1.0000						
T7	-0.0437	0.0547	0.0291	-0.1379	-0.0381	1.0000					
T8	0.2805	-0.1697	0.2231	0.2564	-0.2976	-0.0392	1.0000				
T9	0.2247	-0.0543	0.0689	0.1022	-0.1189	0.1049	0.2510	1.0000			
T11	0.1208	-0.0467	0.0452	0.1271	-0.2822	0.0785	0.3328	0.3814	1.0000		
T12	0.2181	-0.1050	0.0550	-0.0557	-0.1105	-0.2333	0.2725	0.4036	0.3177	1.0000	
T13	0.2662	0.1139	-0.0258	-0.0941	-0.1427	0.0099	0.1518	0.2449	0.1455	0.2910	1.0000
T14	0.1846	0.0365	0.0089	0.3454	-0.1389	-0.0705	0.3415	0.3842	0.2920	0.3533	-0.0383
T15	0.1200	-0.0099	-0.0084	0.0842	-0.1897	-0.0194	0.2427	0.1630	0.2431	0.1516	-0.0761
T18	0.1465	-0.0848	0.0843	0.0742	-0.1477	-0.0352	0.1842	0.1264	0.1234	0.2160	0.0365
T19	0.1087	-0.0775	-0.0623	0.2943	-0.3669	-0.0332	0.3992	0.2997	0.4081	0.2757	0.1050
T20	-0.0836	-0.0598	-0.0919	-0.1112	0.1173	-0.0888	0.0049	0.0035	-0.1988	0.0846	0.1791
T21	0.2739	-0.0044	0.0360	0.1664	-0.0709	0.0592	0.2213	0.0247	0.2068	0.0786	0.0494
T22	-0.0049	-0.1842	0.1427	0.1702	0.0877	-0.0373	-0.1649	-0.0854	0.0005	-0.1845	0.0220
T25	0.1243	-0.0765	0.0087	0.2912	-0.3348	-0.0428	0.2581	0.2252	0.2386	0.1516	-0.0501
T26	0.1545	-0.0756	0.0592	0.3114	-0.2656	0.0600	0.3092	0.2380	0.3035	0.1562	-0.1310
T30	0.1111	-0.2189	0.0407	0.2295	-0.2469	-0.1298	0.3601	0.2988	0.3313	0.1683	-0.1557
T31	0.1350	-0.0435	0.0552	0.4517	-0.3846	0.0074	0.3956	0.2627	0.4150	0.3103	-0.0730
T33	-0.1269	0.0056	-0.0253	-0.0906	0.1410	-0.0030	0.0776	-0.1421	0.0056	-0.2320	-0.0417

Table 6.12 continued. Tetrachoric correlation matrix for all Late Intermediate Period samples.

	T14	T15	T18	T19	T20	T21	T22	T25	T26	T30	T31	T33
T14	1.0000											
T15	0.4087	1.0000										
T18	0.0844	0.1575	1.0000									
T19	0.4479	0.2702	0.1850	1.0000								
T20	-0.1124	-0.1906	-0.0566	-0.2988	1.0000							
T21	0.3808	0.1598	0.1313	0.2896	-0.1774	1.0000						
T22	-0.0113	-0.1041	-0.0833	-0.1723	-0.0555	0.0772	1.0000					
T25	0.3812	0.3237	0.1369	0.4241	-0.1590	0.2309	-0.3235	1.0000				
T26	0.3985	0.2494	0.1555	0.4856	-0.1378	0.0031	-0.0478	0.4026	1.0000			
T30	0.4026	0.1665	0.1647	0.4382	-0.0767	0.0849	-0.1849	0.3917	0.1800	1.0000		
T31	0.4853	0.4194	0.2431	0.4719	-0.3186	0.2137	-0.3095	0.5310	0.2609	0.5223	1.0000	
T33	-0.2514	-0.0414	-0.1595	-0.0864	0.1138	-0.0202	0.0846	-0.1971	-0.1995	-0.0337	-0.1890	1.0000

Table 6.13. Tetrachoric correlation matrix for all Late Intermediate Period samples (no BER_LIP).

	T1	T2	T3	T5	T6	T7	T8	T9	T11	T12	T13
T1	1.0000										
T2	-0.1239	1.0000									
T3	0.1269	-0.7479	1.0000								
T5	0.0920	0.0221	0.0628	1.0000							
T6	-0.2493	0.0064	-0.1331	-0.0883	1.0000						
T7	-0.0450	0.0455	0.0265	-0.1427	-0.0394	1.0000					
T8	0.2913	-0.1694	0.2317	0.2676	-0.3105	-0.0515	1.0000				
T9	0.2331	-0.0564	0.0715	0.1066	-0.1240	0.1080	0.2606	1.0000			
T11	0.1254	-0.0485	0.0469	0.1328	-0.2946	0.0808	0.3457	0.3958	1.0000		
T12	0.2256	-0.1086	0.0569	-0.0579	-0.1149	-0.2394	0.2822	0.4175	0.3286	1.0000	
T13	0.2752	0.1263	-0.0304	-0.0978	-0.1483	0.0102	0.1479	0.2531	0.1504	0.3009	1.0000
T14	0.1918	0.0379	0.0092	0.3609	-0.1450	-0.0727	0.3549	0.3989	0.3033	0.3655	-0.0396
T15	0.1245	-0.0378	-0.0088	0.0880	-0.1980	-0.0235	0.2690	0.1692	0.2525	0.1568	-0.0559
T18	0.1530	-0.1085	0.0768	0.0776	-0.1545	-0.0609	0.1811	0.1321	0.1290	0.2250	0.0379
T19	0.1124	-0.0802	-0.0732	0.3062	-0.3815	-0.0416	0.3944	0.3101	0.4221	0.2852	0.1172
T20	-0.0870	-0.0439	-0.0853	-0.1164	0.1227	-0.0917	0.0156	0.0037	-0.2070	0.0877	0.1786
T21	0.2850	0.0027	0.0553	0.1742	-0.0742	0.0388	0.2004	0.0257	0.2154	0.0815	0.0415
T22	-0.0051	-0.1852	0.1521	0.1765	0.0908	-0.0422	-0.1828	-0.0881	0.0006	-0.1903	0.0180
T25	0.1290	-0.0794	0.0091	0.3038	-0.3492	-0.0441	0.2679	0.2336	0.2477	0.1568	-0.0518
T26	0.1603	-0.0956	0.0518	0.3249	-0.2770	0.0412	0.3114	0.2469	0.3151	0.1616	-0.1289
T30	0.1159	-0.2285	0.0425	0.2408	-0.2590	-0.1343	0.3760	0.3117	0.3459	0.1750	-0.1617
T31	0.1406	-0.0643	0.0469	0.4732	-0.4027	0.0076	0.4017	0.2736	0.4324	0.3220	-0.0686
T33	-0.1327	0.0263	-0.0150	-0.0948	0.1475	0.0221	0.0929	-0.1486	0.0058	-0.2419	-0.0435

Table 6.13, continued. Tetrachoric correlation matrix for all Late Intermediate Period samples (no BER_LIP).

	T14	**T15**	**T18**	**T19**	**T20**	**T21**	**T22**	**T25**	**T26**	**T30**	**T31**	**T33**
T14	1.0000											
T15	0.4242	1.0000										
T18	0.0883	0.1532	1.0000									
T19	0.4634	0.2886	0.1927	1.0000								
T20	-0.1170	-0.1881	-0.0254	-0.2947	1.0000							
T21	0.3965	0.1837	0.1255	0.3003	-0.1743	1.0000						
T22	-0.0117	-0.1026	-0.0864	-0.1729	-0.0611	0.0671	1.0000					
T25	0.3960	0.3360	0.1430	0.4388	-0.1654	0.2403	-0.3337	1.0000				
T26	0.4139	0.2493	0.1300	0.4882	-0.1142	-0.0071	-0.0457	0.4175	1.0000			
T30	0.4202	0.1737	0.1729	0.4557	-0.0800	0.0886	-0.1914	0.4087	0.1878	1.0000		
T31	0.5054	0.4262	0.2200	0.4742	-0.3019	0.2120	-0.3161	0.5529	0.2419	0.5455	1.0000	
T33	-0.2633	-0.0316	-0.1674	-0.0901	0.0841	-0.0086	0.0878	-0.2061	-0.1756	-0.0354	-0.1621	1.0000

Table 6.14. Tetrachoric correlation matrix for all Andahuaylas samples.

	T1	**T2**	**T3**	**T5**	**T6**	**T7**	**T8**	**T9**	**T11**	**T12**	**T13**
T1	1.0000										
T2	-0.1127	1.0000									
T3	0.1886	-0.7656	1.0000								
T5	0.1196	0.1307	-0.0431	1.0000							
T6	-0.1772	-0.0527	-0.1069	-0.1496	1.0000						
T7	-0.0208	0.0085	0.0338	-0.1360	-0.0617	1.0000					
T8	0.4155	-0.2278	0.2022	0.1989	-0.2503	-0.1574	1.0000				
T9	0.3168	-0.1109	0.1500	0.0966	-0.1101	0.0834	0.1450	1.0000			
T11	0.1300	-0.1646	0.2316	0.1258	-0.2561	0.0712	0.2096	0.3590	1.0000		
T12	0.3393	-0.1265	0.1002	0.0264	-0.2110	-0.1787	0.1618	0.4789	0.3005	1.0000	
T13	0.3445	-0.0483	0.0395	0.0664	-0.1957	0.1271	0.0884	0.3121	0.1203	0.2598	1.0000
T14	0.2203	0.0202	0.0326	0.3699	-0.1538	-0.2108	0.2893	0.5214	0.3290	0.4235	0.1282
T15	0.0193	0.0373	-0.0086	0.1355	-0.0884	-0.0980	0.0249	0.0451	0.0522	0.0644	-0.0452
T18	0.1600	-0.1146	0.1444	0.1902	-0.1060	-0.0585	0.2505	0.2458	0.1269	0.2717	0.0464
T19	0.0887	-0.0851	-0.0582	0.3087	-0.3042	-0.0084	0.3160	0.1840	0.2865	0.2697	0.0711
T20	0.0053	-0.1531	-0.0308	-0.1023	0.0542	0.1730	0.1209	0.0813	-0.0211	-0.0210	0.1620
T21	0.2446	-0.0500	0.2982	0.2471	-0.0515	0.0436	0.2246	0.0419	0.2246	0.0910	-0.0598
T22	0.0475	-0.2544	0.1568	0.1170	0.0870	-0.0704	-0.0764	0.0715	0.0633	-0.1786	-0.0638
T25	0.0366	0.0057	-0.0485	0.2644	-0.2598	-0.1135	0.1491	0.1556	0.1549	0.1769	-0.0357
T26	0.2186	-0.0735	0.0719	0.4294	-0.2577	0.0742	0.3417	0.2765	0.2824	0.2766	-0.1197
T30	0.1957	-0.1752	0.1512	0.2622	-0.3463	-0.1752	0.3923	0.3246	0.3277	0.3019	-0.1555
T31	0.2086	-0.0204	0.1060	0.4480	-0.3505	0.0294	0.3645	0.1959	0.4076	0.4449	-0.0487
T33	-0.0429	0.0430	-0.0081	-0.1658	0.0608	0.0547	0.1011	-0.1236	0.0697	-0.0748	0.0731

Table 6.14 continued. Tetrachoric correlation matrix for all Andahuaylas samples.

	T14	**T15**	**T18**	**T19**	**T20**	**T21**	**T22**	**T25**	**T26**	**T30**	**T31**	**T33**
T14	1.0000											
T15	0.4239	1.0000										
T18	0.0815	0.0971	1.0000									
T19	0.4930	0.1253	0.2743	1.0000								
T20	-0.1712	-0.2648	-0.0664	-0.3060	1.0000							
T21	0.3795	0.2895	0.2376	0.3034	-0.3055	1.0000						
T22	-0.1834	0.1108	-0.1463	-0.1717	0.0090	0.1432	1.0000					
T25	0.4375	0.2274	0.1749	0.3866	-0.0673	0.2412	-0.4712	1.0000				
T26	0.5335	0.2019	0.1142	0.5376	0.0189	0.0889	-0.2154	0.4542	1.0000			
T30	0.5581	0.1560	0.3226	0.4232	-0.0210	0.1968	-0.2155	0.4534	0.1573	1.0000		
T31	0.6299	0.3756	0.3185	0.4184	-0.2343	0.3320	-0.4234	0.5357	0.0713	0.6036	1.0000	
T33	-0.3594	-0.1592	-0.1669	-0.0934	0.1167	-0.0418	-0.0155	-0.2044	-0.0491	-0.2249	-0.2095	1.0000

Table 6.15. Tetrachoric correlation matrix for Andahuaylas Late Intermediate Period samples.

	T1	**T2**	**T3**	**T5**	**T6**	**T7**	**T8**	**T9**	**T11**	**T12**	**T13**
T1	1.0000										
T2	-0.1228	1.0000									
T3	0.2056	-0.7584	1.0000								
T5	0.1292	0.1982	-0.0901	1.0000							
T6	-0.1914	-0.0569	-0.1154	-0.1603	1.0000						
T7	-0.0226	-0.0486	0.1143	-0.1023	-0.0667	1.0000					
T8	0.4405	-0.2416	0.2144	0.2096	-0.2660	-0.1671	1.0000				
T9	0.3443	-0.1208	0.1633	0.1043	-0.1189	0.0908	0.1535	1.0000			
T11	0.1414	-0.1795	0.2525	0.1360	-0.2769	0.0775	0.2221	0.3899	1.0000		
T12	0.3672	-0.1372	0.1087	0.0283	-0.2264	-0.1934	0.1705	0.5176	0.3248	1.0000	
T13	0.3725	-0.0028	0.0146	0.0712	-0.2099	0.1133	0.0930	0.3370	0.1299	0.2806	1.0000
T14	0.2367	0.0504	0.0213	0.3669	-0.1650	-0.2481	0.3045	0.5595	0.3531	0.4548	0.1244
T15	0.0205	0.0649	-0.0210	0.1069	-0.0941	-0.0790	0.0261	0.0478	0.0553	0.0683	-0.0593
T18	0.1679	-0.1202	0.1514	0.2000	-0.1115	-0.0615	0.2603	0.2578	0.1332	0.2825	0.0482
T19	0.0960	-0.0923	-0.0631	0.3316	-0.3267	-0.0091	0.3328	0.1990	0.3098	0.2917	0.0769
T20	0.0057	-0.1725	-0.0457	-0.0688	0.0584	0.1426	0.1278	0.0877	-0.0228	-0.0225	0.1552
T21	0.2646	-0.0542	0.3233	0.2665	-0.0556	0.0472	0.2376	0.0453	0.2427	0.0976	-0.0641
T22	0.0513	-0.3243	0.2001	0.1579	0.0930	-0.0905	-0.0801	0.0770	0.0683	-0.1926	-0.0398
T25	0.0393	0.0061	-0.0521	0.2854	-0.2782	-0.1220	0.1568	0.1668	0.1661	0.1887	-0.0381
T26	0.2363	-0.0517	0.0618	0.4277	-0.2782	0.0962	0.3618	0.2984	0.3049	0.2970	-0.1390
T30	0.2095	-0.1877	0.1620	0.2783	-0.3710	-0.1874	0.4128	0.3468	0.3503	0.3228	-0.1661
T31	0.2189	-0.0214	0.1114	0.4699	-0.3675	0.0308	0.3765	0.2053	0.4273	0.4666	-0.0510
T33	-0.0459	0.0717	-0.0510	-0.1833	0.0644	0.0854	0.1060	-0.1320	0.0745	-0.0794	0.0604

Table 6.15 continued. Tetrachoric correlation matrix for Andahuaylas Late Intermediate Period samples.

	T14	**T15**	**T18**	**T19**	**T20**	**T21**	**T22**	**T25**	**T26**	**T30**	**T31**	**T33**
T14	1.0000											
T15	0.4247	1.0000										
T18	0.0847	0.1010	1.0000									
T19	0.5295	0.1328	0.2854	1.0000								
T20	-0.1662	-0.2467	-0.0698	-0.3280	1.0000							
T21	0.4038	0.3033	0.2500	0.3257	-0.3300	1.0000						
T22	-0.1648	0.1365	-0.1509	-0.1851	0.0270	0.1527	1.0000					
T25	0.4664	0.2392	0.1835	0.4124	-0.0715	0.2568	-0.5006	1.0000				
T26	0.5374	0.2139	0.1198	0.5774	0.0383	0.0953	-0.1989	0.4866	1.0000			
T30	0.5912	0.1639	0.3364	0.4527	-0.0224	0.2102	-0.2289	0.4767	0.1667	1.0000		
T31	0.6602	0.3906	0.3316	0.4390	-0.2456	0.3479	-0.4410	0.5573	0.0747	0.6294	1.0000	
T33	-0.3421	-0.1368	-0.1762	-0.0990	0.0988	-0.0450	-0.0257	-0.2181	-0.0283	-0.2374	-0.2206	1.0000

Table 6.16. Mahalanobis D^2 matrix for all samples.

	CON_MH	AYA_LIP	HUA_MH	MAR_LIP	TUR_MH	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP	AJA_MH	CAH_MH	CAN_MH	MAJ_MH	BER_MH	BER_LIP	ANC_MH	ANC_LIP
CON_MH	0.0000																
AYA_LIP	7.8440	0.0000															
HUA_MH	15.2498	12.7236	0.0000														
MAR_LIP	12.5299	10.2552	9.0349	0.0000													
TUR_MH	7.9603	8.2905	8.7576	5.0582	0.0000												
SON_LIP	9.5547	8.8797	9.0467	10.1499	7.6849	0.0000											
MPM_LIP	6.3294	7.0194	11.2597	10.3898	6.4858	9.6390	0.0000										
PUC_LIP	9.0815	9.0495	11.6690	6.8319	3.7615	6.7422	8.3121	0.0000									
RCC_LIP	10.5443	8.7697	13.4516	10.2808	6.7702	7.1306	3.0692	9.0766	0.0000								
AJA_MH	11.6830	11.3939	13.8776	18.6392	12.0668	12.5447	13.2361	16.9752	14.4156	0.0000							
CAH_MH	8.0062	7.5125	11.8110	15.2988	10.0266	8.9318	11.6598	11.5287	14.5053	5.9602	0.0000						
CAN_MH	10.2219	10.0799	14.6321	17.5133	9.9787	12.9308	9.1031	13.7944	10.5086	7.3002	7.1068	0.0000					
MAJ_MH	9.7374	10.6410	6.2223	10.6671	7.2242	6.8751	9.9664	9.9562	11.3866	10.2406	5.6318	7.5664	0.0000				
BER_MH	13.9918	10.1063	14.2247	12.1202	8.7707	10.2040	12.6355	9.8038	13.7973	17.1646	8.6817	9.9297	7.6837	0.0000			
BER_LIP	20.7315	13.3958	23.5414	18.0913	16.4307	17.8152	17.2927	15.8912	17.1276	30.4849	22.2900	17.7076	18.7774	8.2883	0.0000		
ANC_MH	11.7605	17.4667	19.6455	15.9295	11.7880	11.3061	18.2250	15.0724	17.0184	12.9538	12.6244	9.4875	8.5004	12.9502	21.2594	0.0000	
ANC_LIP	10.0993	11.8968	5.7356	11.6319	9.1963	6.8880	13.3303	10.1364	15.9229	8.8426	6.5583	9.7261	4.7891	9.6250	21.4912	9.8258	0.0000

Table 6.17. Mahalanobis D^2 matrix for all samples (AJA_MH and BER_LIP excluded).

	CON_MH	AYA_LIP	HUA_MH	MAR_LIP	TUR_MH	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP	CAH_MH	CAN_MH	MAJ_MH	BER_MH	ANC_MH	ANC_LIP
CON_MH	0.0000														
AYA_LIP	7.7932	0.0000													
HUA_MH	15.4444	12.9955	0.0000												
MAR_LIP	12.6110	10.4492	9.3532	0.0000											
TUR_MH	8.2017	8.5128	8.8193	5.0700	0.0000										
SON_LIP	10.2206	9.4127	9.0546	10.4455	7.8651	0.0000									
MPM_LIP	6.4810	7.0585	11.5258	10.7007	6.9012	10.4132	0.0000								
PUC_LIP	9.7615	9.7804	12.1400	7.1657	4.0227	7.0204	9.3740	0.0000							
RCC_LIP	10.8462	8.8832	13.4898	10.5164	7.1338	7.6639	3.1379	10.0254	0.0000						
CAH_MH	8.3133	7.6977	11.8696	15.6283	10.3649	9.4235	11.8931	12.5608	14.6692	0.0000					
CAN_MH	10.3505	10.1587	14.7491	17.8486	10.3755	13.4983	9.1632	14.8952	10.4937	7.1995	0.0000				
MAJ_MH	10.2012	11.0403	6.1523	10.9249	7.4300	6.9858	10.3972	10.5530	11.5904	5.8035	7.9170	0.0000			
BER_MH	14.6246	10.7541	14.3906	12.2559	8.8701	10.1404	13.6745	9.6669	14.5876	9.4966	11.0350	8.1050	0.0000		
ANC_MH	12.0003	17.5960	19.6286	15.8703	11.7991	11.5337	18.5833	15.5319	17.2473	12.9899	9.7200	8.8121	13.3137	0.0000	
ANC_LIP	10.4964	12.3437	5.9026	12.0328	9.3428	6.9448	14.0623	10.4321	16.3951	7.0008	10.1511	5.0384	9.6275	9.8822	0.0000

Table 6.18. Mahalanobis D^2 matrix for all Middle Horizon.

	CON_MH	HUA_MH	TUR_MH	AJA_MH	CAH_MH	CAN_MH	MAJ_MH	BER_MH	ANC_MH
CON_MH	0.0000								
HUA_MH	19.4055	0.0000							
TUR_MH	13.7104	12.7401	0.0000						
AJA_MH	17.1637	26.4507	17.6954	0.0000					
CAH_MH	7.9967	15.4740	13.4678	9.6391	0.0000				
CAN_MH	15.2238	21.5105	10.1729	15.4841	10.4499	0.0000			
MAJ_MH	12.5673	10.3463	8.0307	21.9640	9.1743	8.4715	0.0000		
BER_MH	36.5512	35.1524	16.2091	40.3116	28.1048	16.6974	15.4613	0.0000	
ANC_MH	24.0578	36.6482	14.9348	26.2664	24.2382	12.5597	14.5845	14.9824	0.0000

Table 6.19. Mahalanobis D^2 matrix for all Middle Horizon (AJA_MH excluded).

	CON_MH	HUA_MH	TUR_MH	CAH_MH	CAN_MH	MAJ_MH	BER_MH	ANC_MH
CON_MH	0.0000							
HUA_MH	19.2408	0.0000						
TUR_MH	18.6172	15.3868	0.0000					
CAH_MH	8.6016	16.0970	18.3538	0.0000				
CAN_MH	18.1608	22.7277	10.3752	13.2623	0.0000			
MAJ_MH	15.6690	11.7056	8.7469	12.8248	8.6383	0.0000		
BER_MH	58.3067	51.1724	22.3525	50.0535	25.7074	23.9454	0.0000	
ANC_MH	39.4287	48.0138	18.0903	39.1171	17.0906	19.8460	15.9951	0.0000

Table 6.20. Mahalanobis D^2 matrix for all Late Intermediate Period samples.

	AYA_LIP	MAR_LIP	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP	BER_LIP	ANC_LIP
AYA_LIP	0.0000							
MAR_LIP	12.4737	0.0000						
SON_LIP	20.3451	13.5040	0.0000					
MPM_LIP	7.9998	11.3511	16.6428	0.0000				
PUC_LIP	17.5200	8.9947	9.1340	13.3159	0.0000			
RCC_LIP	11.4175	10.4649	10.6506	4.7166	13.1551	0.0000		
BER_LIP	15.1007	20.8043	21.6958	15.6260	17.0424	19.5402	0.0000	
ANC_LIP	26.8131	20.0954	8.6879	22.2642	14.2073	23.5384	24.0631	0.0000

Table 6.21. Mahalanobis D^2 matrix for all Late Intermediate Period samples (no BER_LIP).

	AYA_LIP	MAR_LIP	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP	ANC_LIP
AYA_LIP	0.0000						
MAR_LIP	14.8709	0.0000					
SON_LIP	29.6809	16.3800	0.0000				
MPM_LIP	8.2702	12.7465	23.1829	0.0000			
PUC_LIP	26.0225	11.6815	9.9613	19.5324	0.0000		
RCC_LIP	12.5350	11.1603	15.1618	5.1714	18.2349	0.0000	
ANC_LIP	38.3412	25.3115	9.6314	30.4572	15.6404	30.1212	0.0000

Table 6.22. Mahalanobis D^2 matrix for all Andahuaylas samples.

	TUR_MH	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP
TUR_MH	0.0000				
SON_LIP	75.3029	0.0000			
MPM_LIP	33.4092	8.3166	0.0000		
PUC_LIP	21.8302	35.8420	11.6258	0.0000	
RCC_LIP	32.8959	14.9417	3.1147	21.2444	0.0000

Table 6.23. Mahalanobis D^2 matrix for Andahuaylas Late Intermediate Period samples.

	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP
SON_LIP	0.0000			
MPM_LIP	5.4667	0.0000		
PUC_LIP	41.9723	26.3102	0.0000	
RCC_LIP	0.8427	3.1025	42.6787	0.0000

6.2.2 Principal Coordinate Analyses and Plots of Biological Distance

No distinct patterns are observed when all samples are compared. The Aja MH (AJA_MH) and Beringa LIP (BER_LIP) samples are clear outliers. The principal coordinate analysis illustrates a tendency for the Andahuaylas samples to group together (Table 6.24, Figures 6.1 and 6.2). Aside from this group, there is no distinct pattern related to geographical distance or chronology.

Table 6.24. Principal coordinate loadings for all samples.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**
CON_MH	0.0487	0.0490	-0.1419	-0.1011	0.1609	0.0182	0.1580	-0.0704	0.0012
AYA_LIP	-0.0757	0.0233	-0.1291	0.1274	0.1257	-0.0048	-0.0807	-0.0989	0.0315
HUA_MH	0.0570	0.1688	0.2126	0.1564	-0.1057	-0.0070	0.0549	-0.0612	-0.0298
MAR_LIP	-0.1426	0.1611	0.1478	-0.0764	0.0250	-0.1416	-0.0663	-0.0736	0.0784
TUR_MH	-0.0640	0.0978	0.0286	-0.0797	0.0032	-0.1099	-0.0217	0.0798	-0.0279
SON_LIP	-0.0022	0.0597	0.0686	-0.0455	0.0073	0.2333	-0.0785	0.0057	0.0043
MPM_LIP	-0.0875	0.1508	-0.1796	0.0256	-0.0662	0.0001	0.1055	0.0125	0.0086
PUC_LIP	-0.1298	0.1009	0.0570	-0.0826	0.1131	0.0010	-0.0112	0.1291	-0.1094
RCC_LIP	-0.1235	0.1475	-0.1674	-0.0474	-0.1542	0.0767	-0.0508	0.0301	0.0352
AJA_MH	0.3049	0.0087	-0.1193	0.0545	-0.0184	-0.0502	-0.1364	-0.0264	-0.0532
CAH_MH	0.1846	-0.0669	-0.0345	0.1153	0.1292	0.0127	-0.0100	0.0702	0.0720
CAN_MH	0.1185	-0.1455	-0.1542	0.0280	-0.1238	-0.0780	0.0334	0.0391	-0.0497
MAJ_MH	0.1058	-0.0385	0.1117	0.0195	-0.0673	0.0207	0.0831	0.0322	0.1061
BER_MH	-0.1182	-0.2085	0.0812	0.0785	0.0234	-0.0193	-0.0058	0.1195	0.0602
BER_LIP	-0.3789	-0.2728	-0.0060	0.0694	-0.0276	0.0150	0.0025	-0.0847	-0.0562
ANC_MH	0.1385	-0.2080	0.0472	-0.2803	-0.0468	-0.0018	-0.0209	-0.0624	0.0220
ANC_LIP	0.1644	-0.0276	0.1770	0.0385	0.0222	0.0348	0.0449	-0.0405	-0.0931
Variation (%)	24.08	17.53	14.77	10.23	7.56	5.79	4.94	4.64	3.34
Cumulative variation (%)	**24.08**	**41.61**	**56.38**	**66.61**	**74.17**	**79.96**	**84.90**	**89.54**	**92.88**

Table 6.24 continued. Principal coordinate loadings for all samples.

	PC10	**PC11**	**PC12**	**PC13**	**PC14**	**PC15**	**PC16**	**PC17**
CON_MH	0.0335	0.0278	0.0086	0.0278	-0.0160	0.0275	0.0109	0.0335
AYA_LIP	-0.0742	-0.0255	0.0538	-0.0481	0.0015	-0.0043	0.0065	-0.0742
HUA_MH	-0.0253	0.0247	0.0112	0.0246	0.0388	0.0129	0.0213	-0.0253
MAR_LIP	0.0352	-0.0579	-0.0288	0.0253	-0.0102	0.0087	-0.0128	0.0352
TUR_MH	-0.0143	0.0942	0.0671	0.0142	-0.0093	-0.0196	-0.0149	-0.0143
SON_LIP	0.0044	-0.0026	0.0229	0.0233	0.0091	0.0208	-0.0272	0.0044
MPM_LIP	0.0455	-0.0131	-0.0205	-0.0484	0.0417	-0.0185	-0.0232	0.0455
PUC_LIP	-0.0605	-0.0320	-0.0478	-0.0219	0.0066	0.0099	0.0122	-0.0605
RCC_LIP	0.0194	-0.0095	-0.0013	0.0169	-0.0323	-0.0180	0.0318	0.0194
AJA_MH	0.0488	0.0542	-0.0457	-0.0239	-0.0052	0.0216	-0.0013	0.0488
CAH_MH	-0.0119	-0.0010	-0.0345	0.0606	0.0179	-0.0382	0.0010	-0.0119
CAN_MH	-0.0482	-0.0766	0.0291	0.0415	-0.0066	0.0212	-0.0130	-0.0482
MAJ_MH	-0.0770	0.0318	-0.0334	-0.0438	-0.0399	0.0101	-0.0089	-0.0770
BER_MH	0.0918	-0.0090	0.0355	-0.0269	0.0110	0.0246	0.0142	0.0918
BER_LIP	-0.0054	0.0446	-0.0414	0.0206	-0.0072	-0.0076	-0.0064	-0.0054
ANC_MH	-0.0205	-0.0020	0.0050	-0.0180	0.0383	-0.0150	0.0123	-0.0205
ANC_LIP	0.0588	-0.0482	0.0202	-0.0237	-0.0382	-0.0360	-0.0023	0.0588
Variation (%)	2.12	1.66	1.13	1.01	0.55	0.40	0.23	0.02
Cumulative variation (%)	**95.00**	**96.66**	**97.79**	**98.8**	**99.35**	**99.75**	**99.98**	**100**

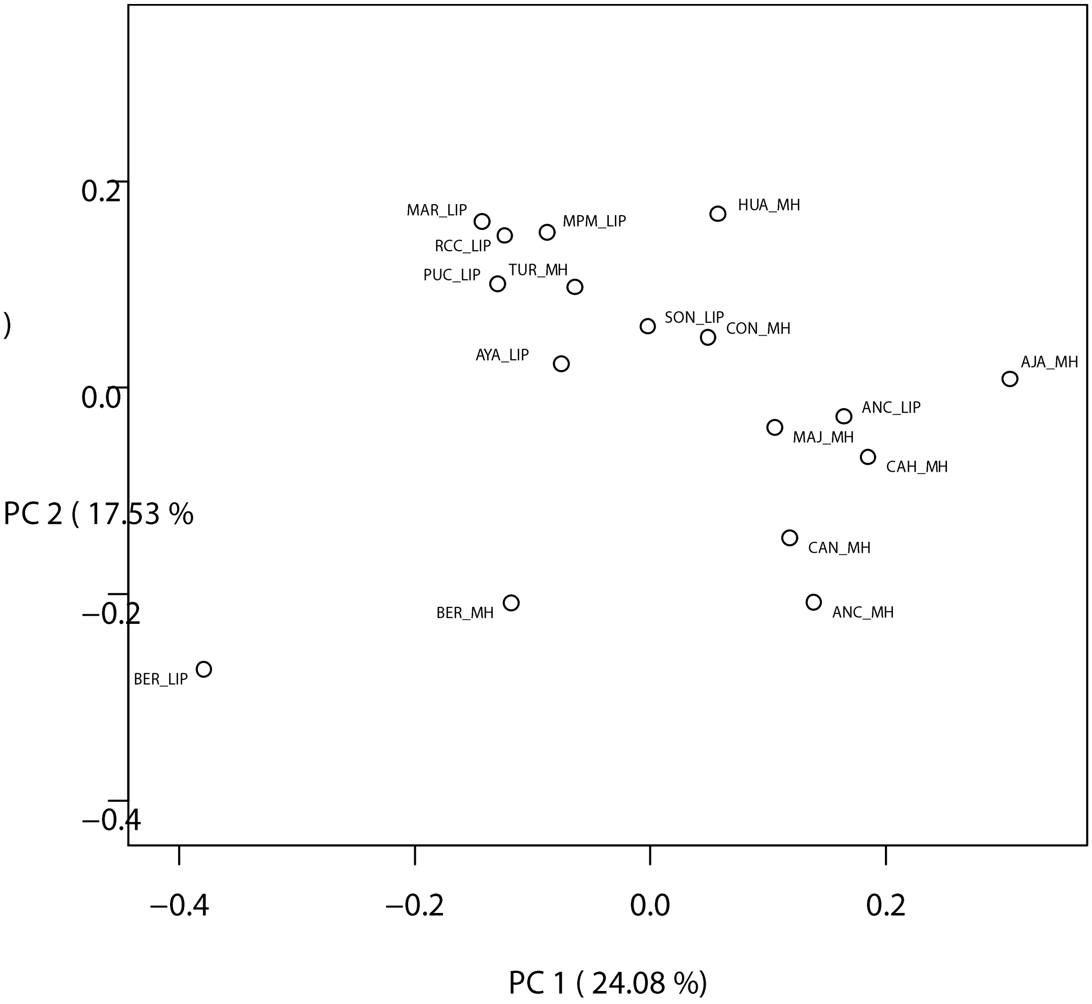


Figure 6.1. All samples, plot of first two principal coordinates.

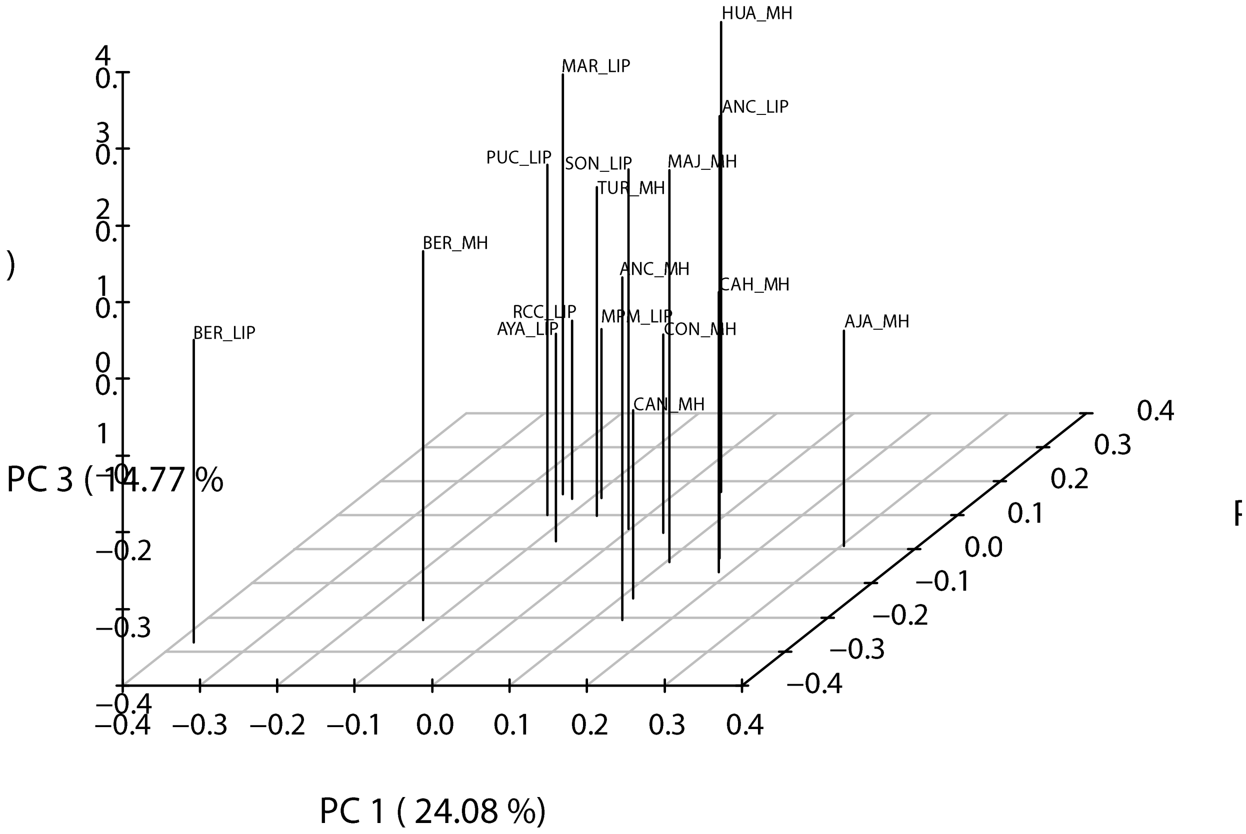


Figure 6.2. All samples, plot of first three principal coordinates.

A comparison of all samples excluding Aja MH (AJA_MH) and Beringa LIP (BER_LIP) was considered to remove the effects of these outliers. The plots of the first two and first three principal coordinates reveal a pattern relative to geographical distance where the highland samples separate from the mid-valley and coastal samples along the first principal coordinate (Figures 6.3 and 6.4).

Table 6.25. Principal coordinate loadings for all samples (AJA_MH and BER_LIP excluded).

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**
CON_MH	-0.0298	-0.1628	-0.0303	-0.0115	0.2291	-0.0301	-0.0472	0.0868	0.0377
AYA_LIP	-0.1079	-0.1109	0.0822	0.1530	0.0544	-0.0025	0.1506	-0.0678	0.0313
HUA_MH	-0.0083	0.2312	0.2158	-0.1101	-0.0168	-0.0456	-0.0015	-0.0136	0.0222
MAR_LIP	-0.1633	0.1873	-0.1040	-0.0017	0.0171	-0.1381	0.1200	0.0192	-0.0089
TUR_MH	-0.0992	0.0585	-0.0897	0.0006	-0.0153	-0.0825	-0.0662	-0.0411	-0.0687
SON_LIP	-0.0064	0.0846	-0.0208	-0.0342	0.0263	0.2455	0.0416	-0.0081	-0.0016
MPM_LIP	-0.2110	-0.1435	0.0732	-0.0622	-0.0269	-0.0220	-0.0579	0.0689	0.0432
PUC_LIP	-0.1294	0.1041	-0.1241	0.0969	0.0499	0.0406	-0.1414	-0.0809	-0.0236
RCC_LIP	-0.2295	-0.1153	-0.0111	-0.1162	-0.1216	0.0936	0.0268	0.0018	-0.0170
CAH_MH	0.1601	-0.0868	0.1370	0.1147	0.0689	0.0125	0.0114	-0.0034	-0.1239
CAN_MH	0.1345	-0.2242	0.0487	-0.0441	-0.1242	-0.0778	-0.0372	-0.0992	0.0230
MAJ_MH	0.1430	0.0591	0.0650	-0.0595	-0.0477	-0.0069	-0.0066	0.0916	-0.0903
BER_MH	0.0963	0.0476	-0.0623	0.2313	-0.1737	0.0112	-0.0207	0.0921	0.0640
ANC_MH	0.2585	-0.0609	-0.2516	-0.1276	0.0094	-0.0099	0.0671	-0.0081	0.0062
ANC_LIP	0.1924	0.1323	0.0720	-0.0292	0.0711	0.0120	-0.0388	-0.0383	0.1063
Variation (%)	23.38	18.37	13.20	10.50	9.11	7.33	5.32	3.71	3.43
Cmulative variation (%)	**23.38**	**41.75**	**54.95**	**65.45**	**74.56**	**81.89**	**87.21**	**90.92**	**94.35**

Table 6.25 continued. Principal coordinate loadings for all samples (AJA_MH and BER_LIP excluded).

	PC10	**PC11**	**PC12**	**PC13**	**PC14**
CON_MH	-0.0002	-0.0216	0.0445	0.0145	0.0099
AYA_LIP	0.0788	-0.0130	-0.0163	0.0061	0.0026
HUA_MH	0.0238	-0.0259	0.0301	-0.0419	0.0207
MAR_LIP	-0.0600	0.0513	0.0146	0.0100	-0.0139
TUR_MH	0.0027	-0.1152	-0.0162	0.0137	-0.0141
SON_LIP	-0.0131	-0.0172	0.0276	-0.0072	-0.0323
MPM_LIP	0.0013	0.0233	-0.0476	-0.0402	-0.0250
PUC_LIP	0.0367	0.0694	0.0022	-0.0106	0.0125
RCC_LIP	-0.0380	-0.0017	-0.0068	0.0312	0.0372
CAH_MH	-0.0786	0.0101	-0.0165	-0.0228	0.0081
CAN_MH	-0.0121	0.0245	0.0453	0.0103	-0.0187
MAJ_MH	0.0865	0.0375	-0.0056	0.0400	-0.0082
BER_MH	-0.0106	-0.0223	0.0125	-0.0072	0.0079
ANC_MH	0.0233	-0.0033	-0.0204	-0.0382	0.0127
ANC_LIP	-0.0406	0.0041	-0.0474	0.0421	0.0005
Variation (%)	2.02	1.75	0.82	0.72	0.34
Cumulative variation (%)	**96.37**	**98.12**	**98.94**	**99.66**	**100**

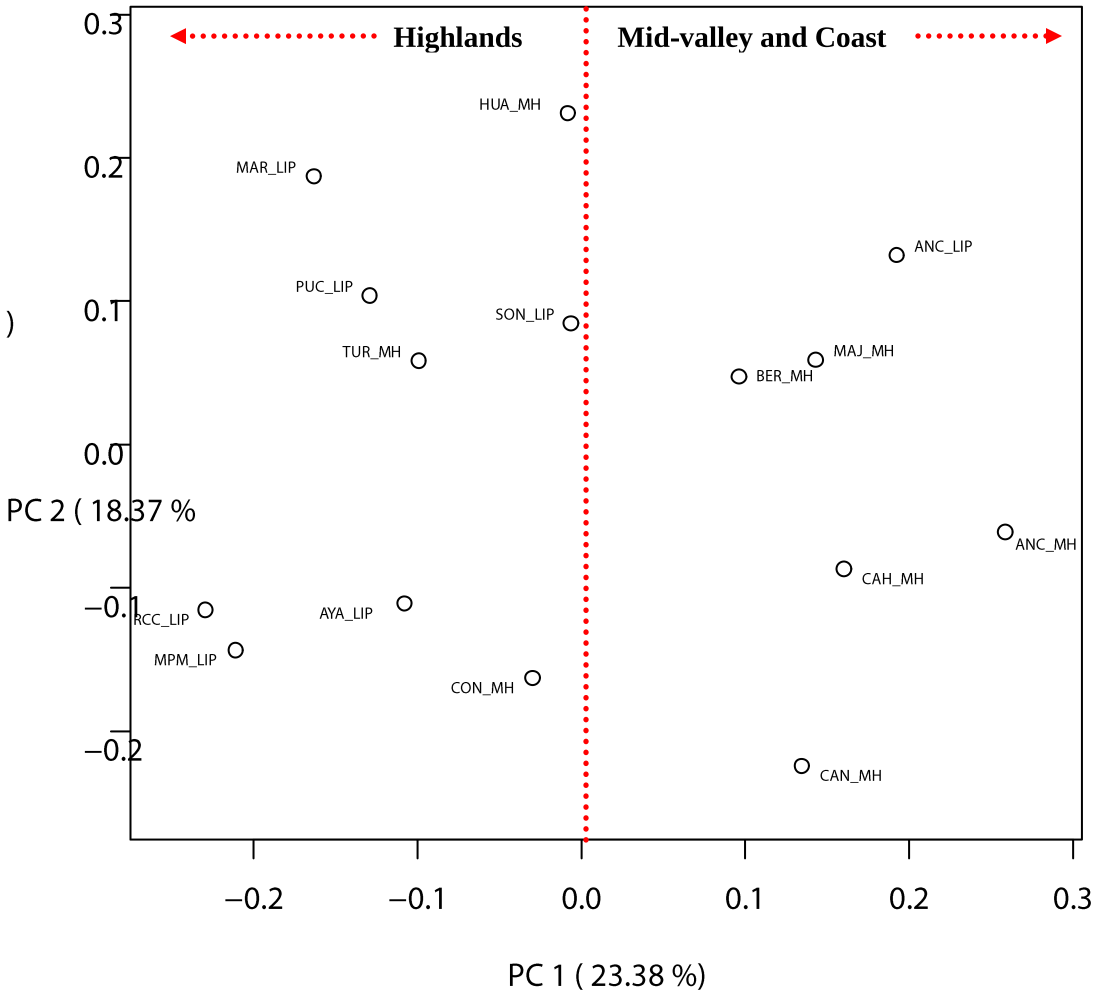


Figure 6.3. All samples (AJA_MH and BER_LIP excluded), plot of the first two principal coordinates.

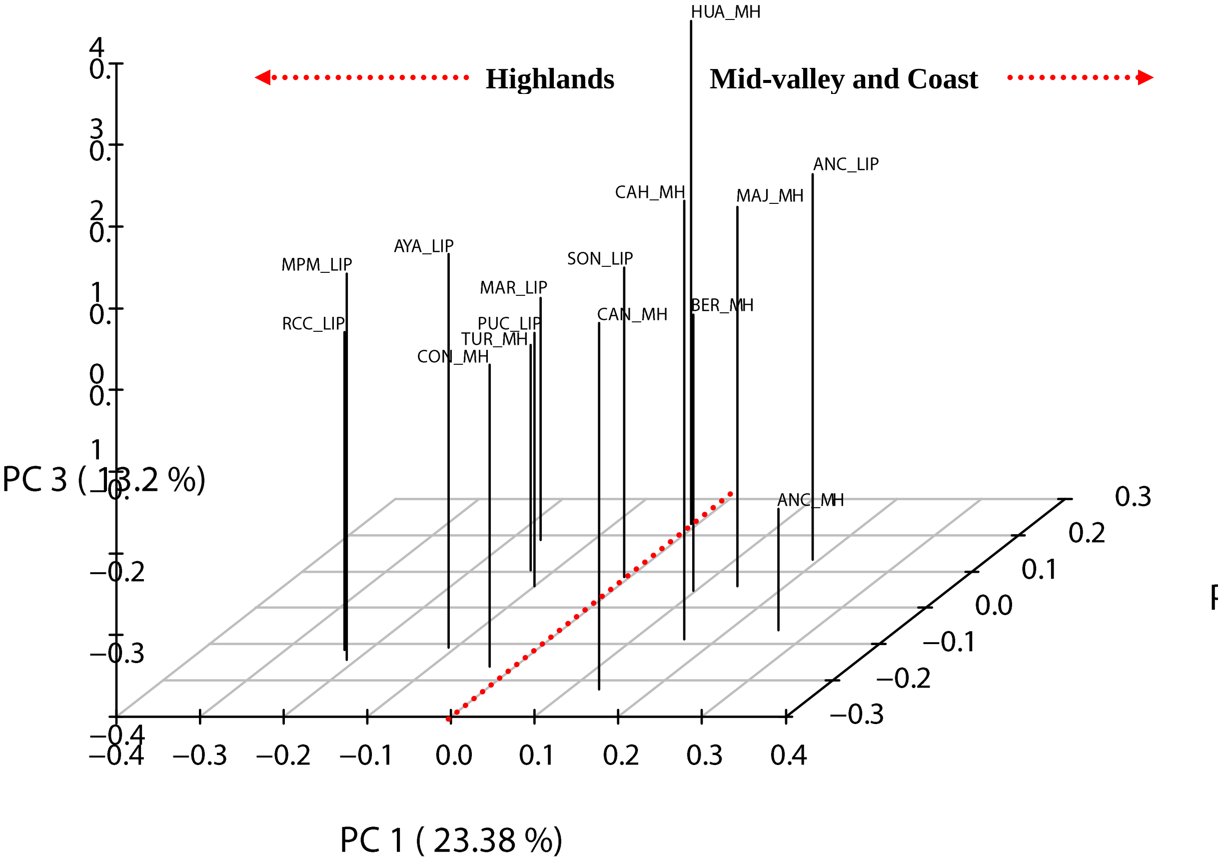


Figure 6.4. All samples (AJA_MH and BER_LIP excluded), plot of the first three principal coordinates.

All MH samples were compared. The two dimensional and three dimensional plots of the principal coordinates revealed several patterns among the samples (Table 6.26, Figures 6.5 and 6.6). The Aja MH (AJA_MH) sample was an outlier in this comparison. There was also a slight geographical pattern revealed in the principal coordinate plots. Beringa MH (BER_MH), representing the southern mid-valley region, Ancón (ANC_MH) representing the coast, and the Hualcayan MH (HUA_MH), representing the north-central highlands region, plotted separate from the rest of the samples (Figures 6.5 and 6.6).

Table 6.26. Principal coordinate loadings for all Middle Horizon samples.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**
CON_MH	-0.2379	-0.0616	0.2785	-0.0300	0.0975	-0.0318	0.0355	0.0386
HUA_MH	-0.2306	0.3749	-0.0690	0.0886	-0.0691	0.0228	0.0651	-0.0047
TUR_MH	0.0387	0.0899	-0.0321	0.1612	0.1439	-0.0872	-0.0634	-0.0396
AJA_MH	-0.2623	-0.2971	-0.2113	0.0610	0.0194	0.0438	-0.0003	0.0505
CAH_MH	-0.2086	-0.0564	-0.0169	-0.1833	0.0163	0.0759	-0.0134	-0.0866
CAN_MH	0.0727	-0.0951	-0.0385	-0.0835	-0.1287	-0.1960	0.0107	-0.0050
MAJ_MH	0.0384	0.1524	0.0676	-0.0484	-0.0998	0.0610	-0.0977	0.0509
BER_MH	0.4699	0.0925	-0.0940	-0.1216	0.1121	0.0306	0.0384	0.0300
ANC_MH	0.3198	-0.1994	0.1158	0.1560	-0.0916	0.0810	0.0250	-0.0340
Variation (%)	41.18	24.15	11.65	8.97	6.19	4.95	1.60	1.31
Cumulative variation (%)	**41.18**	**65.33**	**76.98**	**85.95**	**92.14**	**97.09**	**98.69**	**100**

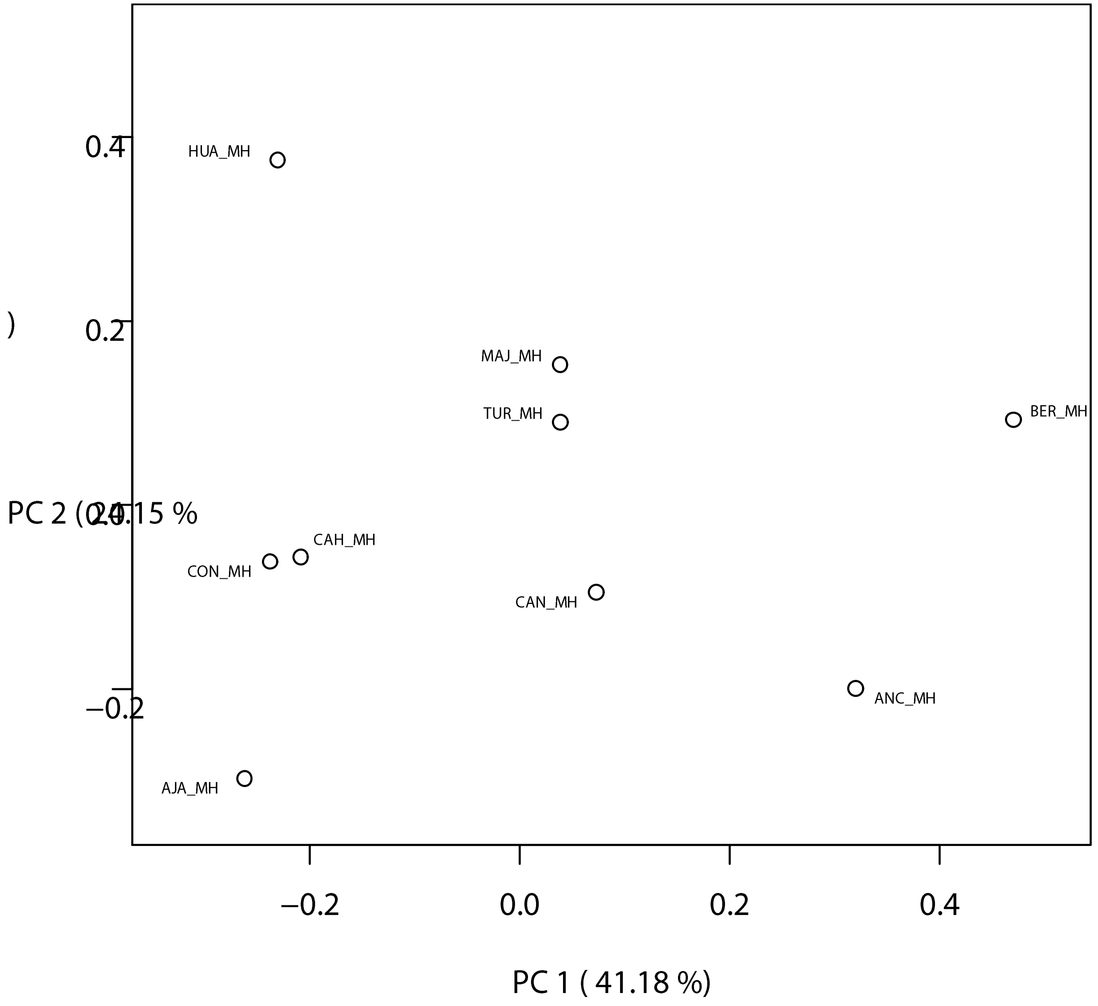


Figure 6.5. All Middle Horizon samples, plot of the first two principal coordinates.

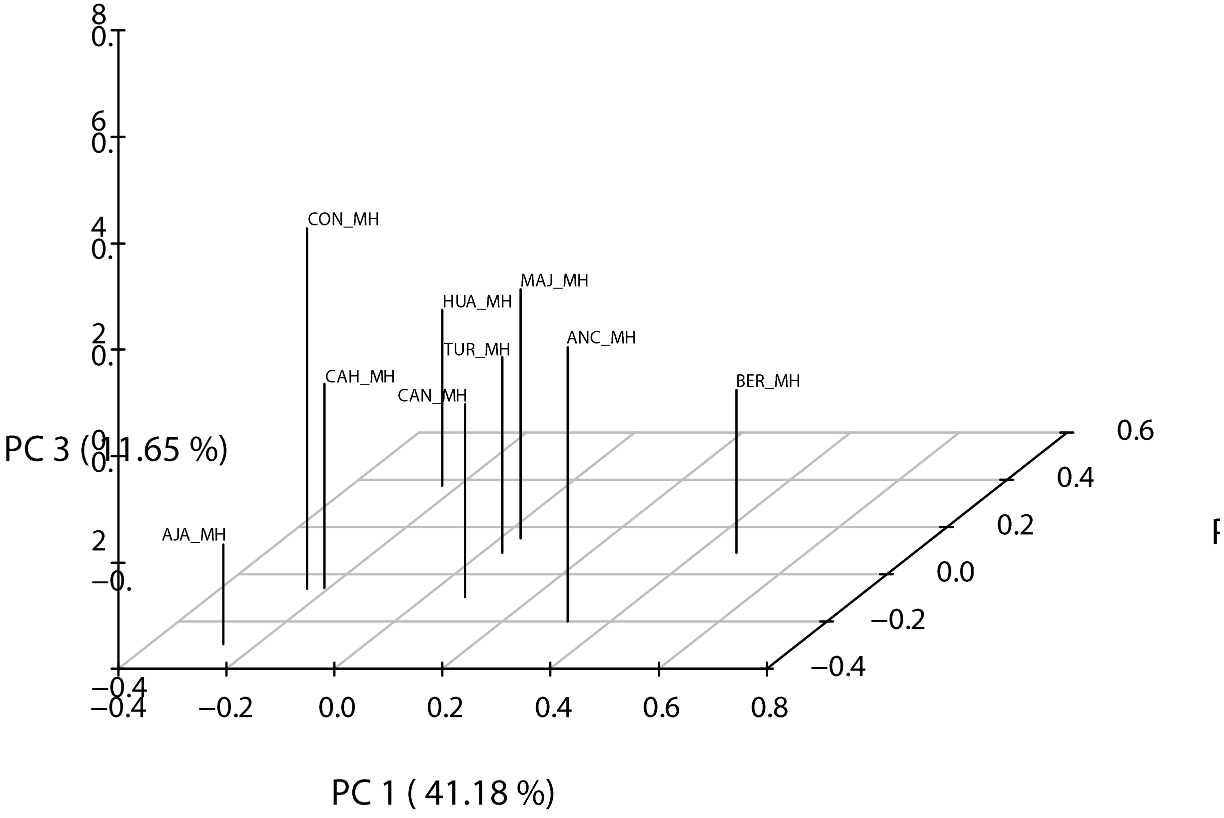


Figure 6.6. All Middle Horizon samples, plot of the first three principal coordinates.

Since the Aja MH (AJA_MH) sample was identified as an outlier in the MH group, the comparison was done again excluding this sample. Patterns that were evident in the comparison of all MH samples were clearer when the outlier sample was removed (Table 6.27, Figures 6.7 and 6.8). Turpo Qatun Rumi MH (TUR_MH), and Mina Puka Machay MH (MPM_MH) groups demonstrate a strong relationship (Figures 6.7 and 6.8). The Beringa MH (BER_MH), Ancón MH (ANC_MH), and Hualcayan MH (HUA_MH) samples still separated from the other samples. The Nazca valley samples form a loose cluster with the samples close to the Wari heartland (Conchopata and Turpo Qatun Rumi) their geographical and chronological proximity (Figures 6.7 and 6.8).

Table 6.27. Principal coordinate loadings for all Middle Horizon samples (AJA_MH excluded).

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**
CON_MH	-0.3680	0.2069	0.0888	-0.1423	0.0253	0.0896	-0.0350
HUA_MH	-0.3317	-0.3221	0.0706	0.0767	0.0302	-0.0223	-0.0653
TUR_MH	0.0404	-0.0902	0.1402	-0.0533	-0.1771	-0.0331	0.0654
CAH_MH	-0.3238	0.1130	-0.1859	-0.0307	0.0029	-0.1381	0.0122
CAN_MH	0.0304	0.1167	-0.1207	0.1629	-0.1135	0.0962	-0.0145
MAJ_MH	-0.0257	-0.0839	-0.0202	0.0346	0.1516	0.0614	0.0972
BER_MH	0.5605	-0.1478	-0.1261	-0.1313	0.0072	0.0227	-0.0367
ANC_MH	0.4178	0.2074	0.1533	0.0834	0.0734	-0.0763	-0.0233
Variation (%)	58.4	17.54	8.42	5.68	5.15	3.33	1.48
Cumulative variation (%)	**58.40**	**75.94**	**84.36**	**90.04**	**95.19**	**98.52**	**100**

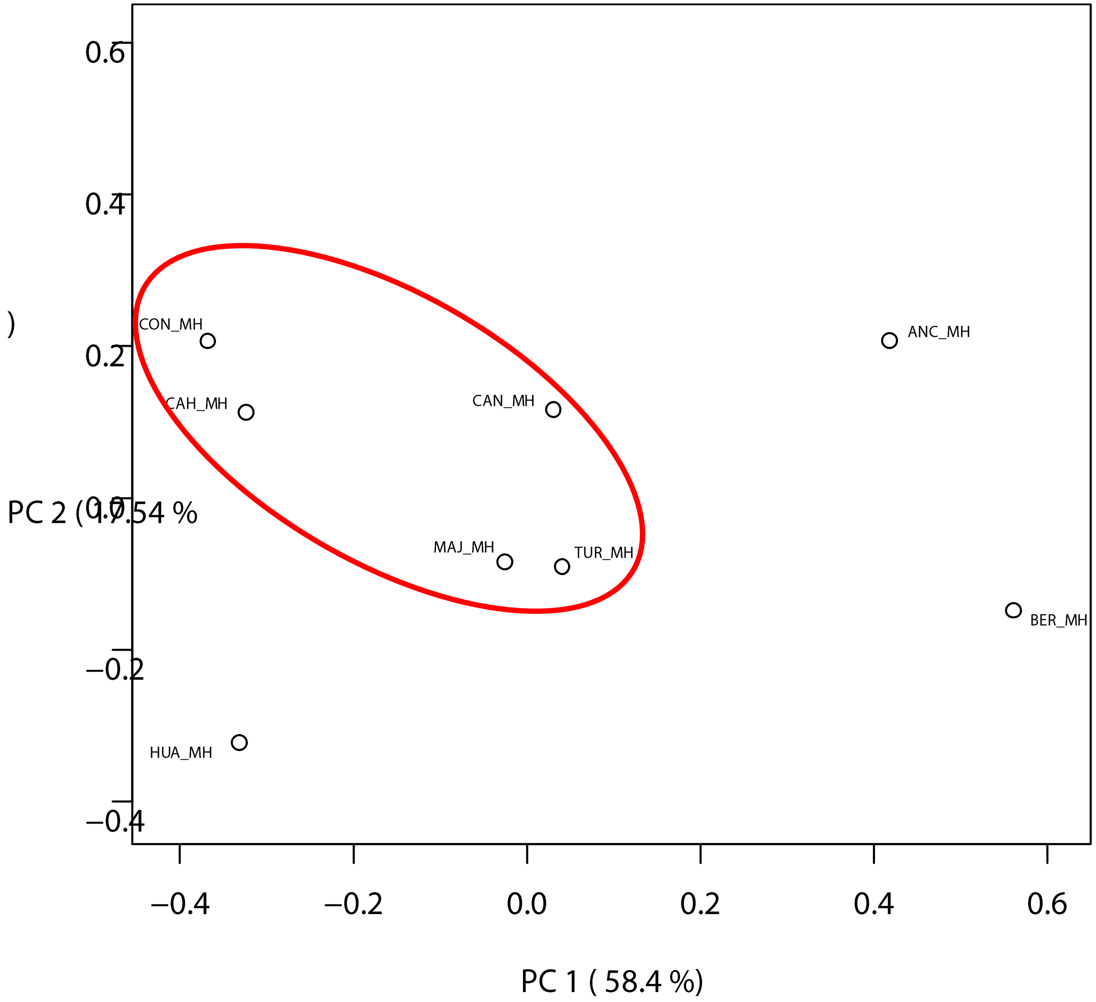


Figure 6.7. All Middle Horizon samples (AJA_MH excluded), plot of the first two principal coordinates. The cluster of Wari heartland and Nazca Valley samples is highlighted by a red circle.

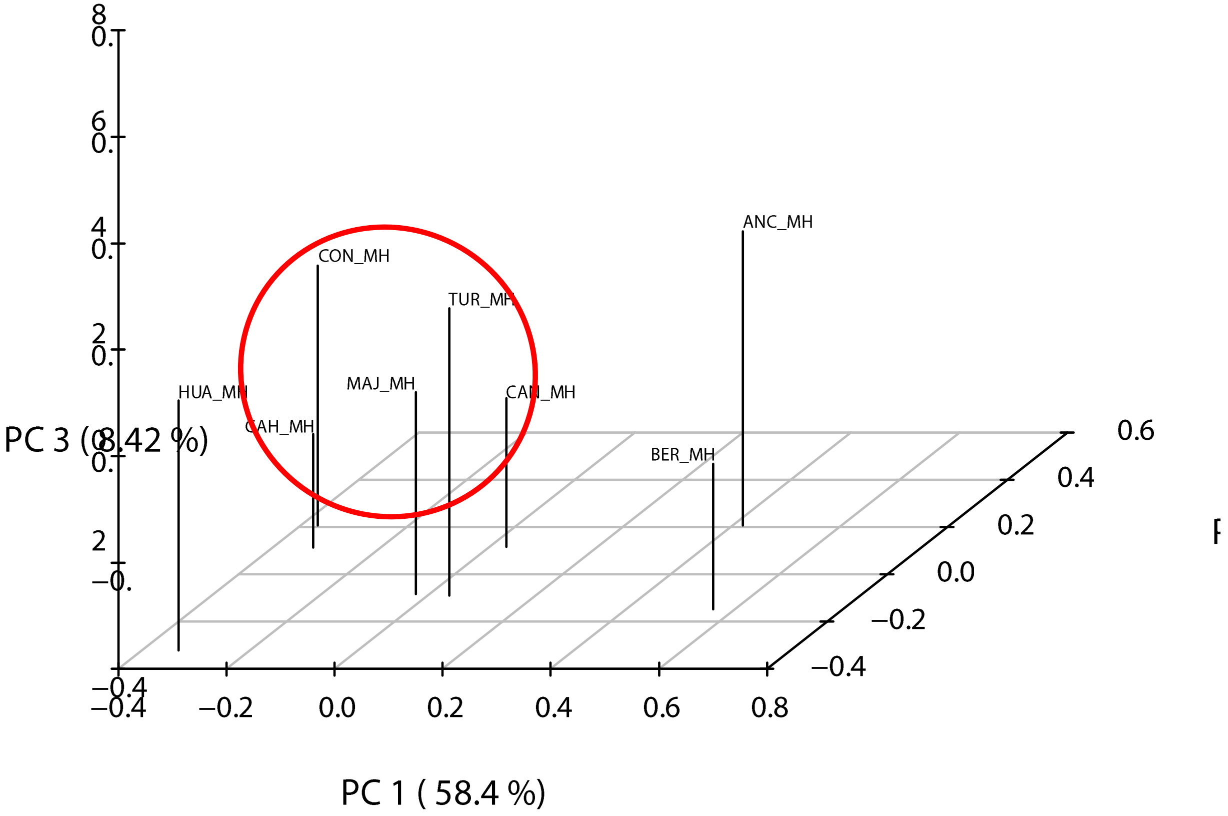


Figure 6.8. All Middle Horizon samples (AJA_MH excluded), plot of the first three principal coordinates. The cluster of Wari heartland and Nazca Valley samples is highlighted by a red circle.

All of the LIP samples were compared. Consistent with the comparison of all samples, the Beringa LIP (BER_LIP) was an outlier (Table 6.28, Figures 6.9 and 6.10). The relationship of the Beringa LIP sample to the rest of the samples seemed to obscure other possible patterns (Figures 6.9 and 6.10). The Andahuaylas samples appeared to separate along the first principal coordinate (Figure 6.9). No other clear patterns associated with geographical or chronological distance were evident.

Table 6.28. Principal coordinate loadings for all Late Intermediate Period samples.

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**
AYA_LIP	-0.2739	-0.0247	-0.0286	0.2008	0.0940	0.1061	0.0099
MAR_LIP	-0.0355	0.1590	0.2244	0.0784	0.0227	-0.1419	-0.0097
SON_LIP	0.2529	0.0797	-0.0850	-0.0803	0.1515	0.0214	-0.0586
MPM_LIP	-0.2007	0.0685	-0.1121	-0.0092	-0.1699	-0.0034	-0.0601
PUC_LIP	0.1247	0.0220	0.2005	-0.0983	-0.0713	0.1494	0.0155
RCC_LIP	-0.1327	0.1853	-0.1292	-0.1352	0.0216	-0.0368	0.0711
BER_LIP	-0.1290	-0.3965	0.0295	-0.1018	0.0286	-0.0607	-0.0001
ANC_LIP	0.3941	-0.0934	-0.0995	0.1457	-0.0772	-0.0340	0.0320
Variation (%)	37.73	23.26	13.57	11.01	7.19	5.91	1.33
Cumulative variation (%)	**37.73**	**60.99**	**74.56**	**85.57**	**92.76**	**98.67**	**100**

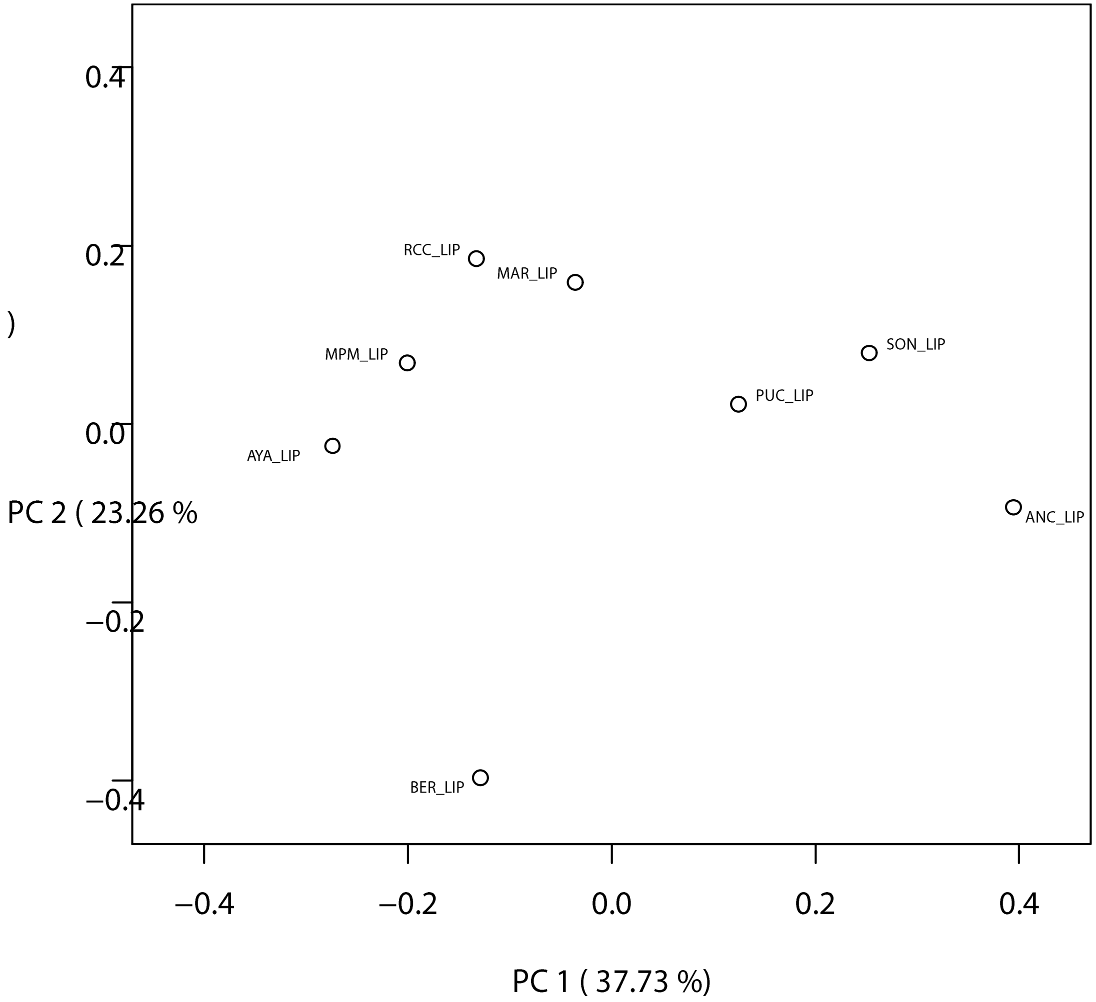


Figure 6.9. All Late Intermediate Period samples, plot of the first two principal coordinates.

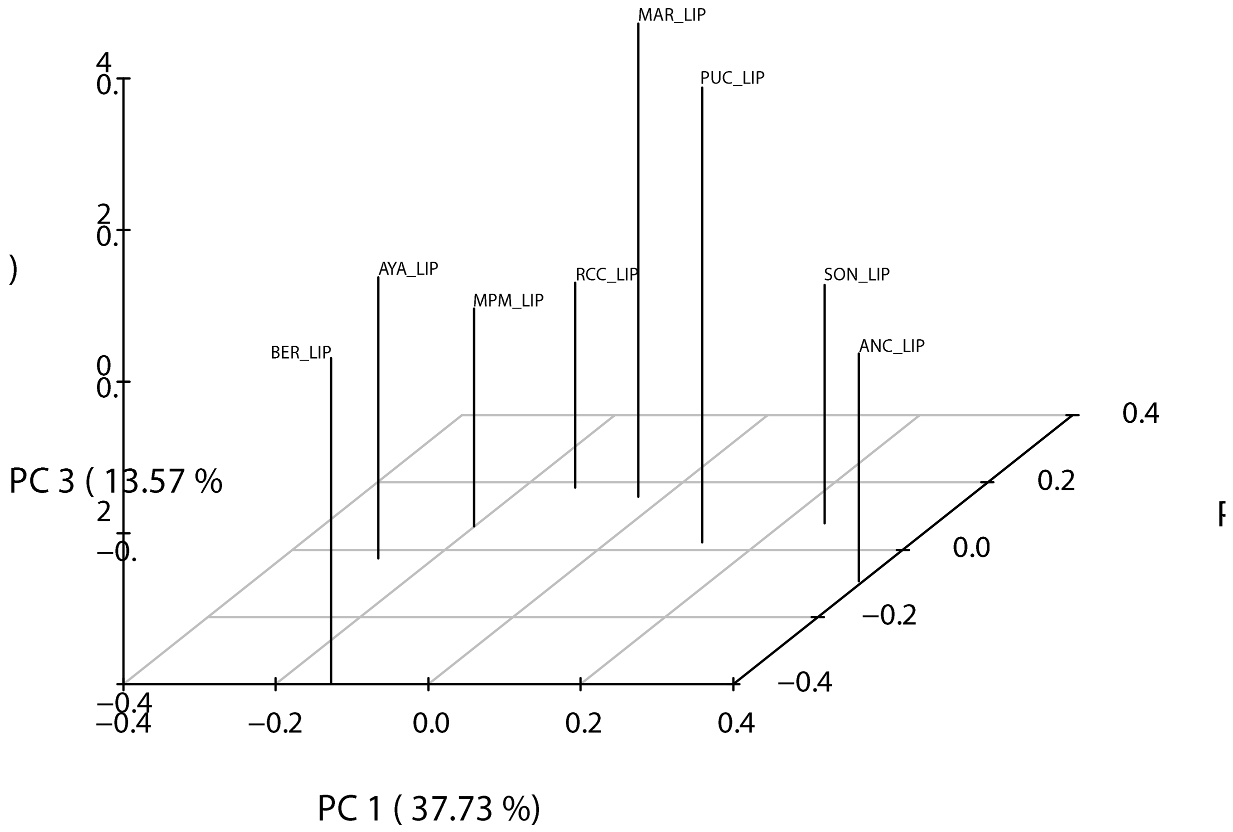


Figure 6.10. All Late Intermediate Period samples, plot of the first three principal coordinates.

When the LIP comparison was calculated excluding the Beringa LIP (BER_LIP) sample the Andahuaylas group separated more dramatically along the first principal coordinate (Table 6.29, Figures 6.11 and 6.12). The Ayacucho LIP (AYA_LIP) appeared similar to the Mina Puka Machay (MPM_LIP) sample (Figures 6.11 and 6.12). The Marcajirca LIP (MAR_LIP) and Ancón LIP (ANC_LIP) groups also appeared distinctive from the rest of the samples.

Table 6.29. Principal coordinate scores for all Late Intermediate Period samples (BER_LIP excluded).

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
AYA_LIP	-0.3667	0.0961	-0.1835	0.0528	0.1356	-0.0098
MAR_LIP	-0.0791	-0.2281	-0.0666	0.1472	-0.1203	0.0093
SON_LIP	0.2864	0.0217	0.1522	0.0911	0.1139	0.0587
MPM_LIP	-0.2729	0.0992	0.0344	-0.1335	-0.1040	0.0626
PUC_LIP	0.1936	-0.2141	-0.0530	-0.1757	0.0727	-0.0176
RCC_LIP	-0.1987	0.0298	0.2318	0.0087	-0.0125	-0.0723
ANC_LIP	0.4374	0.1953	-0.1153	0.0096	-0.0854	-0.0309
Variation (%)	55.48	15.35	12.98	8.01	6.81	1.37
Cumulative variation (%)	**55.48**	**70.83**	**83.81**	**91.82**	**98.63**	**100**

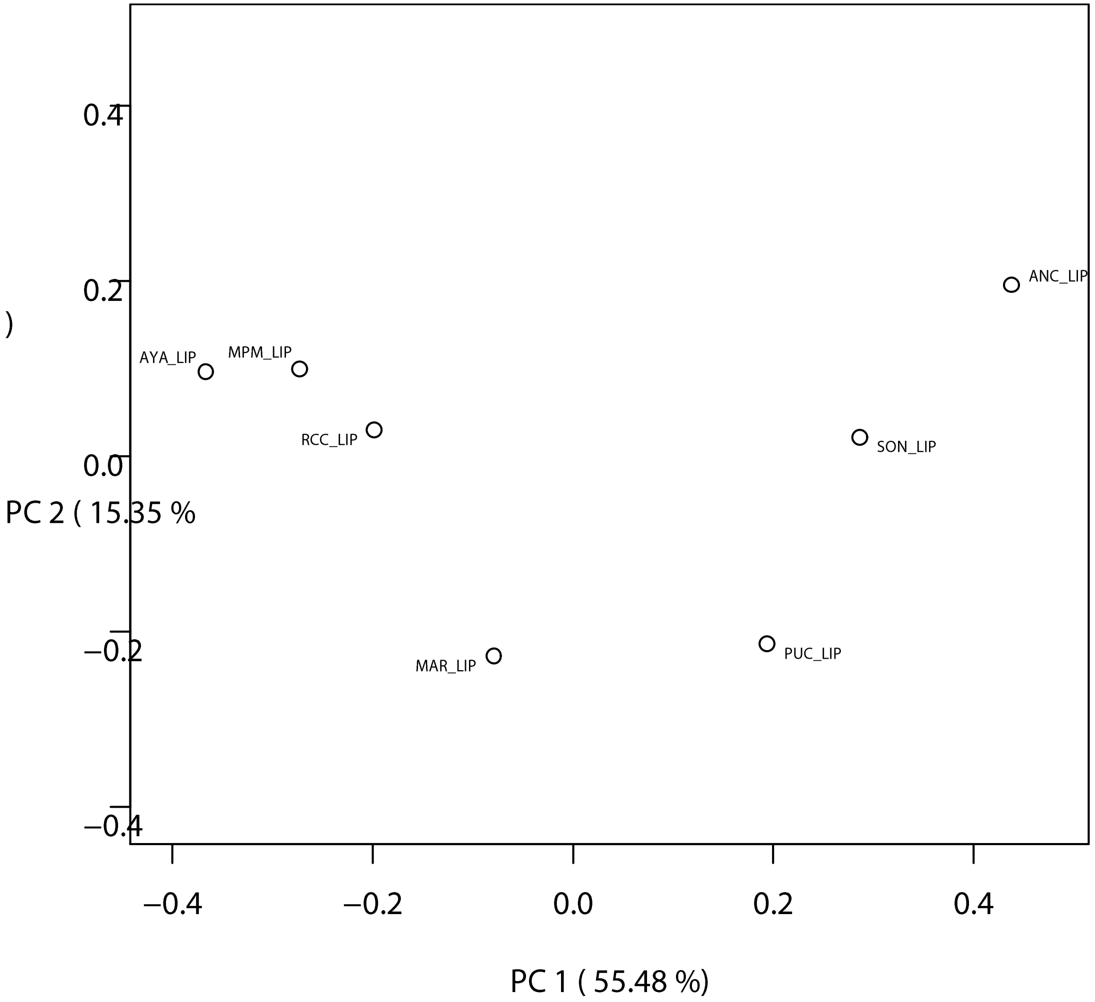


Figure 6.11. All Late Intermediate Period samples (BER_LIP excluded), plot of the first two principal coordinates.

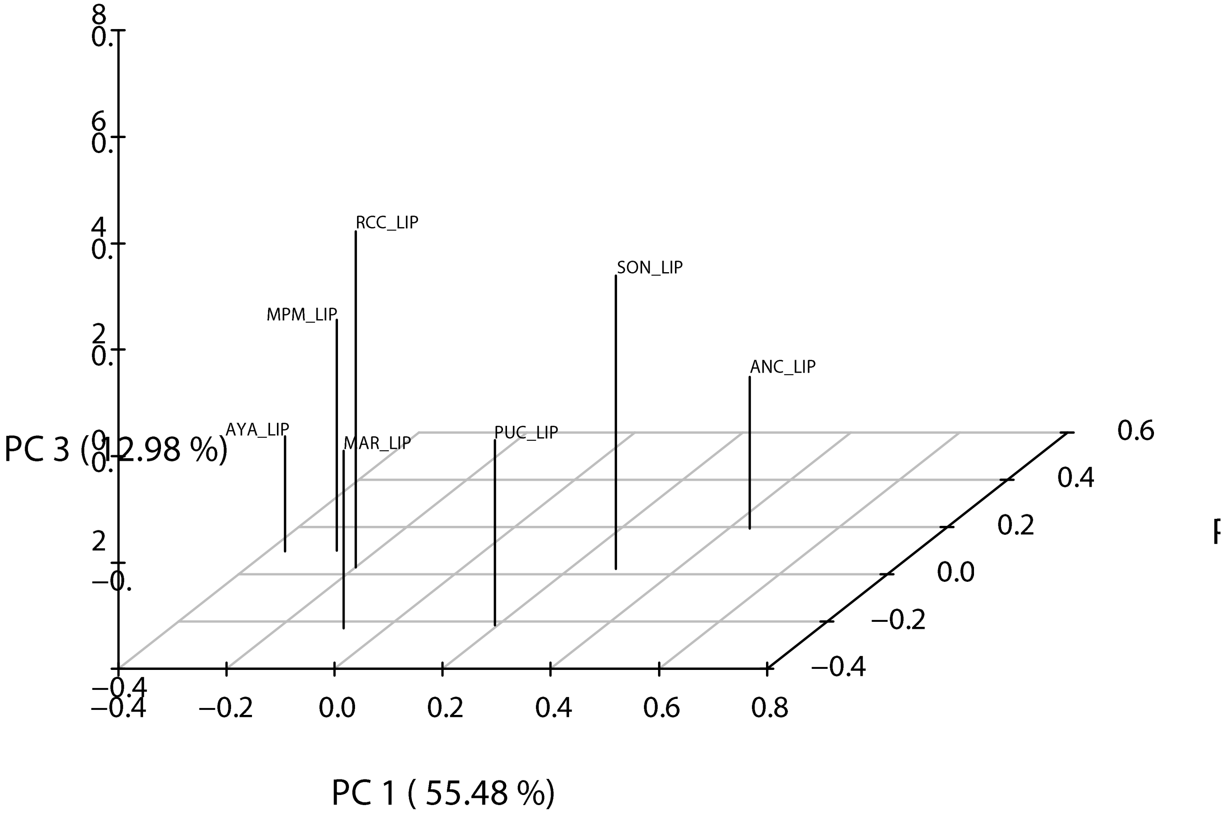


Figure 6.12. All Late Intermediate Period samples (BER_LIP excluded), plot of the first three principal coordinates.

All Andahuaylas samples were compared (Table 6.30, Figures 6.13 and 6.14). The Andahuaylas LIP samples were also compared independently (Table 6.31, Figure 6.15). The Turpo Qatun Rumi MH (TUR_MH) separated from the other four LIP samples. This is more evident in the three-dimensional plot (Figure 6.14) which illustrates a larger percentage of the total variation than the two-dimensional plot (6.13).

When the Andahuaylas LIP samples were compared separately there was a clear division between the Sonhuayo LIP (SON_LIP) and Puccullu (PUC_LIP) samples, and the Mina Puka Machay LIP (MPM_LIP) and Ranra Cancha LIP (RCC_LIP) samples (Figure 6.15). The pattern is not associated with geographical distance as the Sonhuayo LIP and Mina Puka Machay LIP samples are in very close proximity to one another. The pattern may be related to other variables.

Table 6.30. Principal coordinate loadings for all Andahuaylas samples.

	PC1	**PC2**	**PC3**
TUR_MH	0.6129	0.1247	0.0743
SON_LIP	-0.5347	-0.0157	0.0908
MPM_LIP	-0.1471	-0.0052	0.0070
PUC_LIP	0.1906	-0.3143	-0.0542
RCC_LIP	-0.1217	0.2105	-0.1180
Variation (%)	79.48	17.2	3.32
Cumulative variation (%)	**79.48**	**96.68**	**100**

Table 6.31. Principal coordinate loadings for Andahuaylas Late intermediate Period samples.

	PC1	**PC2**
SON_LIP	-0.2676	0.1160
MPM_LIP	-0.0680	-0.1336
PUC_LIP	0.6139	0.0301
RCC_LIP	-0.2782	-0.0125
Variation (%)	94.25	5.75
Cumulative variation (%)	**94.25**	**100**

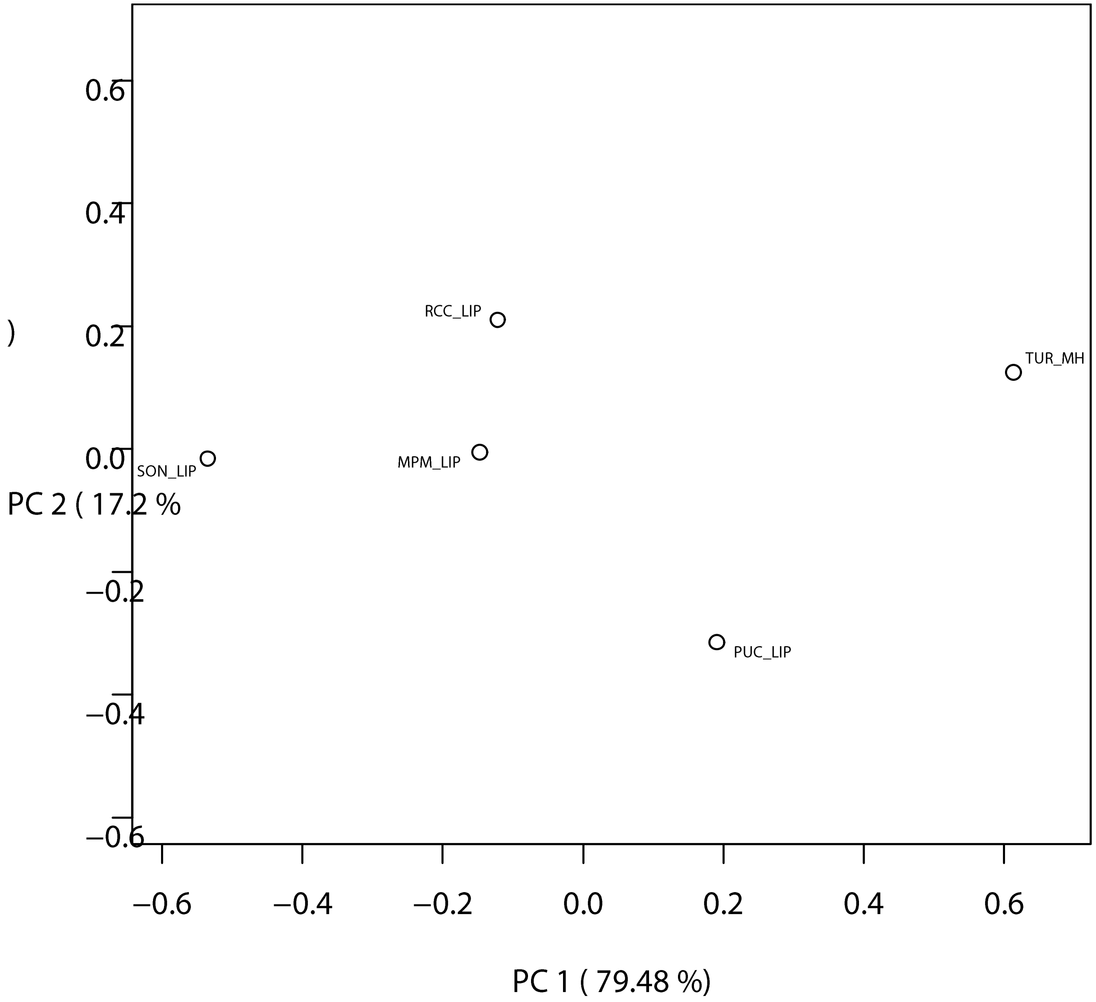


Figure 6.13. All Andahuaylas samples, plot of first two principal coordinates.

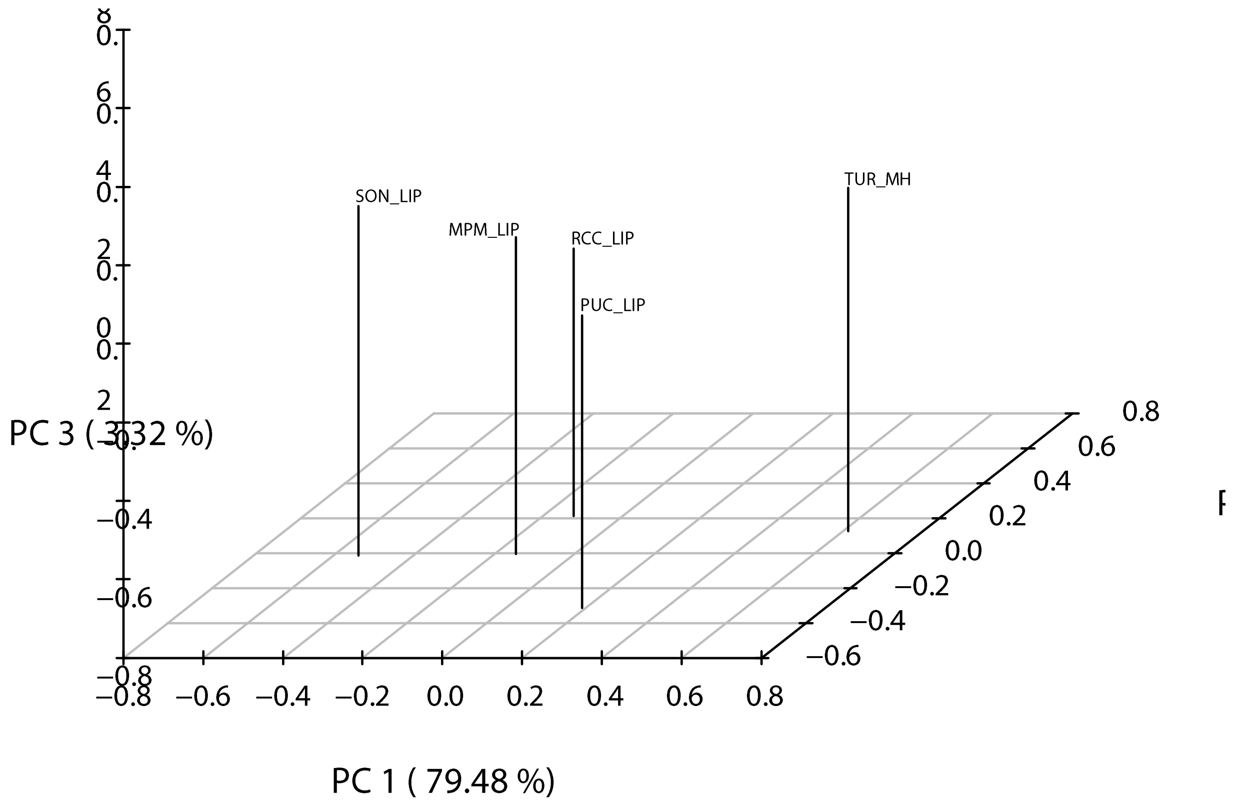


Figure 6.14. All Andahuaylas samples, plot of first three principal coordinates.

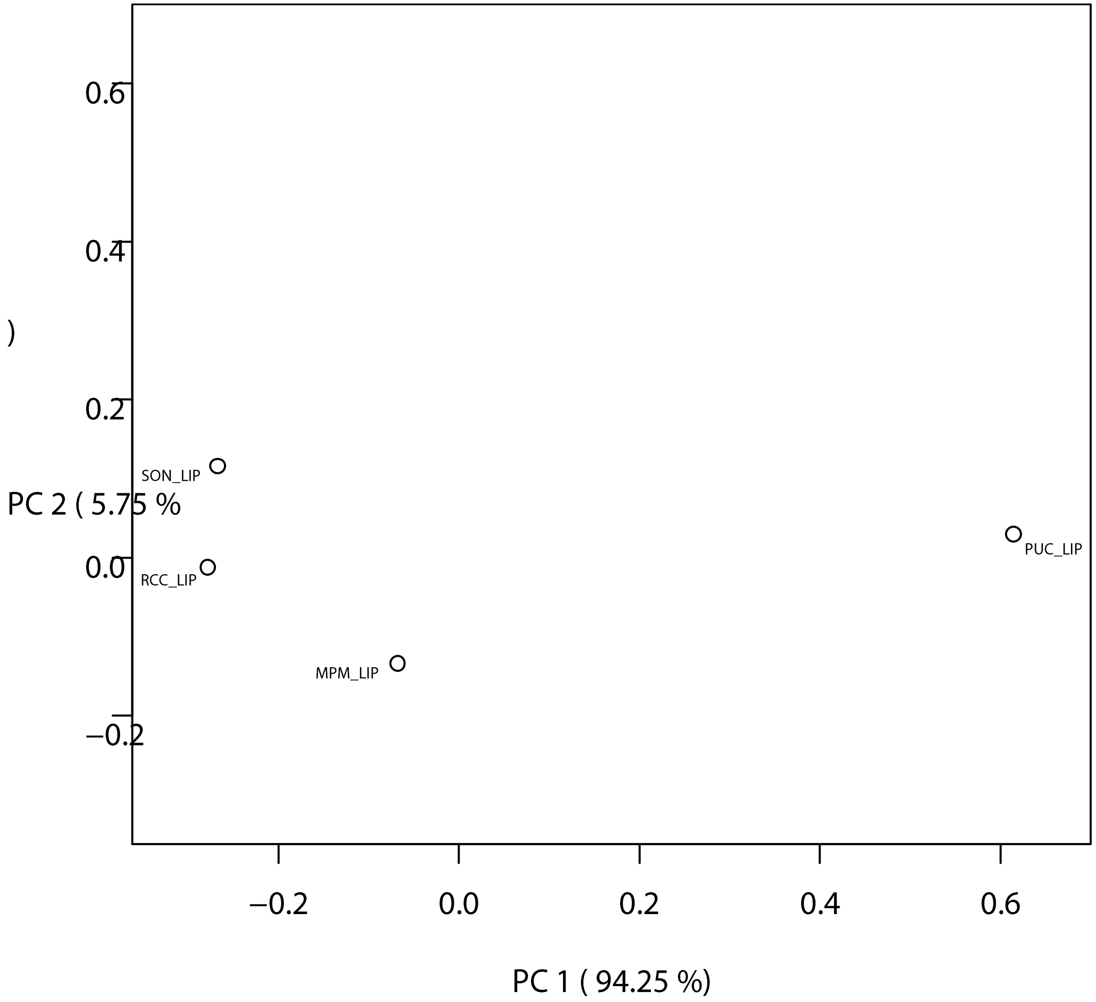


Figure 6.15. Andahuaylas Late Intermediate Period samples, plot of the first two principal coordinates.

6.3 R Matrices

The R matrices were calculated for all comparisons. These matrices are summarized in Tables 6.32 to 6.39. The R matrices were calculated to find the $F_{ST.}$ The F_{ST} is calculated as the mean of the diagonal of the R matrix, and is a measure of between-group microdifferentiation. The F_{ST} values derived from the R matrices are summarized in Table 6.40.

Table 6.32. R matrix for all samples.

	CON_MH	AYA_LIP	HUA_MH	MAR_LIP	TUR_MH	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP	AJA_MH	CAH_MH	CAN_MH	MAJ_MH	BER_MH	BER_LIP	ANC_MH	ANC_LIP
CON_MH	0.0951																
AYA_LIP	0.0131	0.0837															
HUA_MH	-0.0385	-0.0197	0.1244														
MAR_LIP	-0.0158	0.0006	0.0328	0.1170													
TUR_MH	-0.0023	-0.0113	0.0045	0.0368	0.0550												
SON_LIP	-0.0086	-0.0078	0.0109	-0.0035	-0.0105	0.0734											
MPM_LIP	0.0294	0.0169	-0.0039	0.0008	0.0078	-0.0137	0.0867										
PUC_LIP	0.0025	-0.0029	-0.0081	0.0353	0.0341	0.0143	0.0057	0.0864									
RCC_LIP	-0.0026	0.0090	-0.0162	0.0109	0.0141	0.0198	0.0659	0.0073	0.1048								
AJA_MH	0.0058	0.0029	-0.0009	-0.0509	-0.0180	-0.0134	-0.0135	-0.0500	-0.0159	0.1437							
CAH_MH	0.0132	0.0123	-0.0092	-0.0468	-0.0265	-0.0067	-0.0266	-0.0254	-0.0452	0.0574	0.0869						
CAN_MH	-0.0030	-0.0073	-0.0312	-0.0629	-0.0207	-0.0402	0.0037	-0.0421	-0.0009	0.0497	0.0232	0.0977					
MAJ_MH	-0.0164	-0.0309	0.0324	-0.0145	-0.0120	0.0006	-0.0228	-0.0229	-0.0276	0.0030	0.0194	0.0060	0.0614				
BER_MH	-0.0383	-0.0062	-0.0259	-0.0091	-0.0075	-0.0123	-0.0293	-0.0019	-0.0315	-0.0448	0.0093	0.0025	0.0062	0.1005			
BER_LIP	-0.0348	0.0308	-0.0475	0.0018	-0.0130	-0.0173	-0.0056	0.0079	0.0051	-0.1053	-0.0541	-0.0041	-0.0326	0.0889	0.2385		
ANC_MH	0.0097	-0.0515	-0.0524	-0.0200	-0.0107	0.0032	-0.0574	-0.0269	-0.0366	0.0223	-0.0029	0.0331	0.0245	0.0008	-0.0110	0.1529	
ANC_LIP	-0.0086	-0.0318	0.0485	-0.0126	-0.0199	0.0118	-0.0442	-0.0133	-0.0604	0.0279	0.0217	-0.0036	0.0262	-0.0013	-0.0477	0.0230	0.0841

Table 6.33. R matrix for all samples (AJA_MH and BER_LIP excluded).

	CON_MH	AYA_LIP	HUA_MH	MAR_LIP	TUR_MH	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP	CAH_MH	CAN_MH	MAJ_MH	BER_MH	ANC_MH	ANC_LIP
CON_MH	0.0958														
AYA_LIP	0.0174	0.0920													
HUA_MH	-0.0439	-0.0218	0.1196												
MAR_LIP	-0.0191	0.0002	0.0247	0.1135											
TUR_MH	-0.0061	-0.0110	-0.0002	0.0335	0.0531										
SON_LIP	-0.0155	-0.0094	0.0079	-0.0088	-0.0137	0.0739	-0.0200								
MPM_LIP	0.0296	0.0220	-0.0081	-0.0030	0.0041	-0.0200	0.0906	-0.0017							
PUC_LIP	-0.0029	-0.0050	-0.0144	0.0314	0.0321	0.0130	-0.0017	0.0900	0.0006						
RCC_LIP	-0.0046	0.0128	-0.0186	0.0075	0.0105	0.0157	0.0685	0.0006	0.1080	-0.0437					
CAH_MH	0.0126	0.0168	-0.0104	-0.0503	-0.0289	-0.0092	-0.0251	-0.0320	-0.0437	0.0926	0.0302				
CAN_MH	0.0009	0.0009	-0.0304	-0.0639	-0.0207	-0.0410	0.0099	-0.0466	0.0056	0.0302	0.1091	0.0075			
MAJ_MH	-0.0216	-0.0317	0.0300	-0.0199	-0.0158	-0.0010	-0.0261	-0.0280	-0.0291	0.0200	0.0075	0.0612	0.0076		
BER_MH	-0.0391	-0.0030	-0.0249	-0.0070	-0.0040	-0.0061	-0.0324	0.0066	-0.0327	0.0096	0.0028	0.0076	0.1131	0.0046	
ANC_MH	0.0089	-0.0479	-0.0541	-0.0203	-0.0105	0.0025	-0.0584	-0.0287	-0.0365	-0.0024	0.0379	0.0229	0.0046	0.1575	0.0246
ANC_LIP	-0.0123	-0.0323	0.0447	-0.0185	-0.0223	0.0116	-0.0499	-0.0145	-0.0641	0.0204	-0.0022	0.0240	0.0049	0.0246	0.0857

Table 6.34. R matrix for all Middle Horizon samples.

	CON_MH	HUA_MH	TUR_MH	AJA_MH	CAH_MH	CAN_MH	MAJ_MH	BER_MH	ANC_MH
CON_MH	0.1521								
HUA_MH	0.0046	0.2159							
TUR_MH	-0.0155	0.0254	0.0705						
AJA_MH	0.0225	-0.0315	-0.0233	0.2103					
CAH_MH	0.0493	0.0120	-0.0421	0.0631	0.0943				
CAN_MH	-0.0258	-0.0520	-0.0199	0.0009	-0.0105	0.0779			
MAJ_MH	-0.0114	0.0410	-0.0103	-0.0693	-0.0090	-0.0107	0.0574		
BER_MH	-0.1275	-0.0827	0.0198	-0.1332	-0.0783	0.0190	0.0201	0.2688	
ANC_MH	-0.0482	-0.1327	-0.0046	-0.0395	-0.0787	0.0211	-0.0079	0.0941	0.1965

Table 6.35. R matrix for all Middle Horizon samples (AJA_MH excluded).

	CON_MH	HUA_MH	TUR_MH	CAH_MH	CAN_MH	MAJ_MH	BER_MH	ANC_MH
CON_MH	0.2163							
HUA_MH	0.0519	0.2303						
TUR_MH	-0.0232	0.0126	0.0690					
CAH_MH	0.1177	0.0579	-0.0429	0.1723				
CAN_MH	-0.0147	-0.0483	-0.0189	0.0070	0.0780			
MAJ_MH	-0.0087	0.0336	-0.0207	-0.0053	-0.0152	0.0455		
BER_MH	-0.2258	-0.1552	0.0209	-0.1743	-0.0045	-0.0051	0.3711	
ANC_MH	-0.1133	-0.1827	0.0032	-0.1325	0.0166	-0.0242	0.1729	0.2598

Table 6.36. R matrix for all Late Intermediate Period samples.

	AYA_LI	MAR_LI	SON_LI	MPM_LI	PUC_LI	RCC_LI	BER_LI	ANC_LI
AYA_LI	0.1369							
MAR_LI	0.0021	0.1038						
SON_LIP	-0.0690	-0.0207	0.1108					
MPM_LI	0.0377	-0.0107	-0.0573	0.0901				
PUC_LIP	-0.0509	0.0134	0.0156	-0.0344	0.0936			
RCC_LIP	0.0071	-0.0004	0.0014	0.0473	-0.0310	0.0938		
BER_LIP	0.0201	-0.0506	-0.0555	-0.0083	-0.0200	-0.0436	0.1896	
ANC_LI	-0.0841	-0.0370	0.0747	-0.0644	0.0137	-0.0746	-0.0317	0.2033

Table 6.37. R matrix for all Late Intermediate Period samples (no BER_LIP).

	AYA_LIP	MAR_LIP	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP	ANC_LIP
AYA_LIP	0.1986						
MAR_LIP	0.0107	0.0989					
SON_LIP	-0.1112	-0.0375	0.1304				
MPM_LIP	0.0815	-0.0099	-0.0911	0.1181			
PUC_LIP	-0.0811	0.0023	0.0340	-0.0611	0.1226		
RCC_LIP	0.0327	-0.0044	-0.0259	0.0608	-0.0583	0.0995	
ANC_LIP	-0.1312	-0.0601	0.1013	-0.0983	0.0416	-0.1044	0.2511

Table 6.38. R matrix for all Andahuaylas samples.

	TUR_MH	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP
TUR_MH	0.3966				
SON_LIP	-0.3232	0.2936			
MPM_LIP	-0.0897	0.0814	0.0169		
PUC_LIP	0.0735	-0.1024	-0.0258	0.1379	
RCC_LIP	-0.0572	0.0506	0.0172	-0.0832	0.0727

Table 6.39. R matrix for Andahuaylas Late Intermediate Period samples.

	SON_LIP	MPM_LIP	PUC_LIP	RCC_LIP
SON_LIP	0.0850			
MPM_LIP	0.0026	0.0224		
PUC_LIP	-0.1608	-0.0457	0.3777	
RCC_LIP	0.0732	0.0208	-0.1712	0.0772

6.3.1 F_{ST}

The F_{ST} values for all comparisons are listed in Table 6.40. The F_{ST} values for the MH groups are the highest both when all samples are compared, and when the outliers (AJA_MH and BER_LIP) have been excluded. This suggests that populations were more genetically isolated during the MH than the LIP. The F_{ST} values for all MH samples (0.1493) and all LIP samples (0.1277) are not dramatically different, and may not indicate a significant difference in the amount of gene flow in the Peruvian Andes during the respective time periods. The difference between the MH and LIP comparisons when the outlier samples are removed is somewhat more dissimilar (0.1803 and 0.1456 respectively).

The Andahuaylas comparisons have very small F_{ST} values (Table 6.40). This suggests that these groups were genetically very similar to one another. There is a very slight decrease in the F_{ST} value from all Andahuaylas samples to only the LIP Andahuaylas samples. The decrease is only 0.0043 and may not be indicative of a increase in gene flow in this region from the MH to the LIP.

Table 6.40. F_{ST} values for all comparisons.

Comparison	**F_{ST} value**
All samples	0.1054
All samples(AJA_MH and BER_LIP excluded)	0.0970
All Middle Horizon samples	0.1493
All Middle Horizon samples (AJA_MH excluded)	0.1803
All Late Intermediate Period samples	0.1277
All Late Intermediate Period samples (BER_LIP excluded)	0.1456
All Andahuaylas samples	0.1835
Andahuaylas Late Intermediate Period samples	0.1406

6.4 Mantel tests of matrix correlations

The relationship between biological distance and relative geographical and chronological distances were also calculated (Tables 6.41 and 6.42). There were significant correlations at the $\alpha \leq 0.05$ level between the biological distance matrices for all samples, geographic distance, and chronological distance (Table 6.41 and 6.42). The biological distances among all samples were not significantly correlated with chronological distance once the Aja MH and Beringa LIP outlier samples were excluded (Table 6.41).

Partial correlations between the Mahalanobis D^2 matrices and geographic distance while controlling for chronological distance was also calculated (Table 6.42). However, only the partial correlations between all samples and both geographic distance matrices while controlling for time remained significant at the $\alpha \leq 0.05$ level when the Aja MH and Beringa LIP outliers were removed (Figure 6.42). The partial correlation between the biological distance matrix for all samples and chronological distance, while controlling for the geographic distance matrices were also significant (Figure 6.42). It is likely that the Aja MH and Beringa LIP outliers were influencing the significant partial correlations with chronological distance when controlling for geographic distance. Therefore, the significant results regarding chronological distance will not be discussed extensively in the following chapters.

Table 6.41. Mantel correlations.

Comparison	**Road/River Distance**		**Linear Distance**		**Chronological Distance**	
	Mantel statistic	**p-value**	**Mantel statistic**	**p-value**	**Mantel statistic**	**p-value**
All samples	0.3823	**0.019***	0.3828	**0.017***	0.1328	**0.016***
All samples (AJA_MH and BER_LIP excluded	0.3784	**0.002***	0.3774	**0.003***	0.1008	0.13
All Middle Horizon samples	0.3515	0.089	0.3337	0.099	NA	NA
All Middle Horizon samples (AJA_MH excluded)	0.2741	0.148	0.2542	0.177	NA	NA
All Late Intermediate Period samples	0.2107	0.200	0.2406	0.180	NA	NA
All Late Intermediate Period samples (BER_LIP excluded)	-0.0250	0.458	-0.0180	0.453	NA	NA
All Andahuaylas samples	-0.3569	0.781	-0.067	0.652	0.6257	0.191
Andahuaylas Late Intermediate Period samples	-0.0366	0.654	0.5286	0.253	NA	NA

*****Significant at α≤0.05

Table 6.42. Partial Mantel correlations.

Comparison	**Road/River distance controlling for time**		**Linear distance controlling for time**		**Time controlling for road/river distance**		**Time controlling for linear distance**	
	Mantel statistic	**p-value**	**Mantel statistic**	**p-value**	**Mantel statistic**	**p-value**	**Mantel statistic**	**p-value**
All samples	0.389	**0.011***	0.3873	**0.014**	0.1536	**0.014***	0.1469	**0.028***
All samples (AJA_MH and BER_LIP excluded	0.3847	**0.005***	0.3817	**0.002***	0.1253	0.073	0.1182	0.088
All Andahuaylas samples	-0.1205	0.652	-0.0613	0.616	0.5593	0.159	0.6254	0.182

*****Significant at α≤0.05

Chapter VII

Discussion

This chapter outlines the interpretations of the patterns in gene flow and biological distances presented in Chapter 6. Results indicate that gene flow was not affected by the collapse of the Wari empire when considered on the pan-Andean level. However, there are many interesting patterns present in the data when the results are considered on the regional scale. The discussion starts by comparing MH populations to LIP populations. Once outlier samples were removed, the Mantel tests comparing the biological distances to temporal distance did not reveal significant correlation (Tables 6.41 and 6.42). This indicates that if the samples are correctly categorized as MH or LIP populations then the patterns in genetic structure accurately represent changes in gene flow rather than other forces such as natural selection (Konigsberg, 1990). Certainly some populations represented by the study samples appear to have experienced increased gene flow during the MH. This is expected in the context of imperialism where economic and political objectives foment increased contact between regional groups that previously were isolated from each other. The population at the center of the empire (i.e. near or within the capital) would likely have an especially high rate of gene flow as immigrants came to the capital region, and members of the heartland population struck out on economic, militaristic, and political missions. Indeed, the Conchopata population appears to have experienced higher rates of gene flow when compared to the LIP Ayachucho (Huari) sample, and all other study samples.

It is possible that populations integrated into an empire could remain relatively genetically isolated. The Nazca River valley group will be examined as a possible case of resistance to the Wari empire. These samples have only moderate rates of gene flow despite archaeological evidence that suggests they had a close relationship to the Wari. This relationship between the Nasca and Wari may have been much more complex and nuanced than previously thought and deserves further research in the future.

The LIP samples are considered after the discussion of MH populations. The LIP samples reflect a general pattern of isolation by distance. The south-central highlands group of samples derived from sites around the modern city of Andahuaylas will also be discussed as a subset of the LIP group. The F_{ST} and biological distances illustrate patterns that are likely reflective of kin structure and economic interests. Interestingly, gene flow between these groups appears to remain consistent in the post-collapse era despite a dramatic increase in violence in the region (Kurin, 2012). Possible explanations of this pattern will be discussed in the following sections of this chapter.

7.1Cultural horizons

The Conchopata MH sample was the representative Wari heartland population that dates to the apogee of the empire. The F_{ST} for the MH samples (excluding AJA_MH), 0.1803, is higher than the F_{ST} for the LIP samples (excluding BER_LIP), 0.1456, indicating that gene flow was lower during the MH as compared to the LIP. F_{ST} is calculated as an average of the diagonal values of the R matrix (rii values). While the rii values of the R matrix that correspond to the study samples are not directly relatable to the amount of within-group variation, they inform on how each sample was contributing to the F_{ST} value. Though the overall F_{ST} is higher for the MH samples as a group, the value on the diagonal of the R matrix that corresponds to the Conchopata MH sample is moderate at 0.0958 when all samples are compared, and 0.2162 when the MH samples are compared as a subset (Tables 7.1 and 7.2). The population at Conchopata during the MH was experiencing higher gene flow relative to the other sample populations, but not dramatically higher. It is worth noting that the Conchopata skeletal population is somewhat atypical in the distribution by sex. The root cause of the large female population at Conchopata during the MH may also have had an impact on the results of this analysis.

While Wari imperial objectives may not have significantly increased pan-regional gene flow in the Peruvian Andes, it seems that populations near the capital Huari were experiencing higher rates of gene flow. The Conchopata skeletal population consists of significantly more females than males (62% and 38% respectively) (Tung, 2007). The sample used in this study mirrored this pattern. There are several possible explanations for this disparity including the possibility that the males just have not yet been recovered and remain buried at the site. It has been suggested that the “missing males” were warriors and died in regions away from Conchopata during military conquests (Tung, 2007; see also Ochatoma and Cabrerra, 2002). If this were the case, it could explain the relatively higher rate of gene flow for this population. Warriors may have brought wives[4] home to Conchopata from regional populations where Wari military campaigns took them. Tung and Knudson (2011) address the possibility of Wari captives being brought to Conchopata in their recent publication. Their findings based on Strontium (Sr) isotope data indicate the Conchopata burial population was comprised of local individuals (trophy heads recovered at Conchopata have a non-local Sr pattern (Tung, 2003) and were not included in this study). In a sample of 31, only two individuals were non-local (Tung and Knudson, 2011: 256). The two non-local individuals identified by Tung and Knudson were not included in this study. Despite the Sr results, the low R matrix diagonal value for the Conchopata sample may still be due to warriors returning with non-local wives. If so, then those sampled in the Sr study represented later generations of offspring.

---

[4] The use of the word wives here implies women that returned with warriors and later produced offspring thus contributing to the gene pool. It is not meant to indicate that the women were willing migrants, and may more accurately have been captives.

Table 7.1. R matrix rii values arranged is descending order by site for all samples (AJA_MH and BER_LIP excluded).

Sample	rii
TUR_MH	0.0531
MAJ_MH	0.0612
SON_LIP	0.0739
ANC_LIP	0.0857
PUC_LIP	0.0900
MPM_LIP	0.0906
AYA_LIP	0.0920
CAH_MH	0.0926
CON_MH	0.0958
RCC_LIP	0.1080
CAN_MH	0.1091
BER_MH	0.1131
MAR_LIP	0.1135
HUA_MH	0.1196
ANC_MH	0.1575

F_{ST}=0.0970

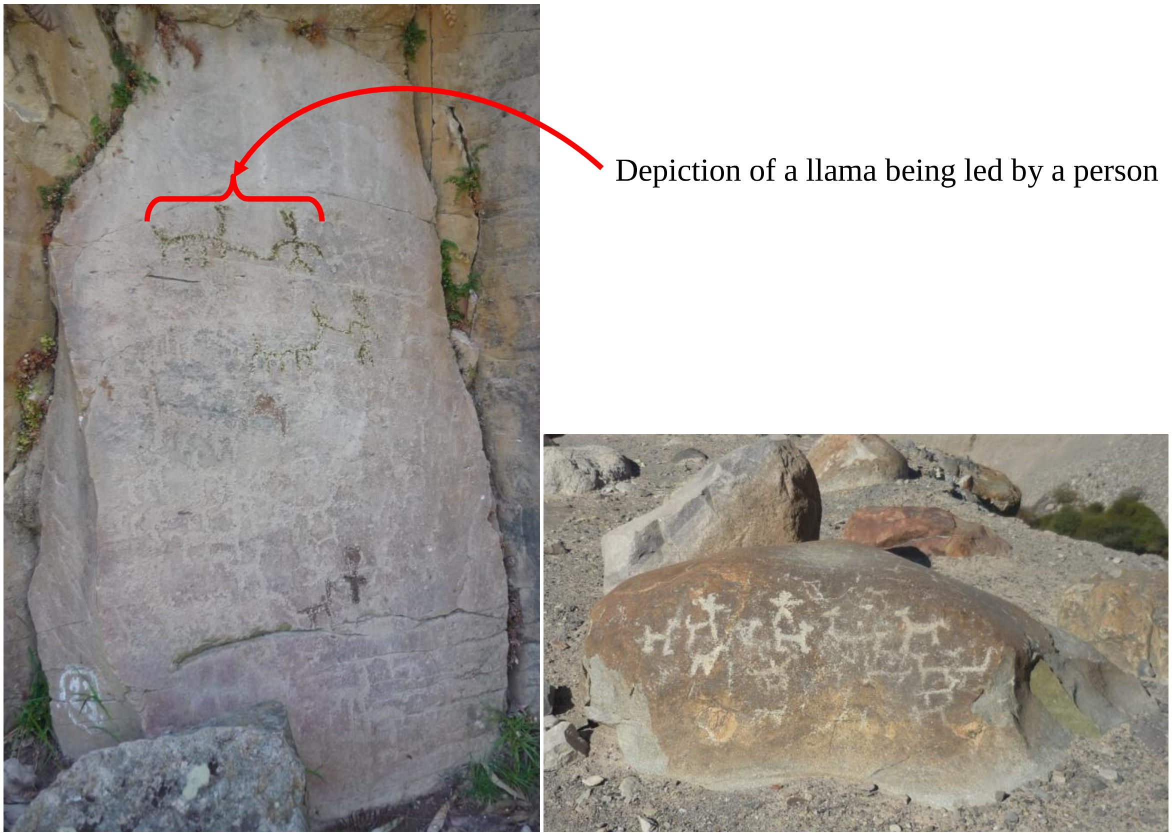
Table 7.2. R matrix rii values arranged is descending order by site for all Middle Horizon samples (AJA_MH excluded).

Sample	rii
MAJ_MH	0.0455
TUR_MH	0.0690
CAN_MH	0.0780
CAH_MH	0.1723
CON_MH	0.2163
HUA_MH	0.2303
ANC_MH	0.2598
BER_MH	0.3711

F_{ST}=0.1803

Populations from the Wari heartland may have been experiencing changes in gene flow consequent to imperial activities other than, or in addition to, military conquest. The Conchopata MH sample separates along the first principal coordinate with the rest of the highland groups when all samples were considered in the biological distance analyses (Figures 6.3 and 6.4). This pattern suggests that interaction between highland populations was probably more intense than interaction between highland populations and those occupying lower elevations. Despite the ubiquity of the Wari cultural influence in the Peruvian Andes during the MH, much less evidence of Wari has been identified in coastal contexts. The results of this study also support a “buffer” (in a genetic sense) between highland populations and those occupying lower elevations.

When considering all MH samples the Conchopata MH, Turpo Qatun Rumi MH, and Nazca Valley samples had a particularly small biological distance (Table 6.17). The probable close biological affinity between the Conchopata and Turpo Qatun Rumi populations during the MH could be explained by their close geographical proximity (Figures 5.2 and 5.3, Table 5.3). Mantel tests of correlation indicate that there is a correlation between geographic distance and biological distance for the study samples (Tables 6.41 and 6.42). The Nasca populations however are not geographically proximate to Conchopata and Turpo Qatun Rumi yet the biological distance results are consistent with a close genetic relationship (Figures 6.3, 6.4, 6.7, and 6.8). This cluster is even more evident when only MH samples are compared (Table 6.19, Figures 6.7 and 6.8). The road and river distance between Conchopata and Turpo Qatun Rumi and the Nazca Valley ranges from 100 to 400 km. This is no small distance even with modern means of transportation, and is even more dramatic when considering that MH populations probably would have covered the distance by llama caravan (Figure 7.1). If the biological distances between these groups do reflect significant contact between populations there must have been a strong incentive to motivate such long distance travel.



Depiction of a llama being led by a person

Figure 7.1 Rock art depicting llama caravans from Andahuaylas (left) and the Tinku site located in the Majes valley near the Beringa site (right).

7.1.1 Ancón's place in the Middle Horizon

While the biological distance results do not indicate a close relationship between Ancón and any of the other populations sampled there is physical evidence that people from the Wari heartland may have been present in Ancón during the MH. Slovak et al. (2009) identified a young female with a non-local Sr signature that overlapped the known Ayacucho range. This in itself is not strong evidence that Wari heartland populations had a significant presence in Ancón. However, the archaeological context of the young girl, including Wari-style dress and mortuary offerings, suggested that she may have been an important Wari figure (Slovak et al., 2009). Taken together, evidence of Wari physical presence in Ancón, without a close genetic relationship to populations in the Wari heartland, may be reflective of Schreiber's (1992) mosaic interpretation of Wari imperialism. Schreiber stated that in regions where a developed infrastructure already existed, the intruding empire may not leave a strong archaeological signature. Ancón existed as a major occupation long before the rise of the Wari empire in the MH. Ancón is also in close proximity to Pachacamac which was an important pilgrimage center since the Early Horizon (Rostworowski, 1992). The Wari would only have had to insert their administration into the existing infrastructure at Ancón, probably through alliance negotiation, to effectively incorporate the territory. An alliance with local elites at Ancón would minimize cost to the empire and allow the Wari to have hegemonic control over a large territory.

7.1.2 Populations in Ayacucho after the Wari Empire

It appears that these populations became genetically isolated after the collapse of the Wari empire. The rii value for the Ayacucho LIP sample is higher than the Conchopata MH sample when all samples are compared. When the LIP subset of samples is compared the Ayacucho LIP sample has the second largest value (Tables 7.1 and 7.3). This suggests that the population in the Wari heartland became more isolated during the LIP. Kemp et al. (2009) found that there was no significant difference between the population at Conchopata and Huari (represented by the Ayacucho LIP sample in this study) on the basis of mitochondrial DNA evidence. The data in this study do not specifically address the exact genetic relationship between the MH and LIP inhabitants of the Ayacucho Basin, but can be interpreted as consistent with the Kemp et al. (2009) study. A larger sample representative of Huari and the Wari heartland both pre- and post collapse is necessary to fully address the question of population continuity in the region.

Table 7.3. R matrix rii values arranged is descending order by site for all Late Intermediate Period samples (BER_LIP excluded).

Sample	Diagonal value
MAR_LIP	0.0989
RCC_LIP	0.0995
MPM_LIP	0.1181
PUC_LIP	0.1226
SON_LIP	0.1304
AYA_LIP	0.1986
ANC_LIP	0.2511

F_{ST}=0.1456

7.2 The Nasca and resistance to the Wari Empire

The Nasca have a well documented relationship with the Wari. Dorothy Menzel (1964) worked extensively with both Nasca and Wari ceramics and proposed the two cultures were very closely tied together. She found that ceramics in Ayacucho dating back to the pre-Wari EIP borrowed both technological and iconographic elements from the Nasca (see also Benavides, 1971; Cook, 1985; and Knobloch, 1976) (Figure 7.2). In addition to strong similarities in ceramic styles, and probably ideology, between Wari and Nasca there is also archaeological evidence of a physical presence of Wari administrators in the Nazca River drainage. Pacheco has long been recognized as a possible Wari administrative center in the lower Nazca Valley (Menze,l 1964; Schreiber, 2001). More recently Pataraya, also located in the lower Nazca drainage just north of sites included in this study, has been identified as a smaller Wari administrative outpost (Edwards, 2010; Schreiber, 1999, 2001). Patarya is located along roads that likely connected Huari to the coast via Jincamocco (Edwards, 2010). This archaeological evidence has interesting implications with regard to biological distance and gene flow during the MH reflected in this study.

Figure 7.2. A comparison of EIP Nasca ceramic style (left, http://precolumbiancivilizations.pbworks.com), and an early Wari ceramic vessel recovered from the Huari site (right). Note the similarity in colors and form of the fish depicted on each vessel.

After the Aja sample was removed from analysis as an outlier, the rii values for MH samples were generally higher than that for the LIP indicating that relatively less gene flow was occurring in the MH (Table 7.1). The notable exceptions to this pattern are Turpo Qatun Rumi MH and Majoro Chico MH which have the lowest rii values (Table 7.1), and appear to have a close biological relationship (Figures 6.7 and 6.8). Plots of biological distances in the MH also illustrate the Nasca samples did not have uniform biological affinity with Conchopata, or with each other (Figures 6.7 and 6.8). The results of this study are indicative of a complex relationship between the Wari heartland and Nasca populations. On a case-by-case basis the biological distance results are quite consistent with the archaeological record in the Nazca Valley.

There is archaeological evidence for a strong Wari presence in the Nazca Valley; however there is also evidence that Nasca populations resisted Wari occupation. Schreiber (2001) found that during the period of Wari expansion into the Nazca drainage there was a decrease in the number of villages and smaller settlements. It appeared that the Nasca population consolidated and moved to the far south part of the Nazca drainage, far away from the Wari settlements including Pacheco, Pataraya, and Incawasi (Schreiber, 2001; Edwards, 2010) (Figure 7.2). This shift in settlement pattern could indicate that Nasca populations were resistant to Wari rule. Conlee and Schrieber (2006) hypothesized that resistance to Wari rule was probably initiated by local Nasca leaders.

Nasca trophy heads also provide a line of evidence for exploring resistance to the Wari. Both the Nasca and the Wari produced trophy heads. However, they were very distinctive in their manufacture and treatment. There is little doubt that the manufacture and display of trophy heads was meant to showcase the power of those that possessed them (Andrushko, 2011; Tung, 2003, 2008b; Forgey, 2006; Forgey and Williams, 2005). In both cases the manufacture of the trophy heads was very consistent indicating that the procedure was controlled possibly by state administration or religious canons. Nasca trophy heads had a hole in the frontal bone where Wari trophy heads consistently have the suspension hole located more superiorly at or near bregma (Andrushko, 2011; Forgey, 2006; Tung, 2008b). Wari trophy heads were ritually destroyed by smashing and burning (Andrushko, 2011; Tung, 2003, 2008b), where Nasca trophy heads were not destroyed (Forgey and Williams, 2005; Forgey, 2006). The origin of individuals that subsequently became trophy heads also differs between the Nasca and Wari. Forgey (2006, 2011) sequenced mtDNA of trophy heads that dated slightly earlier than this study population and found that they were likely derived from the local population. Tung and Knudson (2011, and Tung, 2003, 2008b) used Sr isotope analysis to evaluate the geographical origin of Wari trophy heads from Conchopata and found a number of non-local individuals. The differential use of local versus non-local individuals to make trophy heads suggests they may have served different purposes in each community. Even without a nuanced understanding of the function of trophy heads in Nasca versus Wari cultures, the distinctiveness of their manufacture and treatment indicates that if trophy heads continued to be made into the MH by the Nasca, this practice was not controlled by the Wari administrators.

Although some elites may have resisted imperial rule, others likely allied themselves with the Wari. There is no evidence of a military conquest of the Nazca drainage, and the Wari likely made alliances with local elites affecting their governance through these intermediates. Kolata (2010) termed this kind of imperial incorporation as hegemony without sovereignty. One of the Nasca samples included in this study appears to have experienced more gene flow relative to the others (Table 7.2). Majoro Chico has the lowest rii value (0.0455) when the MH samples are compared. Majoro Chico also clusters tightly with Turpo Qatun Rumi when biological distances were plotted (Figures 6.7 and 6.8). It is possible that the population at Major Chico had a closer relationship with the Wari and did not resist incorporation into the empire. In their study of Nasca remains using Sr isotope analysis of populations near Majoro Chico Conlee et al. (2009) found a largely local population with the exception of two individuals from the MH. Though this further suggests a direct Wari presence in the region, at present there is not enough archaeological evidence available to test this hypothesis.

Figures 6.7 and 6.8 illustrate a close biological relationship between the Wari heartland sample from Conchopata and the Cahuachi sample. Cahuachi had previously been an important ceremonial center for the Nasca during the EIP, and a place where spiritual and political leaders resided (Silverman, 1993; Silverman and Proulx, 2002; Valdez, 1994; Vaughn, 2004). Given the earlier importance of Cahuachi it is not surprising that the Wari rule would implant themselves in this area. Indeed, the ceremonial site Pacheco is within a kilometer of Cahuachi. The biological affinity between Conchopata and Cahuachi may reflect an alliance between these groups. Given the evidence of strong ties between the Nasca and populations in Ayacucho before the rise of the Wari empire this relationship may have even predated the MH.

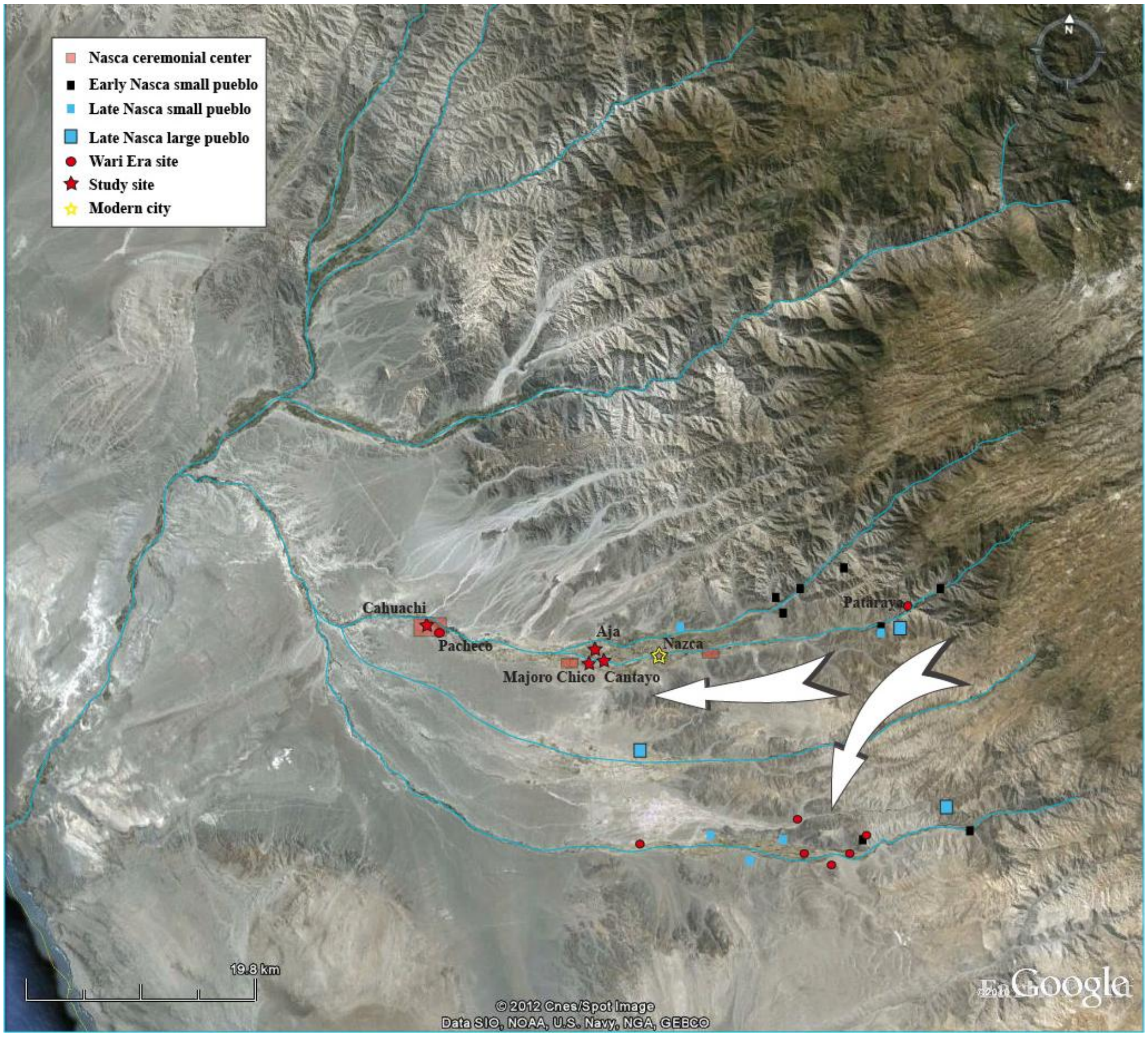


Figure 7.3. Illustration of settlement shift in the lower Nazca River drainage between the EIP and MH (after Schreiber 2000:440-442).

There is another possible interpretation of the pattern observed with the Nazca River Valley samples. Previous research suggests that the Wari withdrew from the Nazca River Valley long before the full collapse of the empire (Conlee, 2000, 2006; Edwards, 2010; Schreiber, 2001). The collapse of the Wari empire in the Nazca drainage caused a major disruption to populations living in the area. Given the relative dating of the Nasca samples used in this study (Kroeber and Collier, 1998), it is possible that they more accurately represent post-collapse populations. As such, they would be more appropriately grouped with the LIP samples. If that is the case then the results can be interpreted and genetic isolation subsequent to the Wari collapse. A pattern of genetic isolation would be consistent with site abandonment and population relocation described by Schreiber (2001).

7.3 Post-collapse societies in the Peruvian Andes

The collapse of a state or empire is often conceptualized as one dramatic, or even cataclysmic, event in prehistory. This is probably because archaeologists do not have the capability to see time at a fine scale, so events that unfold over a hundred years appear instantaneous in the material record. Yoffee (1988; see also Schreiber 2001) reminds archaeologists that collapse is a process by which very complex societies reorganize into a less complex structure. In section 7.1 the post-collapse population in the Wari heartland, represented by the Ayacucho sample, was compared to the pre-collapse Conchopata sample. The post-collapse population appears to have experienced less gene flow than the population that lived during the height of the Wari empire (Table 7.1). Furthermore, when only the LIP samples are compared, the Ayacucho sample has one of the highest rii values suggesting that of all the populations sampled from the LIP they were one of the most genetically isolated (Table 7.3). Kemp and colleagues (2009) sequenced mtDNA of specimens from Conchopata and the population living at Huari after the collapse of the Wari empire. Their study did not find a significant difference between the two populations and could not demonstrate that the people who lived at Huari after the collapse of the empire were not a locally derived population (Kemp et al., 2009). If this was the case then the results of this study suggest a radical change in social interaction in and around the Ayacucho Basin after AD 1000.

A shift in the nature of social interaction is supported by the archaeological record of the Wari heartland. Huari, the Wari capital, was abandoned around AD 1000, and subsequently repopulated (Isbell et al., 1991; Ochatoma and Cabrera, 2002). Evidence of violence consistent with raiding increased significantly during the LIP in this region (Tung, 2009; see also Glowacki, 2005, Kurin, 2012, and Verano, 2005). A sharp increase in interpersonal violence and raiding was likely one of many factors that contributed to the relative genetic isolation of the population in Ayacucho after the collapse of the Wari empire. However, results from this study suggest that increased violence was probably not the singular factor that impacted regional gene flow. The overall F_{ST} for the LIP group is lower than that of the MH group meaning that gene flow was either not significantly impacted by the end of the Wari cultural horizon, or actually increased during the LIP. The Andahuaylas group experienced a similar significant increase in violence after the Wari collapse; however F_{ST} values indicate that the rate of gene flow in the region was unaffected (Table 6.40). It is clear from the results of this study and others that the structural change in social interactions in the Ayacucho Basin after the collapse of the Wari empire is multifaceted and far from well understood.

7.3.1 The Chanka and social structure in the south-central Andes

The populations that the south-central highland samples represent likely identified as ethnic Chanka (Kurin, 2012). When both MH and LIP samples were compared Turpo Qatun Rumi had the lowest R matrix diagonal value consistent with a higher rate of gene flow compared to the LIP samples (Table 7.1). As discussed in section 7.1 of this chapter, the Turpo Qatun Rumi sample clusters with Conchopata MH and the Nasca (especially Majoro Chico MH) when all samples were compared (Figures 6.3 and 6.4) and when only MH groups are compared (Figures 6.7 and 6.8). As might be expected, the population at Turpo Qatun Rumi had a closer biological affinity to MH populations than the LIP samples from the same region.

When all of the south-central highlands samples were compared Turpo Qatun Rumi was an outlier (Figures 6.13 and 6.14). These results are consistent with archaeological findings that Turpo Qatun Rumi was a small Wari outpost. The site is located adjacent to a road that would have connected it with larger Wari administrative centers including Jincamocco and Pikillacta (Kurin, 2012). During the MH the Turpo Valley was a center of intensive maize production, however shortly after the Wari collapse Turpo Qatun Rumi was abandoned (Kurin, 2012). Evidence of a relatively higher rate of gene flow experienced by the population at Turpo Qatun Rumi and their position as an outlier when compared to the LIP samples in the same region is congruent with the archaeological findings. Both lines of evidence suggest that the people at Turpo Qatun Rumi had a much stronger relationship with the population in the Ayacucho Basin than the LIP population.

As discussed previously, although the MH sample from the Andahuaylas group probably had more intensive contact with populations in the Wari heartland, the collapse of the empire does not appear to have significantly affected the overall rate of gene flow in the region. The distance analyses comparing all samples and only LIP samples illustrate the biological affinity of these samples to each other as they consistently cluster together (Figures 6.3, 6.4, 6.11, and 6.12). Bauer and colleagues (2011; see also Kellett, 2010) conclude, based on archaeological survey and radiocarbon dates, that there was a radical shift in settlement patterns in the Andahuaylas region at about AD 1000 concurrent with the demise of the Wari empire. If this is the case, it does not seem to have disrupted rates of gene flow. However, this is a tentative interpretation as this study is not, nor the others mentioned here, exhaustive. Much more research is necessary to accurately describe the population structure and settlement patterns in the south-central highlands during the MH and LIP.

7.3.2 Ethnohistory and biology

The LIP samples from the Andahuaylas group are unique in this study in that there is not only archaeological evidence, but also ethnohistoric information available regarding these populations. During the early colonization of Peru by the Spanish many small villages and towns were consolidated into larger regional *reducciones*. This strategy allowed the Spanish to more easily administrate their new colonies. Andahuaylas was one of these *reducciones* under the charge of Sr. Diego Maldonado. In 1539 Maldonado wrote an *Encomienda de Andahuaylas* (translated by Busto Duthurburu, 1962; Lockhart, 1977:221-223; Puente Brunke, 1992). The *encomienda* was delivered to Francisco Pizzaro and summarized the resources in the region of Andahuaylas. In addition to enumerating resources available for Spanish exploitation, Maldonado also described populations that lived in the region and their social organization. Although the *encomienda* written in 1539 postdates the samples in this study it is reasonable to assume that social organization had not changed significantly during the Inka imperial rule. Maldonado described a moiety system, common to many Andean societies, where the upper (*hanan*) moiety would have included Sonhuayo and Mina Puka Machay, and the lower (*hurin*) moiety would have included Ranra Cancha and eventually Pucullu.

Though it is worth noting that before being subsumed by the Ranra Cancha group Pucullu was identified as an ethnic enclave by Maldonado. The patterns in the biological distance results for this group tend to follow the ethnohistoric evidence. When only the LIP samples from the Andahuaylas region were considered the Sonhuayo and Ranra Cancha samples separated along the second principal coordinate (Figure 6.15). Additionally, Pucullu appears as an outlier, not clustering with any other samples (Figure 6.15). These results strongly support the interpretation of Pucullu as an ethnic enclave that maintained genetic isolation from the other groups. The results are also consistent with a less dramatic genetic distinction between the Sonhuayo and Ranra Cancha groups that could be structured by cultural restrictions on mate choice expected in a moiety kinship system.

Wernke (2007) presents a detailed study of strategies employed by both the Inka and Spanish to embed their administration in existing dualistic kinship systems in the Colca Valley, Peru. The Inka may have introduced the moiety system here to foster competition thus increasing agricultural productivity in the valley. Following the Inka, the Spanish acknowledged the moiety system already functioning in the Colca Valley (Wernke, 2007). The Spanish strategy included the construction of an administrative center at the physical intersection of land used by each half of the moiety system ("right" and "left" in this case). Thus the Spanish colonizers took a different approach than the Inka, while still utilizing the dual organizational structure to their benefit. In the case of the Andahuaylas samples in this study the Inka may have imposed the *hanan/hurin* distinctions on an existing dualistic kin structure to increase agricultural production similar to the Colca Valley. The Spanish recognized the existing moieties when they colonized the region and established the Andahuaylas *reducción* geographically halfway between the Cachi settlements (*hanan*) and Ranra Cancha (*hurin*) (Figure 4.13). Wernke (2007) demonstrated this pattern in social organization over time through detailed archaeological survey, excavation, and spatial analysis. Given the lack of correlation between biological distances and time for the Andahuaylas samples in this study (see Figures 6.41 and 6.42), the genetic structure of these groups supports a similar interpretation of dual social organization.

While the Sonhuayo, Ranra Cancha, and Pucullu samples behaved much as would be expected given the ethnohistorical and archaeological evidence one group did not. The Mina Puka Machay sample was expected to cluster with the Sonhuayo population based both on geographic proximity and its inclusion in the upper moiety. However Mina Puka Machay is an outlier group (Figure 6.15). Mina Puka Machay is also located adjacent to a salt mine that is still intensively exploited. Kurin (2012) cites recent ethnographic evidence that indicates this salt mine was important in antiquity as well. People probably came from as far as 100 km away to mine salt. With the salt mine recognized as an important regional resource, the mortuary program at Mina Puka Machay may have been quite different from that practiced at other regional sites. It is possible that regional groups placed their ancestors in the *machay* to assert rights over the salt resources. Placement of one's ancestors to claim rights over territory and/or resources is not an uncommon practice in the Andes, or any part of the world (see Goldstein's (1981) revision of Saxe's Hypothesis 8). When all samples are considered Mina Puka Machay appears to have a close biological affinity to the Wari heartland samples (Conchopata MH and Ayacucho LIP) (Figures 6.3 and 6.4). Inhabitants from the Ayacucho Basin may have placed mummy bundles in the *machay* to assert their rights to the salt resource. If this was the case at Mina Puka Machay then the sample used in this study is not reflective of the population that lived in the immediate vicinity. It is difficult to say exactly where the remains recovered at Mina Puka Machay were from, but the relative heterogeneity of the group is evident in the results of this analysis. Besides their position as an outlier in the biological distance analysis, the Mina Puka Machay group has a relatively low rii value when compared to all samples (Table 7.1). This is indicative of more within-group heterogeneity for the Mina Puka Machay sample than most other study samples. Elevated within-group heterogeneity would be expected if the group actually represented a multi-regional sampling rather than just the local population. Taken together, the Andahuaylas group is an excellent example of how biological distance analyses can enrich archaeological and ethnohistoric interpretations and vice versa.

7.4 Isolation by distance and by culture? The north-central highland samples.

The north-central highlands are represented by two samples in this study, Hualcayan MH and Marcajirca LIP. In all the comparisons both Hualcayan and Marcajirca tend to separate from the rest of the samples (Figures 6.3 and 6.4). Both samples also appear to have been relatively genetically isolated from the other populations. The rii values for Hualcayan are high in the comparisons of all samples and only MH samples (Tables 7.1 and 7.2). The same can be said for the R matrix diagonal values for Marcajirca when compared to all samples and only the LIP samples (Tables 7.1 and 7.3). Located in the north-central highlands, both Hualcayan and Marcajirca are geographically distant from the other populations (Figure 1.1 and Table 5.3). Results of the Mantel test indicate a significant correlation between biological distances and spatial distance (Tables 6.41 and 6.42). Given these results it is not unexpected that both Hualcayan and Marcajirca would have less of a biological affinity with the other populations. When all groups are compared Hualcayan and Marcajirca do not cluster with each other on the basis of biological distance (Figures 6.3 and 6.2). Consistent with these results, it is not unreasonable for there to be evidence of genetic isolation with regards to these two groups. They are physically separated by the Cordillera Blanca which includes some of the highest peaks in the Andes (Figure 1.1). They are also separated temporally with the Hualcayan sample dating to the MH and Marcajirca to the LIP. Variables such as spatial and temporal distance should result in a pattern of reduced gene flow between these populations.

7.4.1 Hualcayan and the Wari Empire

The population at Hualcayan experienced relatively low rates of gene flow compared to the other MH samples (Table 7.2). There is archaeological evidence to suggest that the Wari had a presence in the north-central highlands. Isbell (1991) offered Honcopampa as a Wari administrative center in the Callejón de Huaylas, not far from Hualcayan. Viracochapampa has also been cited as an example of Wari attempts to incorporate the north-central highlands. However Topic (1991; Topic and Topic, 1987) found the Wari occupation to be brief and construction of Viracochapampa was never finished. Pariamarca, located only eight kilometers south of Hualcayan, has also been cited as a possible Wari administrative center (Jennings and Craig, 2001; Williams and Pineda, 1985). However, survey and test excavations in the plaza structure at Pariamarca by Rebecca Bria in 2009-2010 were unable to date the structure (Bria and Rivas Otaiza, 2010). The mortuary context at Hualcayan has not been radiocarbon dated at this time, but ceramic and architectural evidence strongly suggests the tombs date to the MH (Pink and Bria, 2011; Pink, 2011). Compared to other regions in Peru, very little archaeological investigation has been done in the north-central highlands and especially in the Callejón de Huaylas. The R matrix diagonal values for Hualcayan and Marcajirca suggest that if the Wari had a presence in the north-central highlands their activities did not significantly affect rates of gene flow. This interpretation should be considered a cautious one given the lack of absolute dates for the Hualcayan sample. Furthermore, the Hualcayan and Marcajirca samples used in this study are not a representative sample of the entire north-central highlands which were undoubtedly dynamic with respect to social structure and population movements over the MH to LIP.

Linguistic evidence suggests that populations in the north-central highlands may have maintained relative isolation from other groups over the long durée. Both Hualcayan and Marcajirca are located in the Department of Ancash, Peru. The variant of the indigenous language, Quechua, spoken in Ancash has been recognized as distinctive from other dialects of Quechua (Figure 7.4). Some have even proposed that Ancash Quechua is a unique language (Cole and Hermon, 1994; Isbell, 2010). The distinctive form of Quechua spoken by indigenous people in Ancash is probably due to the region being relatively isolated. Linguistic groups have been shown to correlate to patterns in biological distance in previous studies (for example Greenberg et al., 1986). Cecil Lewis and colleagues (2005) compared variation in the mtDNA of 33 indigenous Ancash residents to other North and South American indigenous groups and found a high level of within-group heterogeneity. The Ancash sample was very also similar to other South American populations with respect to genetic variation and showed no evidence of recent episodes of genetic drift. These results are consistent with other studies of genetic diversity among South Americans that have generally found this group to be a very homogenous one (Barbujani et al., 1997; Fuselli et al., 2003; Luiselli et al., 2000). Lewis et al. (2005) also found correlation between linguistic groups and biological distances. This finding supports the hypothesis that the distinctive Ancash Quechua and relatively large biological distances between Hualcayan, Marcajirca, and the other study samples both reflect population history in this region. Though multiple studies have now shown an association between language and the genetic structure of Andean populations, further empirical testing of prehistoric samples would be needed to draw any conclusions for Hualcayan and Marcajirca.

Figure 7.4. Languages spoken by region from Isbell (2010:201). "Quechua Central" correlates to the Ancash region.

7.5 Central Andean highlanders, ancient DNA, and cranial non-metric traits

The biological affinities of the highland populations sampled in this study suggest that this group was genetically distinct from populations living to the west in the valleys and on the coast (Figures 6.3 and 6.4). Recent studies of both ancient DNA (aDNA) and modern DNA reveal similar patterns where Andean highlanders are very distinct from coastal populations. Many of these studies have been focused on the initial peopling of South America. For example Fuselli and colleagues (2003) have demonstrated a east-west pattern of differentiation where Andean populations comprise a unique and genetically homogeneous group (see also Callegari-Jacques et al, 2011; Hunley and Healy, 2011; Fehren-Schmitz et al., 2010; Shinoda et al., 2006; Lewis et al., 2005). As discussed in the previous section Lewis et al. (2005) found that Ancash highlanders were similar to other Andean populations with respect to genetic heterogeneity. However, his findings also demonstrated a distinction between highland and coastal populations (see also Lewis et al. 2007a, 2007b). Hunley and Healy (2011) explored the possibility that European admixture was masking actual past evolutionary events when modern DNA was being considered. They found that although admixture may heighten the appearance of genetic differences between Andean and Amazonian populations, these large scale differences are accurately identified in DNA studies. Hunley and Healy (2011) also found that gene flow between neighboring populations had little effect on macrogeographic patterns in genetic diversity. Results indicating that the Wari cultural horizon had little impact on the overall central Andean population genetic structure, but almost certainly affected groups on the regional scale as reflected by the R matrices and F_{ST} values are congruent with Hunley and Healy's (2011) findings.

7.6 Summary of findings

The major finding of this study was that the collapse of the Wari empire had no significant impact on gene flow in the Peruvian Andes. A general pattern of isolation by distance was observed in the study populations, but temporal distance was not significantly correlated to biological distances when outlier populations were removed from the analysis. Many more nuanced regional patterns were revealed in their genetic structure when populations were analyzed in subsets. In particular, rates of gene flow in the Wari heartland did appear to have been affected the collapse; and the LIP population is relatively more isolated when compared to the MH populations. The study data also reflect a complicated relationship between Nasca populations and the Wari heartland during the MH. Another interesting, and more subtle, pattern emerged when the south-central highland samples were compared. This group was unique in this study because ethnohistoric data was available for comparison with archaeological and biological distance results. Here the biological distance results appeared to be in congruence with the historic data. In the north-central highlands samples a pattern of isolation emerged. These results were consistent with other studies of South American genetic variation, and may reflect linguistic differences among the sampled populations as well. All of these interpretations warrant further research. The possibility of studying larger, more representative osteological and material culture collections is constantly increasing as the political climate changes in Peru and more researchers and students become interested in the population and culture history of South America.

Chapter VIII

Conclusions and Future Directions of Research

8.1 Conclusions

This study demonstrated that the cultural horizon fomented by the Wari empire in the Peruvian central Andes had no significant impact on social interaction on the pan-regional scale. The results do however; support the argument that imperialism is a dynamic process, and on the small scale there were dramatic variations in social interaction and organization. Furthermore, results indicated that the collapse of an empire is equally dynamic and should also be considered a process not an event. Regionally specific patterns in population genetic structure likely reflect flexibility in Wari imperial strategies and the unique approaches of individual communities when dealing with the Wari cultural horizon whether or not there was direct contact with the Wari empire. There is no strong evidence to suggest any of the populations sampled in this study were incorporated through military coercion (i.e. violence). Therefore, this study is largely reflective of the genetic consequences of hegemonic imperial power.

8.1.1 Complexity during the Middle Horizon

When compared to the LIP groups, populations from the MH did not have a higher rate of gene flow that might be expected during the Wari cultural horizon. However, the rates of gene flow appear to have varied amongst the MH populations that were sampled. The Conchopata sample demonstrated biological affinity with the MH Turpo Qatun Rumi and Nasca populations. Archaeological investigation at Turpo Qatun Rumi and the Nazca Valley also indicated a strong Wari presence in both locations despite the large geographic distance between the Wari heartland and the Nazca Valley. Given archaeological evidence of Wari presence in Andahuaylas and the Nazca Valley and the apparent long-standing relationship between Ayacucho populations and the Nasca the biological distance results were not unexpected.

The Nazca Valley samples, while similar to Wari heartland populations overall, demonstrated some interesting patterns within the valley. This may reflect resistance to incorporation in the Wari empire by some Nasca communities. Others have hypothesized that a settlement shift away from Wari centers in the Nazca River valley during the MH was evidence of non-violent resistance (Schreiber, 2001; Conlee and Schreiber, 2006). Though not conclusive, the results of this study seem to indicate that the Nasca groups were not homogenous in their acceptance of Wari administration. These results may also be an artifact of how samples were grouped in the analysis. The chronology of the Nazca Valley samples groups them with the MH samples. However, the Nazca Valley specimens are relatively dated which introduced the possibility of error in the study. Also, it has been noted that the Wari withdrew from coastal regions, including the Nazca River valley, earlier than in the highlands. In terms of social interaction and its impact on population genetic structure, the Nazca valley samples may be more accurately grouped with the LIP samples. Clearly, the Nasca case warrants further study.

In the north-central highlands the Hualcayan population was an outlier. The evidence for Wari presence in this region is much obvious than for other regions sampled like the south-central highlands. The results probably reflect isolation by distance, but there is also linguistic evidence for isolation of this population. The LIP sample from this region, Marcajirca, also was an outlier. The results concerning these samples are consistent with similar studies of populations in this region. As is the case with the Nasca population, the north-central highlands groups also deserver further study.

8.1.2 Conclusions drawn from the Late Intermediate Period samples

Overall F_{ST} values do not indicate a decrease in the rate of gene flow after the collapse of the Wari empire. However, in the Wari heartland there does appear to have been a decrease in relative rates of gene flow. Other studies have not been able to demonstrate a complete population replacement in the Ayacucho basin (Kemp et al., 2009). If there was not a different group inhabiting Huari after the demise of the empire, then these results indicate that the collapse of the empire had a dramatic impact on population genetic structure in this region. In the absence of any local political autonomous structure a dramatic change in social interaction and organization would be expected. Presently the samples available do not provide for a fine resolution akin to what was found nearby in Andahuaylas. It is also likely that the heartland populations "felt" the effects of the end of the Wari horizon more acutely than other regional populations. A better understanding of the impact of the Wari collapse on the population genetic structure of Ayacucho is certainly in need of further study.

Close to the Wari heartland in the south-central highlands the Andahuaylas samples seemed less affected by the collapse of the Wari with respect to rates of gene flow. Patterns in biological affinities between samples in this subset were also consistent with archaeological and ethnohistorical data. These results were exciting in that they support the hypothesis that kinship structure, especially the moiety which is related to the dualism of Andean cosmology, does have an immense time depth. The results also reinforce the importance of considering multiple lines of evidence when interpreting biological distance results. These patterns could not have been as fully interpreted with only archaeological, or only ethnohistoric data. The Andahuaylas dataset is still being enriched and potential for further analysis will be discussed in the *Future Directions of Research* section.

8.2 Future Directions of Research

As with many research projects, the results of this study have raised more questions than answers. One might expect a dramatic change in the genetic structure of populations between the MH and LIP with a sharp drop in gene flow following the collapse of the Wari empire if imperial incorporation spread evenly and contiguously through the Peruvian Andes and then disappeared in an instant. This however was almost certainly not the case. In the future the Wari heartland populations should be studied in finer detail with regard to population shifts that took place in the late EIP when Huarpa groups coalesced and the Wari rose to a state and imperial level of social complexity. A revision of this study with more samples that have tighter spatial and temporal control for the MH and LIP are also needed. Archaeological studies have demonstrated that Huari had a very large population during the height of Wari power. That population dispersed by the LIP and to date there is not an adequate explanation for this phenomenon. In the recent pass archaeological projects have been impossible in the Wari heartland due to extreme violence in the region associated with the Sendero Luminoso. Renewed excavations at Conchopata were some of the first resumed in Ayacucho. Now is an especially exciting time for Wari archaeology as excavations are planned to resume at Huari very soon as well. With a better understanding of the Wari capital, and hopefully a large skeletal collection dating to the MH from Huari, the nature of social interaction experienced by Huareños can be more effectively studied.

In addition to the Wari heartland the particular relationships within regions and between these communities and the Wari deserve more attention in the Nazca River Valley. Much research has been done regarding Nasca populations dating to the apogee of their culture during the EIP. Forgey (2006) astutely pointed out that the MH coordinate of Nasca culture represents a hole in anthropological knowledge of the prehistoric Andes (see also Buzon et al., 2012; Williams et al., 2011; Kellner and Schoeninger, 2008; Drusini et al., 2001). For many decades the Nasca have been conceived of as having a close relationship with the Wari evidenced by strong similarities in their iconography and presumed ideology (Menzel, 1964; Conlee, 2000). However, it has been suggested more recently by Schreiber (2001; Conlee and Schreiber, 2006) that the Nasca may have resisted Wari administration. The results of this project are consistent with local resistance to Wari incorporation in the Nazca River Valley. Again, to add certainty to this interpretation tighter chronological control is needed for these samples. As proposed for the Wari heartland, in the future a study focused on the Nasca with larger samples and radiometric dates should be undertaken. Currently Italian archaeologists have been working in the Nazca River drainage and are amassing a large skeletal assemblage (Drusini et al., 2001; Orefici and Drusini, 2003). Schreiber's (1992) mosaic model expects that imperial integration will be more difficult to sense archaeologically in regions where a high degree of social complexity already existed. This was certainly the case with the Nasca and very recently researchers have started to decipher the case of Nasca during the MH. This study revealed patterns with the Cahuachi and Cantayo populations that contrasted Majoro Chico. Future research should include samples derived from clear Wari administrative centers in the Nazca Valley like Pataraya. As more datasets become available for comparison with the population genetic research the variation in Nasca interaction with the Wari should become clearer.

Similar to the recent increased interest in MH Nasca populations, the Chanka and LIP populations in the south-central highlands have become the focus of new research programs (Kurin, 2012; Kellett, 2011; and Bauer et al., 2010). At the time this dissertation was written the author and Danielle Kurin submitted ceramic samples for analysis by Neutron Activation Analysis at the Missouri University Research Reactor (MURR) lab. The purpose of the study is to compare ceramic compositional groups to mortuary contexts, ethnic identities interpreted through cranial modification, and the biological distance results from this dissertation. Lofaro and Kurin (2011) have also conducted a small pilot study using Sr isotope analysis to explore the possibility of migrants in the study population. Preliminary results indicate that the population is local (Lofaro and Kurin, 2011; Lofaro personal communication July 2012). The completion of these projects will add even more depth to anthropological understanding of the relationships between the Andahuaylas groups.

Ongoing work in Andahuaylas conducted by Kurin, Gomez Choque and colleagues (Proyecto Bioarqueológico Andahuaylas), as well as Bauer, Kellett and colleagues (Proyecto Arqueológico Andahuaylas) should provide even more resolution to the population history in the region akin to Wernke's (2007) study. There is great potential in Andahuaylas to merge population genetics, bone chemistry, and spatial analyses to gain deep insight into the complexities of community level social organization. Not only is there potential to elucidate patterns of social organization with respect to land use and mortuary programs, but also how those systems have been negotiated over time in the presence of different colonizing regimes including the Wari, Inka, and Spanish.

When all of the populations sampled for this study are considered, the north-central highlands have received the least archaeological study. Both the Hualcayan and Marcajirca data were collected in the context of ongoing archaeological excavations. The author continues to collaborate on the PIARA archaeological project with the director, Rebecca Bria. Excavations during the 2012 field season have added to the MH coordinate of the skeletal collection. Analysis of the artifact assemblage and architecture is ongoing, and grants are in preparation for radiocarbon dating. Strontium isotope analysis is also planned for the MH coordinate of the Hualcayan skeletal collection. As the project progresses the population history at Hualcayan can also be explored as the site has a time depth that spans the Early Horizon through the EIP, MH, and into the LIP. The prospect of continuing research regarding population history in the north-central highlands is especially exciting considering what little is known to date.

8.2.1 Future development of methodology utilizing cranial non-metric traits

In reality cranial non-metric traits are not dichotomously expressed, and the generally accepted model for non-metric trait expression is not a single locus model. The Threshold model acknowledges the polygenic nature of potential non-metric trait expression. Being polygenic, most cranial non-metric traits have a continuum of expression. By collapsing trait scores into a present/absent system data about population variation is being lost. In the future distance analyses using polychoric correlations which do not require trait scores to be collapsed should be explored.

The Relethford-Blangero model (Relethford and Blangero, 1990) has been recognized for its usefulness in evaluating patterned gene flow using relative genetic heterogeneity within and between populations. The model was developed for continuous genetic locus data and has not yet been successfully applied to categorical data like cranial non-metrics (though some have attempted to, for example Schillaci et al. 2009). Konigsberg and Herrmann (2002) provide a method that could be used to estimate a normal distribution from trait threshold values. This would essentially estimate the Threshold model for trait expression and provide the continuous data needed to apply the Relethford-Blangero model to non-metric trait data. Clearly the particulars of this approach have not been worked out. However, this methodological approach has the potential to provide much more powerful and accurate picture of population genetic relationships than existing methodological approaches.

The utility of the Mosaic model as a social theoretical framework for the interpretation of both archaeological and genetic patterns in ancient populations was demonstrated by this study. Patterns in biological affinity and gene flow between populations sampled in this project support several hypotheses about imperialism, local resistance, and regional specificity with respect to the Wari empire. Though this adds to the body of anthropological knowledge, it is clear that much more research is needed to fully understand variability in the process of imperialism.

BIBLIOGRAPHY

Anders MB. 1986. Wari experiments in statecraft: a view from Azángaro. In: Matos M. R, Turpin S, and Eling H, editors. Andean archaeology: papers in memory of Clifford Evans. Los Angeles: Institute of Archaeology, University of California. p 210-224.

Anders MB. 1991. Structure and function at the planned site of Azángaro: cautionary notes for the model of Huari as a centralized secular state. In: Isbell WH, and McEwan GF, editors. Huari political organization: prehistoric monumental architecture and state government. Washington D.C.: Dumbarton Oaks. p 165-198.

Andrushko VA. 2011. How the Wari fashioned trophy heads for display: a distinctive modified cranium from Cuzco, Peru, and comparison to trophies from the capital region. In: Bonogofsky M, editor. The bioarchaeology of the human head. Gainesville: University Press of Florida. p 262–285.

Balakrishnan V, Sanghvi LD. 1968. Distance between populations on the basis of attribute data. Biometrics 24(4):859-865.

Barbujani G, Magagni A, Minch E, Cavalli-Sforza LL. 1997. An apportionment of human DNA diversity. Proceedings of the National Academy of Sciences of the United States of America 94(9):4516-4519.

Bauer TW, and Bauer BS. 1987. Selected aspects of skulls found by the Pikillacta Archaeological Project 1982, Appendix II In: McEwan GF, editor. The Middle Horizon in the Valley of Cuzco, Peru: the impact of the Wari occupation of Pikillacta in the Lucre Basin. Oxford: BAR International Series, vol. 372. British Archaeological Reports.

Bauer BS, Kellett LC. 2011. Cultural transformations of the Chanka homeland (Andahuaylas, Peru) during the Late Intermediate Period (A.D.1000–1400). Latin American Antiquity 21(1):87–111.

Bedrick EJ, Lapídus J, Powell JF. 2000. Estimating the Mahalanobis distance from mixed continuous and discrete data. Biometrics 56:394-401.

Benavides CM. 1971. Análisis de la Cerámica Huarpa. Revista del Museo Nacional, Tomo XXXVII:63-88.

Bennett W. 1953. Excavations at Wari, Ayacucho, Perú, Publications in Anthropology 49. New Haven: Yale University.

Berry RJ. 1968. Biology and non-metrical variation in mice and men. In The Skeletal Biology of Earlier Human Populations. Brothwell DR, editor.). Oxford: Pergamon Press, p. 103-133.

Berry AC. 1974. The use of non-metrical variation of the cranium in the study of Scandinavian population movements. American Journal of Physical Anthropology 40:345-358.

Berry AC. 1975. Factors affecting the incidence of nonmetrical skeletal variants. Journal of Anatomy 120:519-535.

Berry CA, Berry RJ. 1967. Epigenetic variation of the human cranium. Journal of Anatomy 101(2):361-379.

Berry AC, Berry RJ. 1972. Origins and relationships of the ancient Egyptians based on a study of non-metrical variations in the skull. Journal of Human Evolution 1(2):199-208.

Binford, M.W., Kolata, A.L., Brenner, M., Janusek, J., Seddon, M.T., Abbott, M.B., Curtis, J.H., 1997. Climate variation and the rise and fall of an Andean civilization. Quaternary Research 47:235–248.

Brewster-Wray CC. 1989. Huari administration: a view from the capital. In Czwarno RM, Meddens FM, Morgan A, editors. The nature of Wari: a reappraisal of the Middle Horizon Period in Peru. Oxford: B.A.R. International Series Vol. 525, pp. 23-34.

Brown DM, Silverman H, and García R. 1993. A cache of 48 Nasca trophy heads from Cerro Carapo, Peru. Latin American Antiquity 4(3):274-294.

Bria RE. 2012. Remodeling the landscape, remodeling the ceremony: Changing the place and practice of ritual during a period of agricultural intensification at late Formative Period Hualcayan, Callejón de Huaylas, Peru. Abstracts of the 77th Annual Meeting of the Society for American Archaeology, p. 63.

Bria RE, Rivas Otaiza CA. 2010. Proyecto de Investigación Arqueológico Regional Ancash - Huaylas[PIARAH]: Informe final de las labores realizadas durante la temporada de campo 2009. Lima: Instituto Nacional de Cultura.

Bria RE, Cruzado E. 2012. Proyecto de Investigación Arqueológico Regional Ancash [PIARA]: Informe final de las excavaciones realizadas durante la temporada de campo 2011 en Hualcayan [HU01]. Lima: Ministerio de Cultura.

Brumfiel EM, Earle TK. 1987. Specialization, exchange, and complex societies: an introduction. In Brumfiel EM, Earle TK, editors. Specialization, exchange, and complex societies Cambridge: Cambridge University Press, pp. 1-9.

Buikstra JE. 1976. Hopewell in the Lower Illinois Valley. Northwestern University Archeological Program Scientific Papers, No. 2.

Buikstra JE, Ubelaker DH. 1994. Standards for Data Collection from Human Skeletal Remains. Arkansas Archeological Survey Research Series No. 44, Fayetteville, AR.

Burger R. 1984. The prehistoric occupation of Chavín de Huántar. Berkeley: University of California Press.

Burger RL, Mohr Chavez KL, Chavez SJ. 2000. Looking through the glass darkly: prehispanic obsidian procurement and exchange in southern Peru and northern Bolivia. Journal of World Prehistory 14:267-362.

Busto Duthurburu JA. 1962. Maldonado, el Rico, señor de los Andahuaylas. Lima: Revista Histórica.

Buzon MR, Conlee CA, Simonetti A, Bowen GJ. 2012. The consequences of Wari contact in the Nasca region during the Middle Horizon: archaeological, skeletal, and isotopic evidence. Journal of Archaeological Science 39(8):2627-2636.

Cabrera M. 1998. evaluación arqueología en el complejo turistico de Nawimpuquio, Informe de Proyecto Lima, Peru: Instituto Nacional de Cultura.

Carmichael P. 1998 Nasca Ceramics: Production and Social Context. In Shimada I, editor. Andean ceramics: Technology, organization, and approaches. MASCA Research Papers in Science and Archaeology. Supplement to Volume 15. Philidelphia: Museum Applied Center for Archaeology, p. 213-232.

Carson EA. 2006. Maximum-likelihood variance coordinates analysis of heritabilities of cranial nonmetric traits. Human Biology 78:383-402.

Castillo, LJ. 2000. La presencia Wari en San José de Moro. In Kaulicke, P. and Isbell, W. editors. Huari y Tiwanaku: Modelos.vs. Evidencias. Lima: Boletín de Arqueología PUCP 4:143-179.

Cheverud J. 1979. Genetic and environmental morphological variation among social groups of rhesus monkeys (*Macaca mulatta)* on Cayo Santiago. Ph.D. dissertation, Department of Anthropology, University of Wisconsin-Madison.

Cheverud JM. 1988. A comparison of genetic and phenotypic correlations. Evolution 42:958-968.

Cheverud JM, Buikstra JE. 1981a. Quantitative genetics of non-metric traits in the Rhesus Macaques on Cayo Santiago. I. Single trait heritabilities. American Journal of Physical Anthropology 54*:*43-49.

Cheverud JM, Buikstra JE. 1981b. Quantitative genetics of non-metric traits in the Rhesus Macaques on Cayo Santiago. II. Phenotypic genetic and environmental correlations between traits. American Journal of Physical Anthropology 54*:*51-58.

Cheverud JM, Kohn LAP, Konigsberg LW, Leigh S. 1992. The effects of fronto-occipital artificial cranial modification on the cranial base and face. American Journal of Physical Anthropology 88:323-345.

Cole P, Hermon G. 1994. Is there LF *Wh*-movement? Linguistic Inquiry 25(2):239-262.

Conlee CA. 2000. Late prehistoric occupation of Pajonal Alto, Nasca, Peru: Implications for imperial collapse and societal reformation. Ann Arbor: University Microfilms.

Conlee CA. 2010a. Nasca and Wari: Local opportunism and colonial ties during the Middle Horizon. In: Jennings J, editor. Beyond Wari Walls: Regional perspectives on Middle Horizon Perú. Albuquerque : University of New Mexico Press, p. 96-112.

Conlee CA. 2010b. Regeneration as transformation: Postcollapse society in Nasca, Peru. In Schwartz GM, Nichols JJ, editors. After collapse: The regeneration of complex societies. Tuscon: The University of Arizona Press, p. 99-113.

Conlee CA, Schreiber K. 2006. The role of intermediate elites in the balkanization and reformation of post-Wari society in Nasca, Peru. In: Elson CE, Covey A, editors.

Intermediate Elites in Pre-Columbian States and Empires. Tucson: University of Arizona Press, p. 94–111.

Conlee CA, Buzon MR, Gutierrez AN, Simonetti A, Creaser RA. 2009. Identifying foreigners versus locals in a burial population from Nasca, Peru: an investigation using strontium isotope analysis. Journal of Archaeological Science 36(12):2755-2764.

Conrad GW. 1981. Reply to Paulsen and Isbell. American Antiquity 46:38-42.

Cook AG. 1985. The politico-religious implications of the Huari offering traditions. In Rivera MA, editor. La problemática Tiwanaku Huari en el context panandino del desarolllo cultural. Diálogo Andino No. 4, Universidad de Tarapacá, Arica.

Cook AG. 1992. Stone ancestors: idioms of imperial attire and rank among Huari figurines. Latin American Antiquity 3:341-364.

Cook AG. 2001. Huari D-shaped structures, sacrificial offerings, and divine rulership. In Benson E, Cook AG, editors. Ritual Sacrifice in Ancient Peru. Austin: University of Texas Press.

Cook AG, Glowacki M. 2003. Pots, politics, and power: Wari ceramic assemblages and imperial administration. In Bray, T, editor. The archaeology and politics of food and feasting in early states and empires. New York: Kluwer Academic/Plenum Publishers, pp. 173-202.

Cwarzano RM, Meddens FM, Morgan A. 1989. The nature of Wari: a reappraisal of the Middle Horizon period in Peru. Oxford: B.A.R. International Series, 525.

D’Altroy TN. 1992. Provincial power in the Inka Empire. Washington DC: Smithsonian Institution Press.

D’Altroy TN, Earle TK. 1985. Staple Finance, Wealth Finance, and Storage in the Inka Political Economy. Current Anthropology 26:187-206.

DeLeonardis L, Lau GF. 2004. Life, death, and ancestors. In: Silverman H, editor. Andean Archaeology. Malden: Blackwell Publishing Ltd. p 77-115.

Donlon DA. 2000. The value of infracranial nonmetric variation in studies of modern *Homo sapiens*: A n Australian focus. American Journal of Physical Anthropology 113(3):349-368.

Donnan CB, Mackey CJ. 1978. Ancient burial patterns of the Moche Valley, Peru. Austin: University of Texas Press.

Dorsey GA. 1895. Crania from the necropolis of Ancon, Peru. American Anthropologist 43:358-370.

Dow MM, Cheverud JM. 1985. Comparison of distance matrices in studies of population structure and genetic microdifferentiation: Quadratic assignment. American journal of Physical Anthropology 68:367-374.

Droessler J. 1981. Craneometry and biological distance. Biocultural continuity and change at the late-Woodland-Mississippian interface. Evanston: Center for American Archaeology, Northwestern University.

Drusini AG, Carrara N, Orefici G, Bonati MR. 2001. Palaeodemography of the Nasca valley: reconstruction of the human ecology in the southern Peruvian coast. HOMO 52(2):157-172.

Duvoils P. 1973. Huari y Llacuaz: agricultores y pastores. Un dualismo Prehispánico de oposición y complementaridad. Revista del Museo Nacional 39:153-191.

Earle T. 1997. How chiefs come to power: The political economy of prehistory. Stanford: Stanford University Press.

Edgar HJH. 2007. Microevolution of African American dental morphology. American Journal of Physical Anthropology 132(4):535-544.

Edwards MJ. 2010. Archaeological Investigations at Pataraya: A Wari Outpost in the Nasca Valley of Southern Peru. unpublished Ph.D. dissertation. Department of Anthropology, University of California, Santa Barbara.

Eisenstadt SN. 1963. The need for achievement. Economic Development and Cultural Change 11(4):420-431.

Eisenstadt SN. 1967. The Decline of Empires. Englewood Cliffs: Prentice Hall.

Falconer DS. 1965. The inheritance of liability to certain diseases, estimated from the incidence among relatives. Annals of Human Genetics 29:51-76.

Falconer DS. 1989. Introduction to quantitative genetics, 3rd Ed. London: Longman.

Fehren-Schmitz L, Reindel M, Tomasto Cagigao E, Hummel S, Herrmann B. 2010. Pre-Columbian population dynamics in coastal southern Peru: a diachronic investigation of mtDNA patterns in the Palpa region by ancient DNA analysis. American Journal of Physical Anthropology 114:208-221.

Feinman G. and Neitzel J. 1984. Too many types: an overview of sedentary prestate societies in the Americas. *Advances in Archaeological Method and Theory* 7:39-102.

Forgey K. 2006. Investigating the origins and function of Nasca trophy heads using osteological and ancient DNA analyses. Ph.D. Dissertation, Department of Anthropology, University of Illinois ant Chicago.

Forgey K, Williams S. 2005. Were Nasca trophy heads war trophies or revered ancestors? Insights from the Kroeber collection. In: Rakita GFM, Buikstra JE, Beck LA, Williams S, editors. Interacting with the Dead: Perspectives on Mortuary Archaeology for the New Millennium. Gainesville: University Press of Florida, p. 251–276.

Freeman MF, Tukey JW. 1950. Transformations related to the angular and the square root. Annals of Mathematical Statistics 21(4):607-611.

Fried MH. 1960. On the evolution of social stratification and the state. In: Diamond S, editor. Culture in history: essays in honor of Paul Radin. New York: Columbia University Press. p 713-731.

Fuselli S, Tarazona-Santos E, Dupanloup I, Soto A, Luiselli D, Pettener D. 2003. Mitochondrial DNA diversity in South America and the genetic history of Andean highlanders. Molecular Biology and Evolution 20(10):1682-1691.

Glatz C. 2009. Empire as network: spheres of material interaction in Late Bronze Age Anatolia. Journal of Anthropological Archaeology 28(2):127-141.

Glowacki M. 2002. The Huaro archaeological site complex: rethinking the Huari occupation of Cuzco. In: Isbell WH, and Silverman H, editors. Andean Archaeology I: variations in sociopolitical organization. New York: Kluwer Academic/Plenum Publishers. p 267-286.

Glowacki M. 2005: Dating Pikillacta. In McEwan G, editor. Pikillacta: the Wari Empire in Cuzco. University of Iowa Press, p. 115-24.

Glowacki M, Malpass M. 2003. Water, huacas, and ancestor worship: traces of Wari sacred landscape. Latin American Antiquity 14:431-448.

Goldstein LG. 1981. One-dimensional archaeology and multidimensional people: spatial organization and mortuary analysis. In Chapman R, Kinnes I, and Randsborg, editors. The Archaeology of Death. Cambridge: Cambridge University Press, p 53-69.

González-José R, Pucciarelli HM, Neves WA, Hernández M. 2002. Paleoamerican and archaic remains from Patagonia as viewed from modern variation. Collegium Anthropologicum 26:75.

Green R, Suchey J.1976. The use of inverse sine transformation in the analysis of non-metrical data. American Journal of Physical Anthropology 45:61-68.

Green RF, Suchey J, Gokhale DV. 1979. The statistical treatment of correlated bilateral traits in the analysis of cranial material. American Journal of Physical Anthropology 50:629-634.

Greene DL. 1982. Discrete dental variations and biological distances of Nubian populations. American Journal of Physical Anthropology 58:75–79.

Grewal MS. 1962. The development of an inherited tooth defect in the mouse. Journal of Embryology and Experimental Morphology 10(2):202-211.

Grüneberg H. 1952. Genetical studies on the skeleton of the mouse. IV. Quasicontinuous variations. Journal of Genetics 51:95-114.

Grüneberg H. 1963. The pathology of development. Oxford: Blackwell Scientific Publications.

Hallgrímsson B, Donnabháin BO, Walters GB, Cooper DML, Guôbjartsson D, Stefánsson K. 2004. Composition of the founding population of Iceland: biological distance and morphological variation in early historic Atlantic Europe. American Journal of Physical Anthropology 124:257-274.

Hanihara T, Ishida H, Dodo Y. 2003. Characterization of biological diversity through analysis of discrete traits. American Journal of Physical Anthropology 121:241-251.

Harris EF, Sjøvold T. 2004. Calculation of Smith's Mean Measure of Divergence for intergroup comparisons using nonmetric data. Dental Anthropology 17(3):83-93.

Hassig R. 1985. Trade, Tribute, and Transportation: The Sixteenth-Century Political Economy of the Valley of Mexico. Civilization of the American Indian series, no. 171. Norman: University of Oklahoma Press.

Hauser G, DeStefano GF. 1989. Epigenetic variants of the human skull. Stuttgart: E. Schweizerbartsche Verlagsbuchhandlung.

Hintze J. 2007. NCSS 2007. NCSS, LLC. Kaysville, Utah, USA. www.ncss.com.

Hirth KG. 1996. Political economy and archaeology: perspectives on exchange and production. Journal of Archaeological Research 4:203-239.

Ibarra Asencios B (editor). 2003. Arqueología de la sierra Ancash: propuestas y perspectivas. Lima: Instituto Cultural RVNA.

Irish JD. 1998a. Ancestral traits in recent Sub-Saharan Africans and the origins of modern humans. Journal of Human Evolution 34(1):81-98.

Irish JD. 1998b. Diachronic and synchronic dental trait affinities of Late and post-Pleistocene peoples from North Africa. Homo 49: 138-155.

Irish JD. 1997. Characteristic high- and low-frequency dental traits in sub-Saharan African populaitons. American Journal of Physical Anthropolgy 102(4):455-467.

Irish JD. 2010. The mean measure of divergence: Its utility in model-free and model-bound analyses relative to the Mahalanobis D^2 distance for nonmetric traits. American Journal of Human Biology 22(3):378-395.

Irish JD, Turner CG II. 1990. West African dental affinity of late Pleistocene Nubians: Peopling of the Eurafrican-South Asian triangle II. Homo 41: 42-53.

Isbell WH. 1991. Honcopampa. Expedition 33(3):27-36.

Isbell WH. 1997. Mummies and mortuary monuments: a postprocessual prehistory of central Andean social organization. Austin: University of Texas Press.

Isbell WH. 2004. Palaces and politics in the Andean Middle Horizon. In: Toby Evans S, and Pillsbury J, editors. Palaces of the ancient New World. Washington D.C.: Dumbarton Oaks. p 191-246.

Isbell WH. 2010. La arqueología Wari y la dispersión del Quechua. Boletín de Arqueología PUCP No. 14, p. 199-220.

Isbell WH, Brewster-Wray C, and Spickard L. 1991. Architecture and spatial organization at Huari. In: Isbell WH, and McEwan GF, editors. Huari administrative structure: prehistoric monumental architecture and state government. washington D.C.: Dumbarton Oaks. p 19-53.

Isbell WH, and Schreiber KJ. 1978. Was Huari a state? American Antiquity 43(3):372-389.

Isbell WH, Cook AG. 1987. Ideological origins of an Andean conquest state. Archaeology 40:26-33.

Isbell WH, Cook AG. 2002. A new perspective on Conchopata and the Andean Middle Horizon. In Silverman H, Isbell WH, editors. Andean archaeology II: art, landscape, and society. New York: Kluwer Academic Press.

Jantz RL. 1973. Microevolutionary change in Arikara crania: A multivariate analysis. American Journal of Physical Anthropology 38(1):15-26.

Jennings J. 2006. Core, peripheries, and regional realities in Middle Horizon Peru. Journal of Anthropological Archaeology 25:346-370.

Jennings J, and Craig N. 2001. Politywide analysis and imperial political economy: the relationship between valley politicla complexity and administrative centers in the Wari Empire of the Central Andes. Journal of Anthropological Archaeology 20:479-502.

Jorde LB. 1980. The genetic structure of subdivided human populations: a review. In: Mielke JH, Crawford MH, editors. Current developments in anthropological genetics. Vol 1. New York: Plenum Press. p. 135-208.

Kamp KA, Yoffee N. 1980. Ethnicity in ancient western Asia during the early second millennium B. C.: Archaeological assessments and ethnoarchaeological prospectives. *Bulletin of the American Schools of Oriental Research*, No. 237:85-104.

Kellett LC. 2010. Chanka settlement ecology: Hilltop sites, land use and warfare in late prehispanic Andahuaylas, Peru. Ph.D. Dissertation, Department of Anthropology, University of New Mexico.

Kemp BM, Tung TA, Summar ML. 2009. Genetic continuity after the collapse of the Wari empire: Mitochondrial DNA profiles from Wari and post-Wari populations in the ancient Andes. American Journal of Physical Anthropology 140(1):80-91.

Kellner CM, Schoeninger MJ. 2008. Wari’s imperial influence on local Nasca diet: The stable isotope evidence. Journal of Anthropological Archaeology 27(2):226-243.

Kettemen WG. 2002. New dates from the Huari Empire: chronometric dating of the prehistoric occupation of Conchopata, Ayacucho, Peru, unpublished Master’s thesis. Department of Anthropology, Binghamton State University, New York.

Kolata AL. 2010. Before and after collapse: Reflections on the regeneration of social complexity. In Schwartz GM, Nichols JJ, editors. After collapse: The regeneration of complex societies. Tuscon: The University of Arizona Press, p. 208-221.

Knobloch PJ. 1976. A study of the Huarpa ceramic style of the Andean Early Intermediate Period. Master's Thesis, Department of Anthropology, State University of New York at Binghamton.

Knudson KJ. 2009. Oxygen isotope analysis in a land of environmental extremes: the complexities of isotopic work in the Andes. International Journal of Osteoarchaeology 19(2):171-191.

Konigsberg LW. 1987. Population genetic models for interpreting prehistoric intra-cemetery biological variation, unpublished Ph.D. dissertation. Department of Anthropology, Northwestern University.

Konigsberg LW. 1990. Analysis of prehistoric biological variation under a model of isolation by geographic and temporal distance. Human Biology 62:49-70.

Konigsberg LW. 2006. A post-Neumann history of biological distance studies in bioarchaeology. In Buikstra JE, Beck LA, editors. Bioarchaeology: The contextual analysis of human remains. Burlington: Academic Press, pp. 263-279.

Konigsberg LW, *Ousley SD.* 1995. Multivariate quantitative genetics of anthropometric traits from the Boas data. *Human Biology* 67(3)**:**481-498.

Konigsberg LW and Herrmann NP. 2002. Markov chain Monte Carlo estimation of hazard model parameters in paleodemography. In: RD Hoppa and JW Vaupel, editors. Paleodemography: Age Distributions from Skeletal Samples. Cambridge University Press: New York, pp. 222-242.

Konigsberg LW, Kohn LAP, Cheverud JM. 1993. Cranial deformation and nonmetric trait variation. American Journal of Physical Anthropology 90:35-48.

Kroeber A, and Strong W. 1924. The Uhle Collections from Chincha. Berkeley: University of California Press.

Kroeber AL, Collier D, Carmichael PH. 1998. The archaeology and pottery of Nazca, Peru: Alfred Kroeber's 1926 expedition. Chicago: Field Museum of Natural History.

Kurin DS. 2012. The bioarchaeology of collapse: Ethnogenesis and ethnocide in post-imperial Andahuaylas, Peru (AD 900-1250). Ph.D. Dissertation, Department of Anthropology, Vanderbilt University.

La Lone, D. 2000 'Rise, fall, and semiperipheral development in the Andean world-system', Journal of World-Systems Research 6.1:68-99

Lanning EP. 1967. Peru before the Incas. Engelwood Cliffs: Prentice-Hall.

Larco H. R. 1948. Cronología arqueológica del norte del Perú. Buenas Aires: Sociedad Geográfica Americana.

Lasker GW, Mascie-Taylor CGN. 1988. Biological aspects of human migration. Cambridge: Cambridge University Press.

Lewis CM, Tito RY, Lizárraga B, Stone AC. 2005. Land, language, and loci: mtDNA in Native Americans and the genetic history of Peru. American Journal of Physical Anthropology 127(3):351-360.

Lewis CM, Buikstra JE, Stone AC. 2007a. Ancient DNA and genetic continuity in the south central Andes. Latin American Antiquity 18:145-160.

Lewis CM, Lizarraga B, Tito RY, Medina A, Martinez R, Polo S, Caceres AM, Stone AC. 2007b. Mitochondrial DNA and the peopling of South America. Human Biology 79:159-178.

Lightfoot, KG and Martinez A. 1995. Frontiers and boundaries in archaeological perspective. Annual Review of Anthropology 24:471-492.

Lockhart J. 1972. The men of Cajamarca: A social and biographical study of the first conquerers of Peru. Austin: University of Texas Press.

Lofaro E, Kurin DS, Krigbaum J.. 2012. Isotopic analysis of Chanka mobility in the central highlands of Peru. Abstracts of the 77th Annual Meeting of the Society for American Archaeology, p. 219.

Luiselli D, Simoni L, Tarazona-Santos E, Pastor S, Pettener D. 2000. Genetic structure of Quechua-speakers of the Central Andes and geographic patterns of gene frequencies in South Amerindian populations. American Journal of Physical Anthropology 113(1):5-17.

Lumbreras L. 1960. La cultura Wari, Ayacucho. Instituto de Etnología y Arqueología, Universidad Nacional Mayor de san Marcos, Lima, Perú 1:130-227.

Lumbreras L. 1969. De los pueblos, las culturas y las artes del antiguo Peru. Lima: Monclos-Campodonico.

Lumbreras L. 1974a. Las Fundaciones de Huamanga: Hacia una prehistoria de Ayacucho Lima: Editorial Nueva Educación.

Lumbreras L. 1974b. The peoples and cultures of ancient Peru. Washington D.C.: Smithsonian Institution Press.

Lumbreras L. 1981. Arqueología de la América Andina. Lima: Milla Batres.

Luttwak EN. 1976. Strategic power: Military capabilities and political utility. Beverly Hills: Sage Publications.

Mahalanobis PC. 1936. On the generalized distance in statistics. Proceedings of the National Institutes of Science India 2:49.

Manly BJF. 1986. Multivariate statistical methods. A primer. London: Chapman and Hall.

Manly BJF. 1997. Randomization, bootstrap and monte carlo methods in biology, 2nd edition. London: Chapman and Hall.

Mann M. 1977. States ancient and modern. European Journal of Sociology 18(2): 262-298.

Mann M. 1986. The Sources of Social Power, Volume I: A History of Power from the Beginning to 1760 AD. New York: Cambridge University Press.

Mantel N. 1967. The detection of disease clustering and a generalized regression approach. Cancer Research 27:209-220.

Martinez-Abadías N, Esparza M, Sjøvold T, González-José R, Santos M, Hernández M. 2009. Heritability of human cranial dimensions: Comparing the evolvability of different cranial regions. Journal of Anatomy 214(1):19-35.

McEwan GF. 1991. Investigations at the Pikillacta site: a provincial Huari center in the valley of Cuzco. In Isbell WH, McEwan GF, editors. Huari administrative structure: prehistoric monumental architecture and state government. Washington D.C.: Dumbarton Oaks, pp. 93-119.

McEwan GF. 1996. Archaeological investigations at Pikillacta, a Wari site in Peru. Journal of Field Archaeology 23:169-186.

McEwan GF. 2005. Pikillacta: the Wari Empire in Cuzco. Iowa City: University of Iowa Press.

Menzel D. 1964. Style and time in the Middle Horizon. Ñawpa Pacha 2:1-105.

Menzel D. 1969. Some of Rowe’s contributions in the field of Andean culture history. The Kroeber Anthropological Society Papers 40:100-111.

Menzel D. 1977. The Archaeology of ancient Peru and the work of Max Uhle. Berkeley: Robert H. Lowie Museum of Anthropology.

Morrison, KD. 2001. Sources, approaches, definitions. In Alcock, SE, D'Altroy, TN, Morrison, KD, and Sinopoli, CM, editors. Empires: Pespectives from Archaeology and History. New York: Cambridge University Press. p. 1-9.

Moseley ME, Feldman RA, Goldstein PS, Watanabe L. 1991. Colonies and conquest: Tiahuanaco and Huari in Moquegua. In Isbell WH, McEwan GF, editors. Huari administrative structure: prehistoric monumental architecture and state government. Washington DC: Dumbarton Oaks, pp. 121-140.

Nash DJ, Williams PR. 2004. Architecture and power on the Wari-Tiwanaku frontier. In Vaughn KJ, Ogburn D, Conlee CA editors. Foundations of Power in the Prehispanic Andes. Archaeological Papers of the American Anthropological Association 14: 151–174.

Nikita E, Mattingly D, Mirazón Lahr M. 2012. Saharra: Barrier or corridor? Nonmetric cranial traits and biological affinities of North African late holocene populations. American Journal of Physical Anthropology 147(2):280-292.

Ochatoma JA. 1992. Informe final del proyecto: Protección, limpieza y puesta en valor del nacimiento arqueológico de Conchopata. Ayacucho, Peru: Instituto Nacional de Cultura.

Ochatoma JA. 2007. Alfareros del Imperio Huari: Vida cotidiana y areas de actividad ed Conchopata. Ayacucho: Universidad Nacional de San Cristóbal de Huamanga.

Ochatoma JA, Cabrera MR. 2002. Religious ideology and military organization in the iconography of a D-shaped ceremonial precinct at Conchopata. In Silverman H, Isbell WH, editors. Andean Archaeology II: Art, Landscape, and Society. New York : Kluwer Academic Press, p. 225–247.

Oden NL, Sokal RR. 1992. An investigation of three-matrix permutation tests. Journal of Classification 9(2):275-290.

Oksanen J, Blanchet FG, Kindt R, Legendre P, Minchin PR, O'Hara RB, Simpson GL, Solymos P, Stevens MHH, Wagner H. 2012. Community ecology package (vegan). URL: http://cran.r-project.org, http://vegan.r-forge.r-project.org/.

Orefici G, Drusini A. 2003. Nasca: hipótesis y evidencias de su desarrollo cultural. Centro Italiano Studi E Ricerche Archeologiche Precolombiane, Brescia, Italy.

Owen B. 2007. The Wari heartland on the Arequipa coast: Huamanga ceramics from Beringa, Majes. Andean Past 8:287-373.

Pink CM, Ibarra Asencios B.2009. *Chullpas*, Caves, and biological affinity: a case study from Marcajirca, Peru. American Journal of Physical Anthropology Supplement 138 (S48):297.

Pink CM, Bria RE. 2012. Mortuary ritual at the Hualcayan site in the Callejón de Huaylas, Peru. Abstracts of the 77th Annual Meeting of the Society for American Archaeology, p. 281.

Pomeroy E, Stock JT, Zakrzewski SR, Lahr MM. 2010. A metric study of three types of artificial cranial modification from north-central Peru. International Journal of Osteoarcheology 20:317-334.

Pozzi-Escot D. 1999. Conchopata, un poblado de especialistas durante el Horizonte Medio. Boletín del Instituto Francés de Estudios Andinos 14(3-4):115-129.

Puente Brunke J. 1992. Encomienda y encomenderos en el Perú: estudio social y político de una institución colonial. Sevilla: Excma. Diputación Provincial de Sevilla.

R Development Core Team. 2008. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL http://www.R-project.org.

Ravines R. 1977. Practicas Funerarios en Ancón (Primera Parte). Revisita del Museo Nacional 43:327-397.

Ravines R. 1981. Practicas Funerarios en Ancon (Segunda Parte). Revisita del Museo Nacional 45:89-166.

Relethford JH. 1994. Craniometric variation among modern human populations. American Journal of Physical Anthropology 95:53.62.

Relethford JH, Lees FC. 1982. The use of quantitative traits in the study of human population structure. Yearbook of Physical Anthropology 25:113-132.

Relethford JH, Blangero J. 1990. Detection of differential gene flow from patterns of quantitative variation. Human Biology 62:5-25.

Relethford JH, Crawford MH, Blangero J. 1997. Genetic drift and gene flow in post-famine Ireland. Human Biology 69(4):443-465.

Rhode MP, Arriaza BT. 2006. Influence of cranial deformation on facial morphology among prehistoric South Central Andean populations. American Journal of Physical Anthropology 130:462-470.

Ricaut FX, Auriol V, von Cramon-Taubadel N, Keyser C, Murail P, Ludes B, Crubézy E. 2010. Comparison between morphological and genetic data to estimate biological relationship: The case of the Egyin Gol necropolis (Mongolia). American Journal of Physical Anthropology 143(3):355-364.

Roseman CC. 2004. Detecting interregionally diversifying natural selection on modern human cranial form by using matched molecular and morphometric data. Proceedings of the national Academy of Sciences 101:12824-12829.

Roseman CC, Weaver TD. 2004. Multivariate apportionment of global human Craniometric diversity. American Journal of Physical Anthropology 125:257-263.

Rostworowski M. 1992. Pachacamac y el Señor de Milagros: una trayectoria milenaria. Lima: Instituto de Estudios Peruanos.

Rowe JH. 1956. Archaeological explorations in southern Peru, 1954-1955. American Antiquity 22:135-151.

Rowe J, Collier D, and Willey G. 1950. Reconnaissance notes on the site of Huari, near Ayacucho, Perú. American Antiquity VI(2):120-137.

Sack RD. 1986. Human territoriality: its theory and history. Cambridge: Cambridge University Press.

Sangrvi LD, Balakrishnan V. 1972. Comparison of different measures of genetic distance between human populations. In Weiner JS and Huizinga J, editors. p. 25-36.

Scheps S. 1982. Statistical blight. American Antiquity 47(4):836-851.

Schillaci MA, Irish JD, Wood CCE. 2009. Further analysis of the population history of ancient Egyptians. American Journal of Physical Anthropology 139(2):235-243.

Shinoda K, Adachi N, Guillen S, Shimada I. 2006. Mitochondrial DNA analysis of ancient Peruvian highlanders. American Journal of Physical Anthropology 131:98-107.

Schortman E. 1989. Interregional interaction in prehistory: The need for a new perspective. American Antiquity 54:52–65.

Schortman EM, Urban PA. 1998. Culture contact structure and process. In Cusick JG, editor. Studies in culture contact: interaction, culture change, and archaeology. Carbondale: Center for Archaeological Investigations Occasional Paper No. 25, p 102-125.

Schreiber K. 1987a. From state to empire: the expansion of the Wari outside the Ayacucho basin. In: Pozorski S, Haas J, and Pozorski T, editors. The origins and development of the Andean state. Cambridge: Cambridge University Press. p 91-96.

Schreiber K. 1987b. Conquest and consolidation: a comparison of the Wari and Inka occupations of a highland Peruvian valley. American Antiquity 52(2):266-284.

Schreiber K. 1991. Jincamocco: a Huari administrative center in the south central highlands. In: Isbell WH, and McEwan GF, editors. Huari administrative structure: prehistoric monumental architecture Washington D.C.: Dumbarton Oaks. p 199-214.

Schreiber K. 1992. Wari imperialism in Middle Horizon Peru. Ann Arbor: Museum of Anthropology, University of Michigan.

Schreiber KJ. 1999. Regional approaches to the study of prehistoric empires: examples from Ayacucho and Nasca, Peru. In Billman, BR Feinman, GM, editors. Settlement pattern studies in the Americas: fifty years since Virú. Washington D.C.: Smithsonian Institution Press, pp. 160-171.

Schreiber K. 2001. The Wari empire of Middle Horizon Peru: the epistemological challenge of documenting an empire without documentary evidence. In: Alcock S.E. DTN, Morrison K.D., Sinopoli C.M., editors. Empires: perspectives from archaeology and history. Cambridge: Cambridge University Press. p 70-92.

Schreiber K. 2005. Imperial agendas and local agency: Wari colonial strategies. In: Stein GJ, editor. The archaeology of colonial encounters: comparative perspectives. Santa Fe: School of American Research Press. p 237–262.

Shady Solis R. 1989. Cambios significativos ocurridos en el mundo andino durante el Horizonte Medio. In Czwarno RM, Meddens FM, Morgan A. editors. Nature of Wari: a Reappraisal of the Middle Horizon Period in Peru. Oxford: B.A.R. International Series Vol. 525, pp. 1-22.

Shady R and Ruiz A. 1979. Evidence for interregional relationships during the Middle Horizon on the north-central coast of Peru. American Antiquity 44(4):676-684.

Shimada I. 1990. Cultural continuities and discontinuities in the northern North Coast of Peru, Middle-Late Horizons. In Moseley ME, Cordy-Colins A, editors. The northern dynasties: kingship and statecraft in Chimor: a symposium at Dumbarton Oaks, 12th and 13th Washington D.C.: Dumbarton Oaks, pp. 297-392.

Silverblatt IM. 1987. Moon, sun, and witches: gender ideologies and class in Inca and colonial Peru. Princeton: Princeton University Press.

Silverman H. 1993. Cahuachi in the Ancient Nasca World. Iowa City: University of Iowa Press.

Silverman H, Isbell WH. 2002. Introduction: landscapes of power. In Silverman H, Isbell WH, editors. Andean archaeology II: art, landscape, and society. New York: Kluwer Academic Press, pp. 181-188.

Silverman H, Proulx D. 2002. The Nasca. Malden: Blackwell Publishers.

Sinopoli CM. 1994. The archaeology of empires. Annual Review of Anthropology 23:159–180.

Sinopoli CM. 1995. The archaeology of empires: A view from South Asia. *Bulletin of the American Schools of Oriental Research* No. 299/300, The Archaeology of Empire in Ancient Anatolia (Aug. - Nov., 1995), pp. 3-11.

Sinopoli CM. 2001. Empires. In Feinman GM, Price TD, editors. Archaeology at the millennium: a sourcebook. New York: Kluwer Academic/Plenum Publishers, p. 439-471.

Sjøvold T. 1984. A report on the heritability of some cranial measurements and non metric traits. In van Vark G, Howells, WW, editors. Multivariate statistical methods in physical anthropology. Dordrecht: D. Reidel Publishing Company, p. 223-246.

Slovak NM. 2007. Examining imperial influence on Peru's central coast: isotopic and cultural analyses of Middle Horizon burials at Ancón, unpublished Ph.D. dissertation. Stanford University.

Slovak NM, Paytan A, Wiegland BA. 2009. Reconstructing Middle Horizon mobility patterns on the coast of Peru through strontium isotope analysis. Journal of Archaeological Science 36:157-165.

Smouse PE, Long JC, Sokal RR. 1986. Multiple regression and correlation extensions of the Mantel test of matrix correspondence. Systematic Zoology 35(4):627-632.

Smouse PE, Long JC. 1992. Matrix correlation analysis in anthropology and genetics. Yearbook of Physical Anthropology 35:187-213.

Stein GJ. 1998. World system theory and alternative models of interaction in the archaeology of culture contact. In Cusick JG, editor. Studies in culture contact: interaction, cultural change, and archaeology. Center for Archaeological Investigations Occasional Paper, 25. Carbondale: Southern Illinois University Press, p 220-255.

Stein GJ. 2002. From passive periphery to active agents: emerging perspectives in the archaeology of interregional interaction. American Anthropologist 104:903–916.

Sutter RC, Verano JW. 2007. Biodistance analysis of the Moche sacrificial victims from Huaca de la Luna plaza 3C: matrix method test of their origins. American Journal of Physical Anthropology 132: 193-206.

Tello JC. 1931. Las ruinas de Wari en Ayacucho. Lima: El Peru.

Tello JC. 1939. Origen y desarollo de las civilizaciones prehistoricas Andinas. Actas y Trabajos Címtificos, 27th International Congress of Americanists 1:589-720.

Thompson, LG, Mosley-Thompson E, Henderson KA. 2000. Ice-core palaeoclimate records in tropical South America since the Last Glacial Maximum. Journal of Quaternary Science 15:377–394.

Tilley C. 1991. Material culture and text: The art of ambiguity. New York: Routledge.

Topic JR. 1986. A sequence of monumental architecture from Huamachuco. In: Sandweiss DH, and Kvietok DP, editors. Perspectives on Andean prehistory and protohistory. Ithaca: Latin American Studies Program, Cornell University. p 63-83.

Topic JR. 1991a. Huari and Huamachuco. In: Isbell WH, and McEwan GF, editors. Huari administrative structure: prehistoric monumental architecture and state government. Washington D.C.: Dumbarton Oaks. p 141–164.

Topic JR. 1991b. Middle Horizon in northern Peru. In Isbell WH, McEwan GF, editors. Huari administrative structure: prehistoric monumental architecture and state government. Washington D.C.: Dumbarton Oaks, pp. 233-246.

Tschauner H. 2003. Honco Pampa: arquitectura de élite del Horizonte medio en el Callejón de Huaylas. In: Ibarra BA, editor. Arqueología de la sierra de Ancash: propuestas y perspectivas. Lima: Instituto cultural Runa. p 193-220.

Tung TA. 2003. A bioarchaeological perspective on Wari imperialism in the Andes of Peru: a view from the heartland and hinterland populations, unpublished Ph.D. dissertation. Department of Anthropology, University of North Carolina at Chapel Hill.

Tung TA. 2007. The village of Beringa at the periphery of the Wari Empire: a site overview and new radiocarbon dates. Andean Past 8:253-286.

Tung TA. 2008a. Violence after imperial collapse: A study of cranial trauma among Late Intermediate Period burials from the former Huari capital, Ayacucho, Peru. Ñawpa Pacha 29:101-118.

Tung TA. 2008b. Dismembering bodies for display: a bioarchaeological study of trophy heads from the Wari site of Conchopata, Peru. American Journal of Physical Anthropology 136(3):294-308.

Tung TA, Cook AG. 2005. Intermediate elite agency in the Wari Empire: the bioarchaeological and mortuary evidence. In Elson C, Covey RA, editors. Intermediate elites in pre-Columbian states and empires. Tucson: University of Arizona Press, pp. 68-93.

Tung TA, Owen B. 2006. Violence and rural lifeways at two peripheral Wari sites in the Majes Valley of southern Peru. In Isbell WH, Silverman H, editors. Andean archaeology III: north and south. New York: Springer, pp. 435-467.

Tung TA, Knudson KJ. 2008. Social identities and geographical origins of Wari trophy heads from Conchopata, Peru. Current Anthropology 49:915-925.

Tung TA, Knudson KJ. 2011. Identifying locals, migrants, and captives in the Wari Heartland: A bioarchaeological and biogeochemical study of human remains from Conchopata, Peru. Journal of Anthropological Archaeology 30(3):247-261.

Valdez LM. 1994. Cahuachi: new evidence for an early Nasca ceremonial role. Current Anthropology 35:675–679.

Valdez LM. 2011. Wari e Inca: El significado de Vilcabamba. Arqueología Iberoamericana 10:3-7.

Vaughn KJ. 2004. Crafts and the materialization of chiefly power in Nasca. Archaeological Papers of the American Anthropological Association 14(1):113-130.

Verano JW. 2005. Human skeletal remains from Pikillacta. In: McEwan GF, editor. Pikillacta: the Wari Empire in Cuzco. Iowa City: University of Iowa Press. p 125-130.

Verano JW, Uceda S, Chapdelaine C, Tello R, Paredes MI, and Pimentel V. 1999. Modified human skulls from the urban sector of the pyramids of Moche, northern Peru. Latin American Antiquity 10(1):59-70.

Wallerstein IM. 1974. The modern World System, Vol. I: capitalist agriculture and the origins of European world-economy in the sixteenth century. New York: Academic Press.

Wernke SA. 2007. Negotiating community and landscape in the Peruvian Andes: a transconquest view. American Anthropologist 109(1):130-152.

Williams-Blangero S, Blangero J. 1989. Anthropometric variation and the genetic structure of the Jirals of Nepal. Human Biology 61:1-12.

Williams C, and Pineda J. 1985. Desde Ayacucho hasta Cajamarca: formas arquitectónicas con filiación Wari, unidad del espacio andino. Boletin de Lima 7(40):55-61.

Williams PR. 2001. Cerro Baúl: a Wari center on the Tiwanaku frontier. Latin American Antiquity 12(1):67-83.

Witt R, Pink CM, Bria RE. 2012. Testing the nature of Wari's presence in the north-central highlands of Peru: A bioarchaeological perspective. Abstracts of the 77th Annual Meeting of the Society for American Archaeology, p. 378.

Wright SE. 1951. The genetical structure of populations. Annals of Eugenics 15:323-354.

Wright HT, and Johnson G. 1975. population exchange and early state formation in southwestern Iran. American Anthropologist 77(2):267-289.

Yoffee N. 1988. Orienting collapse. In: Yoffee N,Cowgill GL, editors. The Collapse of Ancient States and Civilizations. Tucson: University Arizona Press, p.1-19.

APPENDICES

CRANIAL NON-METRIC TRAIT SCORING RUBRIC

No.	Trait	Expression	Original Score	Collapsed Score	Hauser and DeStefano (1989)
1	Metopic suture	absent	0	0	p. 41-45
		partial	1	1	
		complete	2		
		unobservable	9	9	
2	Supraorbital notch	absent	0	0	p. 50-58
		present; < ½ occluded by spicules	1	1	
		present; > ½ occluded by spicules	2		
		present; degree of occlusion unknown	3		
		unobservable	9	9	
3	Supraorbital foramen	absent	0	0	p. 50-58
		present	1	1	
		multiple foramina	2		
		unobservable	9	9	
4	Infraorbital suture	absent	0	0	p. 67-68
		partial	1		
		complete	2	1	
		unobservable	9	9	
5	Multiple infraorbital foramina	absent	0	0	p. 70-74
		internal division only	1	1	
		two distinct foramina	2		
		more than 2 distinct foramina	3		
		unobservable	9	9	
6	Zygomatico-facial foramina	absent	0	0	p. 224-226
		one large	1		
		one large + smaller foramina	2	1	
		two large	3		
		two large + smaller foramina	4		
		one small	5	0	
		multiple small	6	1	
		unobservable	9	9	

No.	Trait	Expression	Original Score	Collapsed Score	Hauser and DeStefano

					(1989)
7	Parietal foramen	absent	0	0	p. 78-82
		present on parietal	1	1	
		present sutural	2		
		unobservable	9	9	
8	Epiteric bone	absent	0	0	p. 210-213
		present	1	1	
		unobservable	9	9	
9	Coronal ossicle	absent	0	0	p. 84-98
		present	1	1	
		unobservable	9	9	
10	Bregmatic bone	absent	0	0	p. 84-98
		present	1	1	
		unobservable	9	9	
11	Sagittal ossicle	absent	0	0	p. 84-98
		present	1	1	
		unobservable	9	9	
12	Apical bone	absent	0	0	P. 84-98
		present	1	1	
		unobservable	9	9	
13	Lambdoid ossicle	absent	0	0	p. 84-98
		present	1	1	
		unobservable	9	9	
14	Asterionic bone	absent	0	0	p. 196-200
		present	1	1	
		unobservable	9	9	
15	Ossicle in occipito-mastoid suture	absent	0	0	p. 196-200
		present	1	1	
		unobservable	9	9	
16	Parietal notch bone	absent	0	0	p. 207-210
		present	1	1	
		unobservable	9	9	
17	Divided parietal bone	absent	0	0	p. 192-193
		horizontal incomplete	1	1	
		horizontal complete	2		
		vertical incomplete	3		
		vertical complete	4		
		oblique from bregma	5		
		oblique from lambda	6		
		oblique from asterion	7		
		unobservable	9	9	

No.	**Trait**	**Expression**	**Original**	**Collapsed**	**Hauser and**

			Score	Score	DeStefano (1989)
18	Os japonicum	absent	0	0	p. 222-224
		partial suture	1		
		complete division	2	1	
		unobservable	9	9	
19	Inca bone	absent	0	0	p. 99-103
		complete single bone	1	1	
		bipartite	2		
		tripartite	3		
		partial	4		
		unobservable	9	9	
20	Condylar canal	not patent	0	0	p. 114-116
		patent	1	1	
		unobservable	9	9	
21	Divided hypoglossal canal	absent	0	0	p. 120-123
		partial; internal surface	1		
		partial; within canal	2		
		complete; internal surface	3	1	
		complete; within canal	4		
		unobservable	9	9	
22	Flexure of superior sagittal sulcus	right	1	1	Buikstra and Ubelaker (1994)
		left	2	0	
		bifurcate	3		
		unobservable	9	9	
23	Foramen ovale incomplete	absent	0	0	p. 149-156
		partial formation	1		
		no definition of foramen	2	1	
		unobservable	9	9	
24	Foramen spinosum incomplete	absent	0	0	p. 149-156
		partial formation	1		
		no definition of foramen	2	1	
		unobservable	9	9	
25	Pterygo-spinous bridge	absent	0	0	p. 156-161
		trace (spicule only)	1		
		partial bridge	2	1	
		complete bridge	3		
		unobservable	9	9	
26	Pterygo-alar bridge	absent	0	0	p. 156-161
		trace (spicule only)	1		
		partial bridge	2	1	
		complete bridge	3		
		unobservable	9	9	
No.	**Trait**	**Expression**	**Original**	**Collapsed**	**Hauser and**

			Score	**Score**	**DeStefano (1989)**
27	Tympanic dehiscence	absent	0	0	p. 143-147
		foramen only	1	1	
		full defect present	2		
		unobservable	9	9	
28	Auditory exostosis	absent	0	0	p. 186-191
		< 1/3 canal occluded	1	1	
		1/3-2/3 canal occluded	2		
		> 2/3 canal occluded	3		
		unobservable	9	9	
29	Mastoid foramen	absent	0	0	p. 202-205
		one temporal	1		
		multiple temporal	2	1	
		single sutural	3	0	
		multiple sutural	4	1	
		single occipital	5	0	
		multiple occipital	6	1	
		sutural and temporal	7		
		occipital and temporal	8		
		unobservable	9	9	
30	Double (occipital) condylar facet	absent	0	0	p. 116-119
		right only	1	1	
		left only	2		
		bilateral	3		
		unobservable	9	9	
31	Bridging of jugular foramen	absent	0	0	p. 130-133
		external bridging; incomplete	1		
		external bridging; complete	2	1	
		internal bridging; incomplete	3	0	
		internal bridging; complete	4	1	
		unobservable	9	9	
32	Pharyngeal tubercle	absent	0	0	p. 136-137
		weak expression	1		
		strong expression	2	1	
		divided	3		
		unobservable	9	9	

No.	Trait	Expression	Original Score	Collapsed Score	Hauser and DeStefano (1989)
33	Palatine torus	absent	0	0	p. 174-179
		trace	1	1	
		moderate (elevation 2-5mm)	2		
		marked (elevation >5mm)	3		
		unobservable	9	9	
34	Mental foramen	absent	0	0	p. 230-233
		one	1		
		two	2	1	
		>2	3		
		unobservable	9	9	
35	Mandibular torus	absent	0	0	p. 182-185
		trace	1	1	
		moderate (elevation 2-5mm)	2		
		marked (elevation >5mm)	3		
		unobservable	9	9	
36	Mylohyoid bridge	absent	0	NA	p. 234-236
		near mandibular foramen	1		
		center of groove	2		
		both 1 and 2, with hiatus	3		
		both 1 and 2, no hiatus	4		
		unobservable	9		
37	Degree of mylohyoid bridge	absent	0	0	p. 234-236
		partial	1	1	
		complete	2		
		unobservable	9	9	

APPENDIX B

Non-metric Trait Frequencies

		Trait scores (0=absent; 1=present; 9=unobservable)											
		Trait 1			Trait 2			Trait 3			Trait 5		
Sample	**n**	0	1	9	0	1	9	0	1	9	0	1	9
CON_MH	*22*	0.9091	0.0909	0.0000	0.4545	0.5000	0.0455	0.5000	0.4545	0.0455	0.5909	0.0000	0.4091
AYA_LIP	*17*	0.8235	0.1765	0.0000	0.3529	0.6471	0.0000	0.4706	0.5294	0.0000	0.7647	0.0000	0.2353
HUA_MH	*24*	1.0000	0.0000	0.0000	0.2917	0.6667	0.0417	0.4167	0.5417	0.0417	0.5833	0.1250	0.2917
MAR_LIP	*35*	0.9143	0.0857	0.0000	0.2571	0.7429	0.0000	0.5143	0.4857	0.0000	0.5143	0.2857	0.2000
TUR_MH	*12*	1.0000	0.0000	0.0000	0.2500	0.7500	0.0000	0.6667	0.3333	0.0000	0.5833	0.1667	0.2500
SON_LIP	*65*	0.7538	0.2000	0.0462	0.4000	0.5538	0.0462	0.4769	0.4769	0.0462	0.6769	0.0923	0.2308
MPM_LIP	*26*	0.8462	0.1154	0.0385	0.2692	0.6154	0.1154	0.6154	0.2692	0.1154	0.5769	0.0769	0.3462
PUC_LIP	*18*	0.8333	0.1667	0.0000	0.2222	0.7778	0.0000	0.8333	0.1667	0.0000	0.8889	0.1111	0.0000
RCC_LIP	*33*	0.6970	0.3030	0.0000	0.2424	0.7273	0.0303	0.7273	0.2424	0.0303	0.6667	0.1818	0.1515
AJA_MH	*9*	1.0000	0.0000	0.0000	0.2222	0.7778	0.0000	0.4444	0.5556	0.0000	0.8889	0.0000	0.1111
CAH_MH	*18*	0.9444	0.0556	0.0000	0.3333	0.6667	0.0000	0.5000	0.5000	0.0000	0.8889	0.0000	0.1111
CAN_MH	*12*	1.0000	0.0000	0.0000	0.2500	0.6667	0.0833	0.7500	0.1667	0.0833	0.8333	0.0833	0.0833
MAJ_MH	*23*	1.0000	0.0000	0.0000	0.3043	0.6957	0.0000	0.6087	0.3913	0.0000	0.6957	0.2174	0.0870
BER_MH	*10*	1.0000	0.0000	0.0000	0.6000	0.3000	0.1000	0.5000	0.4000	0.1000	0.7000	0.2000	0.1000
BER_LIP	*9*	1.0000	0.0000	0.0000	0.7778	0.2222	0.0000	0.6667	0.3333	0.0000	1.0000	0.0000	0.0000
ANC_MH	*62*	0.9839	0.0161	0.0000	0.3065	0.6935	0.0000	0.6935	0.3065	0.0000	0.7258	0.2419	0.0323
ANC_LIP	*55*	1.0000	0.0000	0.0000	0.3273	0.6727	0.0000	0.6182	0.3818	0.0000	0.9091	0.0909	0.0000

		Trait scores (0=absent; 1=present; 9=unobservable)											
		Trait 6			Trait 7			Trait 8			Trait 9		
Sample	**n**	0	1	9	0	1	9	0	1	9	0	1	9
CON_MH	*22*	0.0455	0.8636	0.0909	0.1364	0.6818	0.1818	0.5000	0.0455	0.4545	0.6818	0.0909	0.2273
AYA_LIP	*17*	0.0588	0.8235	0.1176	0.5294	0.3529	0.1176	0.6471	0.1765	0.1765	0.8235	0.1176	0.0588
HUA_MH	*24*	0.1667	0.5417	0.2917	0.5000	0.4583	0.0417	1.0000	0.0000	0.0000	0.9167	0.0833	0.0000
MAR_LIP	*35*	0.0286	0.8286	0.1429	0.5714	0.3429	0.0857	0.8286	0.0857	0.0857	0.9143	0.0000	0.0857
TUR_MH	*12*	0.0000	0.7500	0.2500	0.3333	0.6667	0.0000	0.6667	0.0000	0.3333	1.0000	0.0000	0.0000
SON_LIP	*65*	0.0462	0.7077	0.2462	0.4769	0.4615	0.0615	0.8615	0.0923	0.0462	0.8308	0.1538	0.0154
MPM_LIP	*26*	0.0000	0.6923	0.3077	0.2308	0.7692	0.0000	0.9231	0.0000	0.0769	0.8462	0.1538	0.0000
PUC_LIP	*18*	0.1111	0.8889	0.0000	0.3889	0.5556	0.0556	0.9444	0.0556	0.0000	0.9444	0.0556	0.0000
RCC_LIP	*33*	0.0000	0.8485	0.1515	0.3030	0.6667	0.0303	0.8788	0.0909	0.0303	0.8788	0.1212	0.0000
AJA_MH	*9*	0.1111	0.7778	0.1111	0.1111	0.7778	0.1111	0.8889	0.1111	0.0000	0.8889	0.1111	0.0000
CAH_MH	*18*	0.1111	0.8333	0.0556	0.3333	0.6111	0.0556	0.7778	0.0000	0.2222	0.9444	0.0556	0.0000
CAN_MH	*12*	0.0833	0.8333	0.0833	0.3333	0.6667	0.0000	1.0000	0.0000	0.0000	1.0000	0.0000	0.0000
MAJ_MH	*23*	0.0870	0.8696	0.0435	0.4783	0.5217	0.0000	0.7391	0.0000	0.2609	0.9565	0.0435	0.0000
BER_MH	*10*	0.0000	1.0000	0.0000	0.7000	0.3000	0.0000	1.0000	0.0000	0.0000	1.0000	0.0000	0.0000
BER_LIP	*9*	0.0000	1.0000	0.0000	0.6667	0.1111	0.2222	0.6667	0.3333	0.0000	1.0000	0.0000	0.0000
ANC_MH	*62*	0.0161	0.9355	0.0484	0.2742	0.6774	0.0484	0.7903	0.1129	0.0968	0.8710	0.0161	0.1129
ANC_LIP	*55*	0.1273	0.8727	0.0000	0.3818	0.6000	0.0182	0.9455	0.0364	0.0182	0.9455	0.0545	0.0000

		Trait scores (0=absent; 1=present; 9=unobservable)											
		Trait 11			Trait 12			Trait 13			Trait 15		
Sample	**n**	**0**	**1**	**9**	**0**	**1**	**9**	**0**	**1**	**9**	**0**	**1**	**9**
CON_MH	*22*	0.7727	0.0000	0.2273	0.5455	0.1818	0.2727	0.3182	0.5455	0.1364	0.3182	0.0909	0.5909
AYA_LIP	*17*	0.8824	0.0000	0.1176	0.7059	0.0000	0.2941	0.2353	0.7059	0.0588	0.7059	0.0588	0.2353
HUA_MH	*24*	0.8750	0.0417	0.0833	0.7500	0.2083	0.0417	0.6250	0.3333	0.0417	0.9583	0.0000	0.0417
MAR_LIP	*35*	0.8000	0.0857	0.1143	0.8000	0.1143	0.0857	0.5714	0.3714	0.0571	0.8000	0.1143	0.0857
TUR_MH	*12*	1.0000	0.0000	0.0000	0.9167	0.0000	0.0833	0.5833	0.3333	0.0833	0.6667	0.1667	0.1667
SON_LIP	*65*	0.9385	0.0462	0.0154	0.7231	0.2462	0.0308	0.3538	0.6308	0.0154	0.9385	0.0462	0.0154
MPM_LIP	*26*	1.0000	0.0000	0.0000	0.9231	0.0385	0.0385	0.5000	0.4615	0.0385	0.8462	0.0385	0.1154
PUC_LIP	*18*	0.8889	0.0556	0.0556	0.8889	0.0556	0.0556	0.5000	0.4444	0.0556	0.8333	0.1667	0.0000
RCC_LIP	*33*	1.0000	0.0000	0.0000	0.9091	0.0606	0.0303	0.5455	0.4545	0.0000	0.9697	0.0303	0.0000
AJA_MH	*9*	0.8889	0.0000	0.1111	0.7778	0.1111	0.1111	0.5556	0.3333	0.1111	0.7778	0.1111	0.1111
CAH_MH	*18*	0.9444	0.0000	0.0556	0.8889	0.0556	0.0556	0.6111	0.3333	0.0556	0.7778	0.1111	0.1111
CAN_MH	*12*	1.0000	0.0000	0.0000	1.0000	0.0000	0.0000	0.5833	0.4167	0.0000	0.6667	0.3333	0.0000
MAJ_MH	*23*	1.0000	0.0000	0.0000	0.7826	0.1739	0.0435	0.5652	0.3913	0.0435	0.7391	0.1304	0.1304
BER_MH	*10*	1.0000	0.0000	0.0000	1.0000	0.0000	0.0000	0.5000	0.5000	0.0000	0.6000	0.3000	0.1000
BER_LIP	*9*	1.0000	0.0000	0.0000	0.8889	0.0000	0.1111	0.3333	0.5556	0.1111	0.6667	0.3333	0.0000
ANC_MH	*62*	0.9194	0.0484	0.0323	0.6935	0.2903	0.0161	0.3226	0.6129	0.0645	0.7581	0.1129	0.1290
ANC_LIP	*55*	0.9636	0.0364	0.0000	0.7273	0.2727	0.0000	0.5273	0.4727	0.0000	0.9091	0.0909	0.0000

		Trait scores (0=absent; 1=present; 9=unobservable)											
		Trait 18			Trait 19			Trait 20			Trait 21		
Sample	**n**	**0**	**1**	**9**	**0**	**1**	**9**	**0**	**1**	**9**	**0**	**1**	**9**
CON_MH	*22*	0.8182	0.0000	0.1818	0.7727	0.0455	0.1818	0.2273	0.6364	0.1364	0.8636	0.1364	0.0000
AYA_LIP	*17*	0.8824	0.0000	0.1176	0.6471	0.0588	0.2941	0.0588	0.6471	0.2941	0.5882	0.1765	0.2353
HUA_MH	*24*	0.6667	0.0417	0.2917	1.0000	0.0000	0.0000	0.0833	0.8333	0.0833	0.8333	0.0833	0.0833
MAR_LIP	*35*	0.8000	0.0571	0.1429	0.8571	0.0857	0.0571	0.2857	0.6286	0.0857	0.7143	0.2000	0.0857
TUR_MH	*12*	0.4167	0.0000	0.5833	0.9167	0.0000	0.0833	0.2500	0.5833	0.1667	0.8333	0.0000	0.1667
SON_LIP	*65*	0.7077	0.0000	0.2923	0.9231	0.0308	0.0462	0.2308	0.6308	0.1385	0.7231	0.1385	0.1385
MPM_LIP	*26*	0.6154	0.0000	0.3846	0.8462	0.0769	0.0769	0.2692	0.5769	0.1538	0.7308	0.1154	0.1538
PUC_LIP	*18*	0.9444	0.0556	0.0000	0.8889	0.0556	0.0556	0.3333	0.6667	0.0000	0.7222	0.2222	0.0556
RCC_LIP	*33*	0.6667	0.0303	0.3030	0.9091	0.0909	0.0000	0.4242	0.5455	0.0303	0.8485	0.0909	0.0606
AJA_MH	*9*	0.8889	0.0000	0.1111	0.8889	0.0000	0.1111	0.2222	0.5556	0.2222	0.4444	0.2222	0.3333
CAH_MH	*18*	0.9444	0.0000	0.0556	0.9444	0.0000	0.0556	0.0556	0.8889	0.0556	0.6111	0.2778	0.1111
CAN_MH	*12*	0.8333	0.0000	0.1667	0.9167	0.0833	0.0000	0.1667	0.7500	0.0833	0.7500	0.1667	0.0833
MAJ_MH	*23*	0.9565	0.0000	0.0435	0.9130	0.0870	0.0000	0.0000	0.7826	0.2174	0.6522	0.0870	0.2609
BER_MH	*10*	0.9000	0.0000	0.1000	1.0000	0.0000	0.0000	0.0000	1.0000	0.0000	0.5000	0.5000	0.0000
BER_LIP	*9*	0.8889	0.1111	0.0000	0.6667	0.2222	0.1111	0.1111	0.8889	0.0000	0.6667	0.3333	0.0000
ANC_MH	*62*	0.8710	0.0645	0.0645	0.8710	0.1129	0.0161	0.1935	0.7581	0.0484	0.7581	0.2097	0.0323
ANC_LIP	*55*	1.0000	0.0000	0.0000	0.9818	0.0182	0.0000	0.1273	0.8727	0.0000	0.6545	0.3273	0.0182

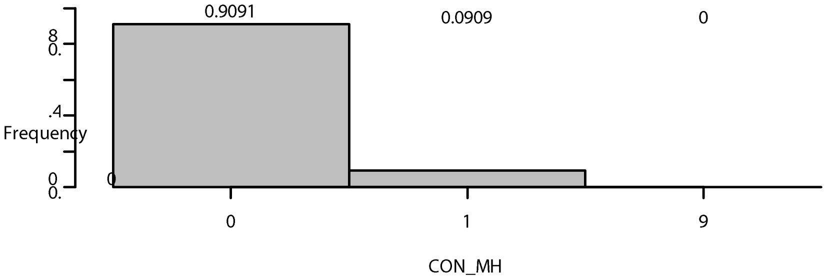
Sample	n	Trait scores (0=absent; 1=present; 9=unobservable)											
		Trait 22			Trait 25			Trait 26			Trait 30		
		0	1	9	0	1	9	0	1	9	0	1	9
CON_MH	22	0.3182	0.5909	0.0909	0.4545	0.0000	0.5455	0.6364	0.0909	0.2727	0.9545	0.0000	0.0455
AYA_LIP	17	0.1176	0.6471	0.2353	0.8824	0.0588	0.0588	0.8235	0.1176	0.0588	0.7647	0.0000	0.2353
HUA_MH	24	0.2500	0.6250	0.1250	0.8750	0.0417	0.0833	0.8333	0.0833	0.0833	0.8333	0.0000	0.1667
MAR_LIP	35	0.1714	0.7714	0.0571	0.8857	0.0857	0.0286	0.8571	0.1143	0.0286	0.7143	0.0000	0.2857
TUR_MH	12	0.1667	0.6667	0.1667	0.8333	0.0000	0.1667	0.8333	0.0833	0.0833	0.6667	0.0000	0.3333
SON_LIP	65	0.3077	0.6000	0.0923	0.9385	0.0462	0.0154	0.9692	0.0154	0.0154	0.7538	0.0308	0.2154
MPM_LIP	26	0.2308	0.6923	0.0769	0.9231	0.0385	0.0385	0.8462	0.1154	0.0385	0.7692	0.0000	0.2308
PUC_LIP	18	0.2222	0.6667	0.1111	1.0000	0.0000	0.0000	1.0000	0.0000	0.0000	0.9444	0.0556	0.0000
RCC_LIP	33	0.1818	0.7576	0.0606	0.9394	0.0606	0.0000	0.9091	0.0909	0.0000	0.8485	0.0303	0.1212
AJA_MH	9	0.1111	0.7778	0.1111	0.8889	0.0000	0.1111	0.7778	0.1111	0.1111	0.5556	0.1111	0.3333
CAH_MH	18	0.1667	0.6111	0.2222	0.8333	0.1111	0.0556	0.8889	0.0000	0.1111	0.8889	0.0000	0.1111
CAN_MH	12	0.0833	0.9167	0.0000	1.0000	0.0000	0.0000	0.7500	0.2500	0.0000	0.7500	0.0000	0.2500
MAJ_MH	23	0.2174	0.6957	0.0870	0.7826	0.0000	0.2174	0.7391	0.0435	0.2174	0.7391	0.0000	0.2609
BER_MH	10	0.2000	0.8000	0.0000	0.8000	0.1000	0.1000	0.9000	0.0000	0.1000	1.0000	0.0000	0.0000
BER_LIP	9	0.3333	0.4444	0.2222	1.0000	0.0000	0.0000	0.8889	0.1111	0.0000	1.0000	0.0000	0.0000
ANC_MH	62	0.3065	0.6774	0.0161	0.9677	0.0161	0.0161	0.8871	0.0968	0.0161	0.9516	0.0323	0.0161
ANC_LIP	55	0.2909	0.6545	0.0545	0.9455	0.0364	0.0182	0.9091	0.0727	0.0182	0.9455	0.0364	0.0182

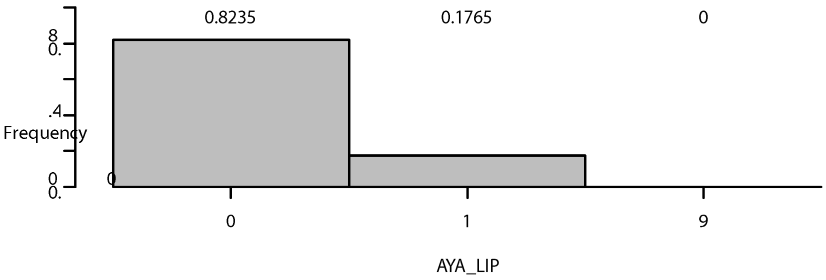
Sample	n	Trait scores (0=absent; 1=present; 9=unobservable)					
		Trait 31			Trait 33		
		0	1	9	0	1	9
CON_MH	22	0.1364	0.0000	0.8636	0.6364	0.1364	0.2273
AYA_LIP	17	0.5882	0.0000	0.4118	0.2353	0.5294	0.2353
HUA_MH	24	0.7917	0.0417	0.1667	0.0833	0.5833	0.3333
MAR_LIP	35	0.8286	0.1143	0.0571	0.1143	0.6571	0.2286
TUR_MH	12	0.5000	0.0000	0.5000	0.1667	0.4167	0.4167
SON_LIP	65	0.8308	0.0154	0.1538	0.2308	0.4308	0.3385
MPM_LIP	26	0.6923	0.1538	0.1538	0.1923	0.4615	0.3462
PUC_LIP	18	0.9444	0.0556	0.0000	0.2222	0.6667	0.1111
RCC_LIP	33	0.8485	0.0909	0.0606	0.1818	0.6667	0.1515
AJA_MH	9	0.6667	0.0000	0.3333	0.5556	0.2222	0.2222
CAH_MH	18	0.7778	0.0000	0.2222	0.6667	0.1667	0.1667
CAN_MH	12	0.7500	0.0000	0.2500	0.7500	0.1667	0.0833
MAJ_MH	23	0.6087	0.0000	0.3913	0.4783	0.3478	0.1739
BER_MH	10	0.9000	0.0000	0.1000	0.3000	0.5000	0.2000
BER_LIP	9	0.8889	0.1111	0.0000	0.1111	0.8889	0.0000
ANC_MH	62	0.8226	0.0161	0.1613	0.9032	0.0645	0.0323
ANC_LIP	55	0.9273	0.0182	0.0545	0.4909	0.4909	0.0182

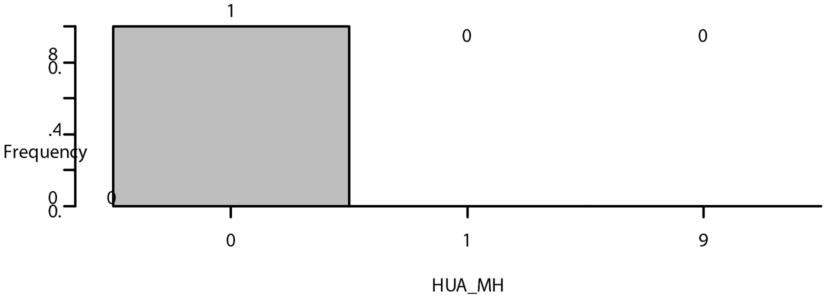
APPENDIX B

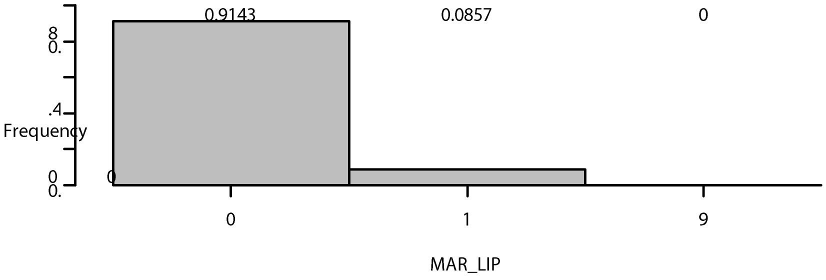
TRAIT FREQUENCIES BY SAMPLE

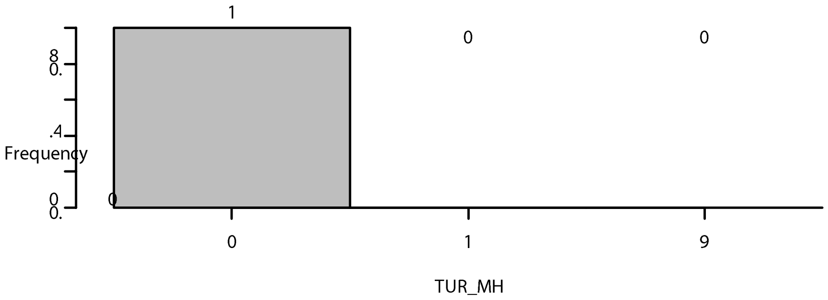
Trait 1 Presence of Metopic suture

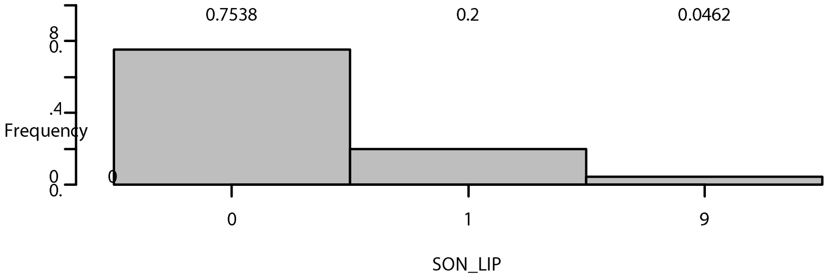


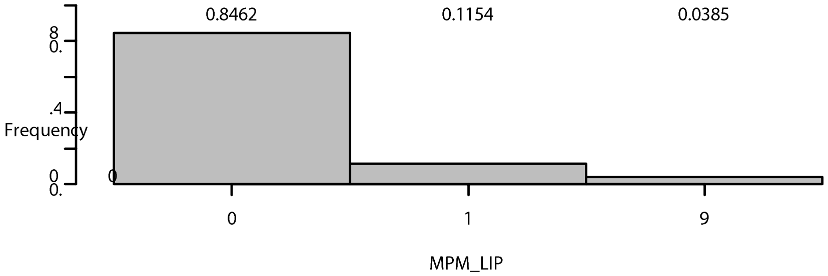


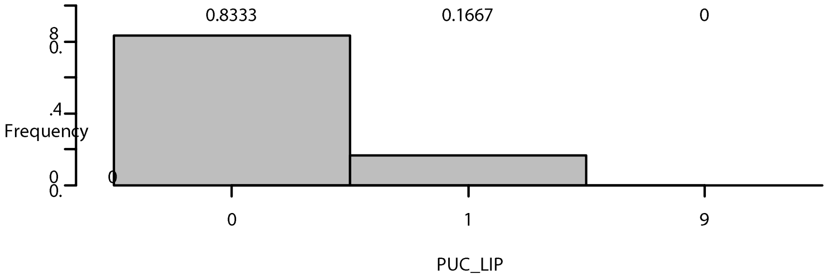


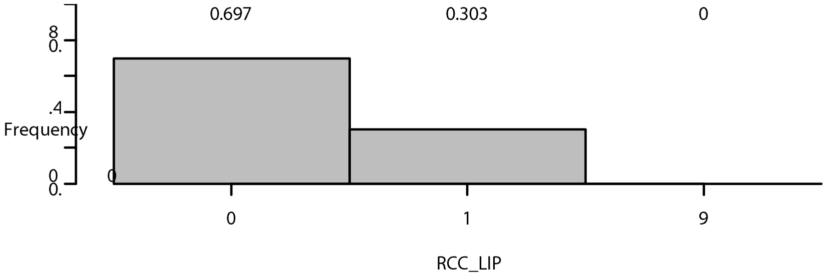


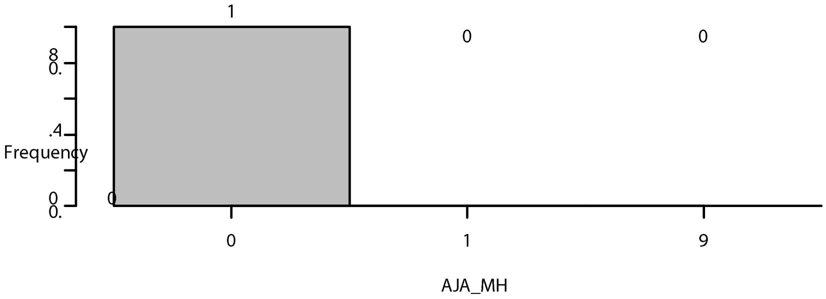

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

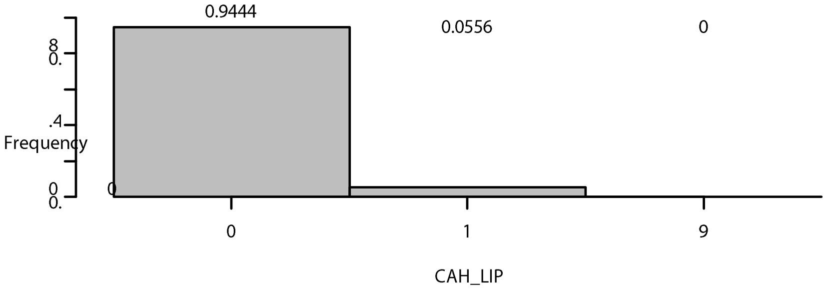

0.7538
0.2
0.0462
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

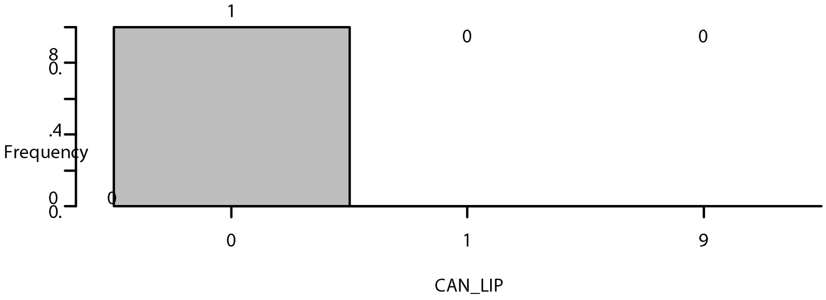

0.8462
0.1154
0.0385
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

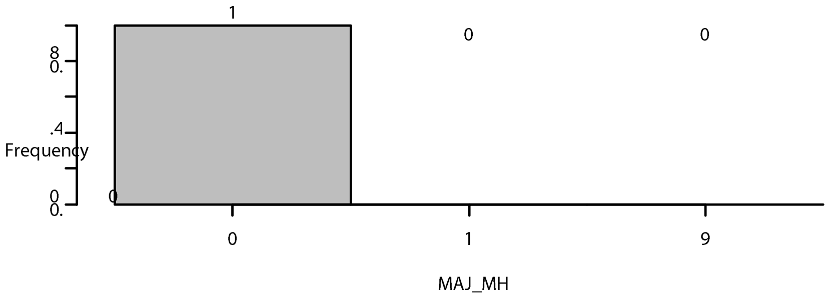

0.8333
0.1667
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

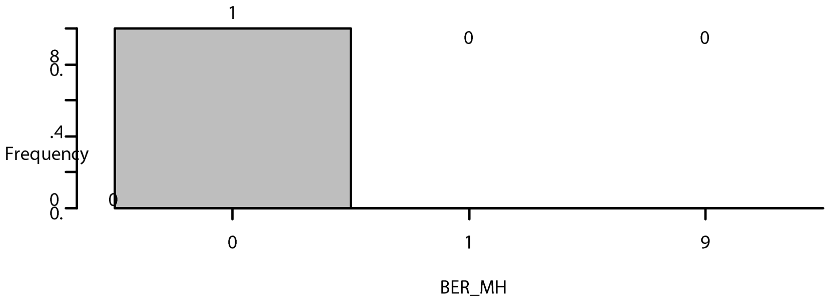

0.697
0.303
0
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

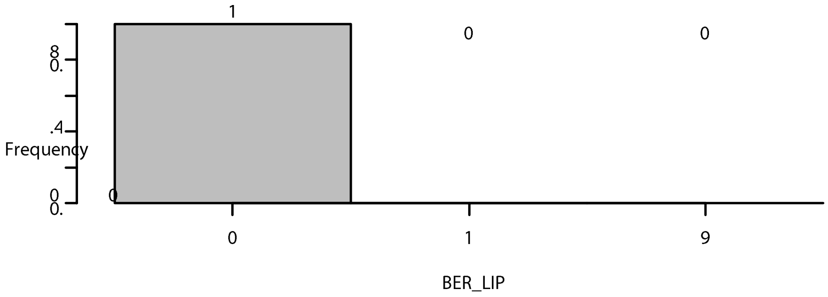

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

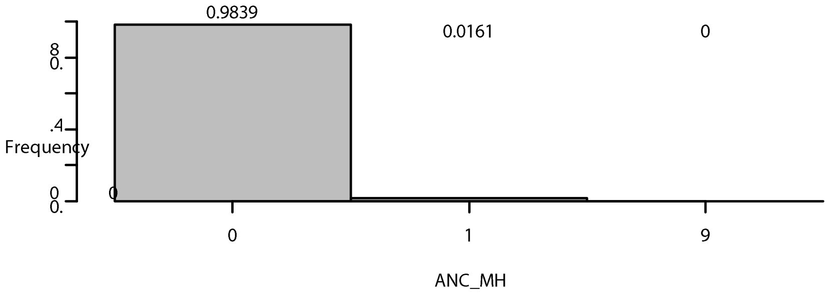

0.9444
0.0556
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

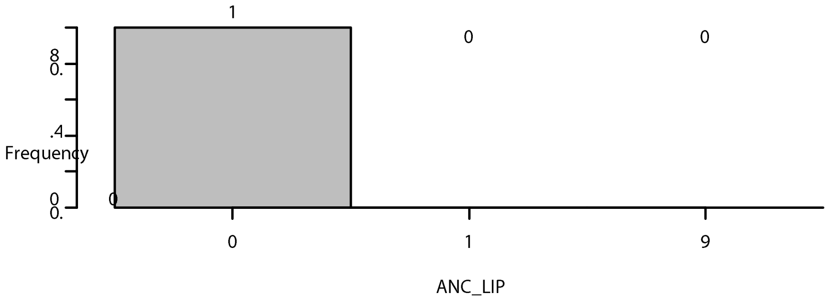

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


1
0
0
0.8
.4
Frequency
0.0
0
0
1
9
MAJ_MH

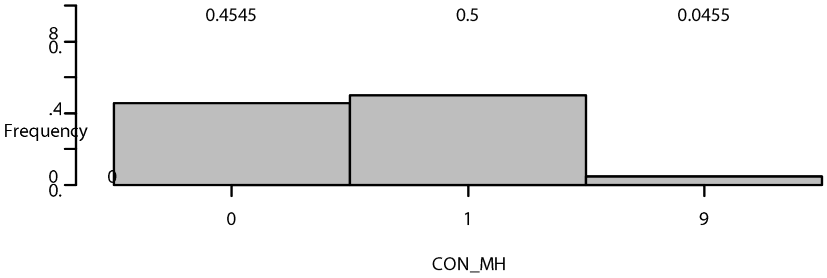

1
0
0
0.8
.4
Frequency
0.0
0
0
1
9
BER_MH

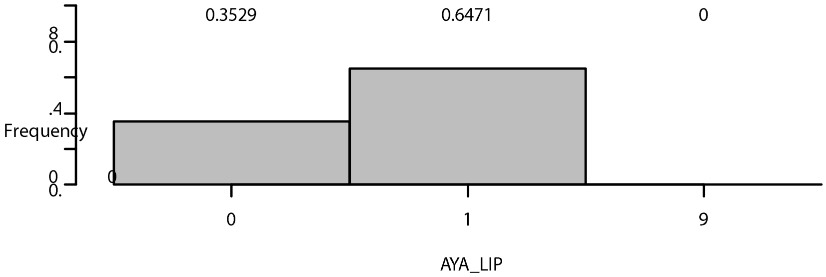

1
0
0
0.8
.4
Frequency
0.0
0
0
1
9
BER_LIP

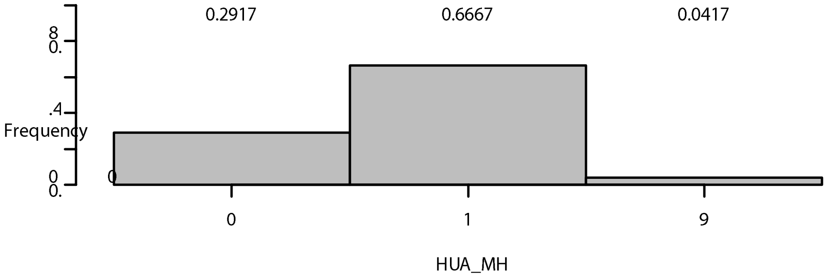

0.9839
0.0161
0
0.8
.4
Frequency
0.0
0
0
1
9
ANC_MH

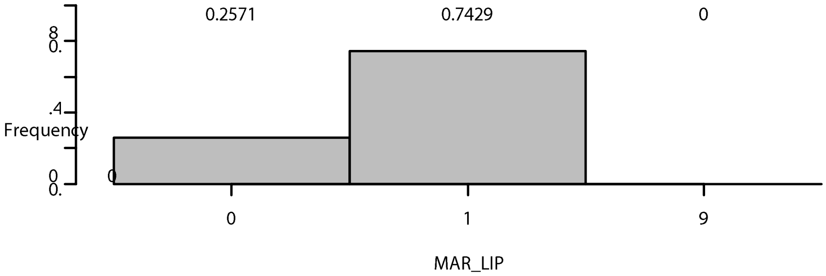

1
0
0
0.8
.4
Frequency
0.0
0
0
1
9
ANC_LIP

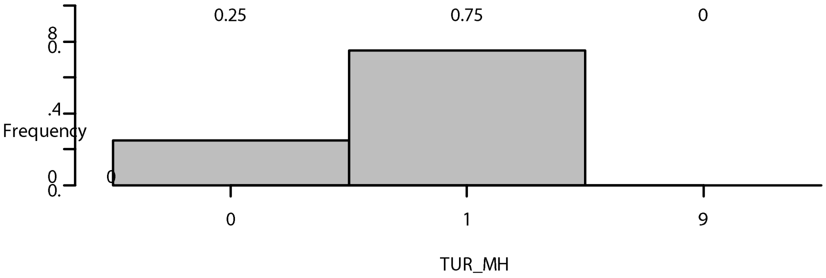
Trait 2 Presence of Supraorbital notch

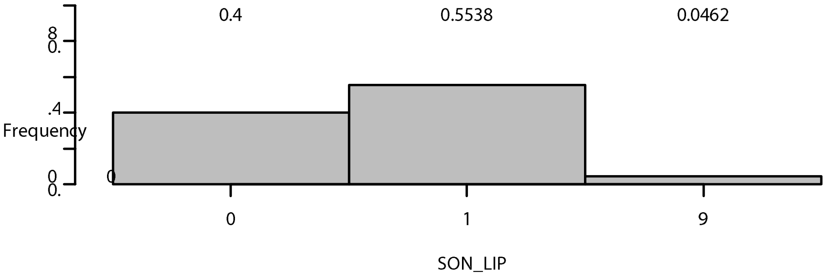


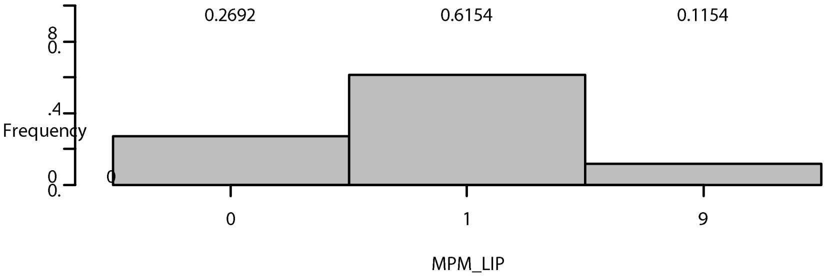


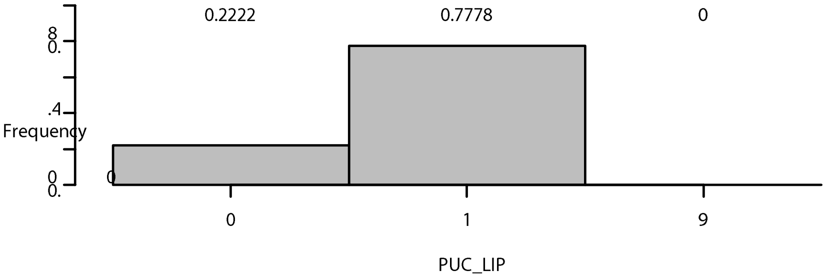


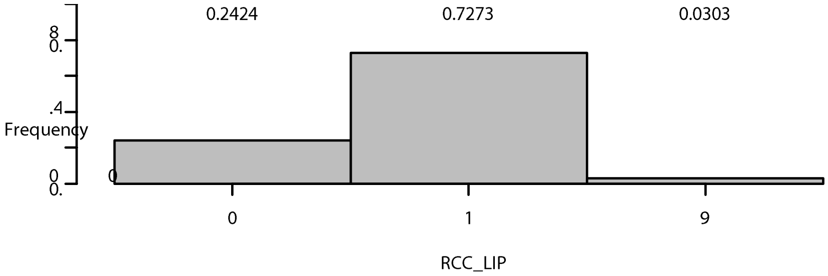


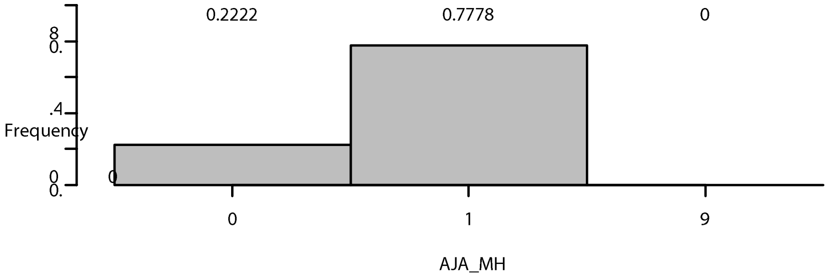

0.25
0.75
0
0.8
0.4
Frequency
0.0
0
1
9
TUR_MH

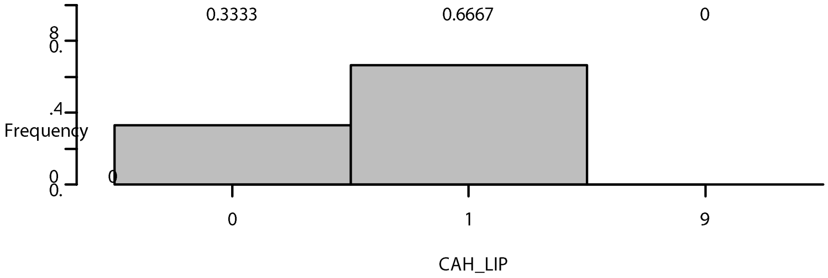

0.4
0.5538
0.0462
0.8
0.4
Frequency
0.0
0
1
9
SON_LIP

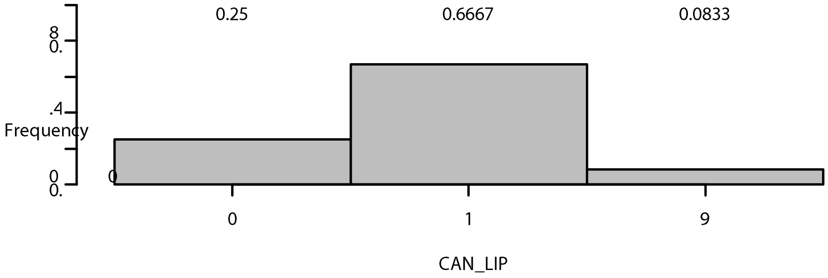

0.2692
0.6154
0.1154
0.8
0.4
Frequency
0.0
0
1
9
MPM_LIP

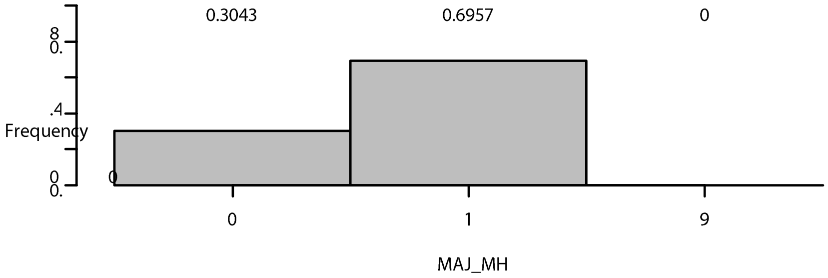

0.2222
0.7778
0
0.8
0.4
Frequency
0.0
0
1
9
PUC_LIP

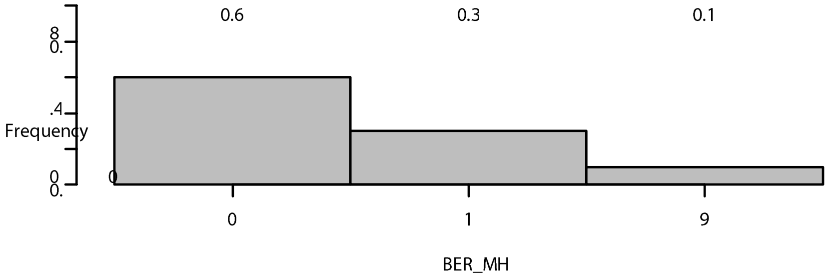

0.2424
0.7273
0.0303
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

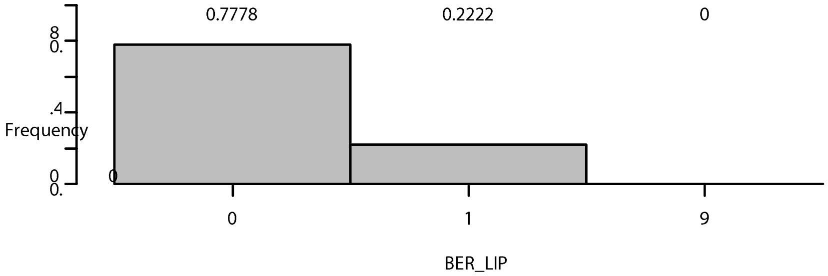

0.2222
0.7778
0
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

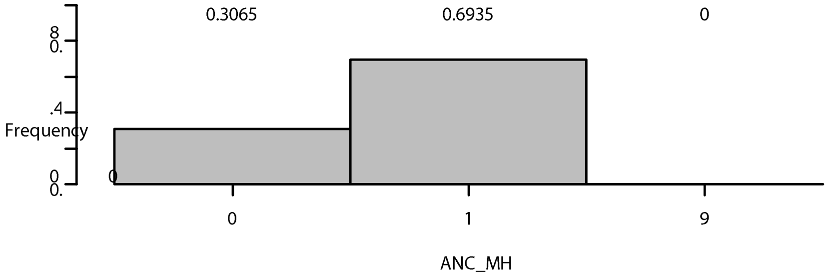

0.3333
0.6667
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

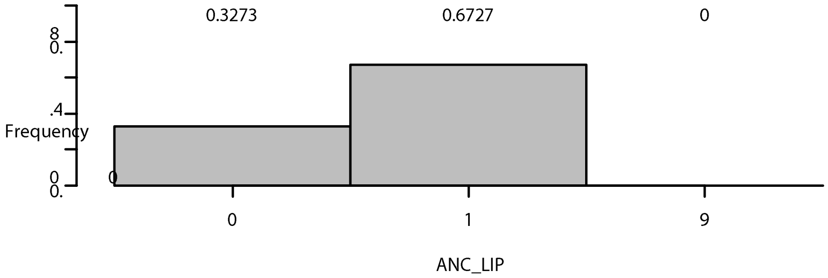

0.25
0.6667
0.0833
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.3043
0.6957
0
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

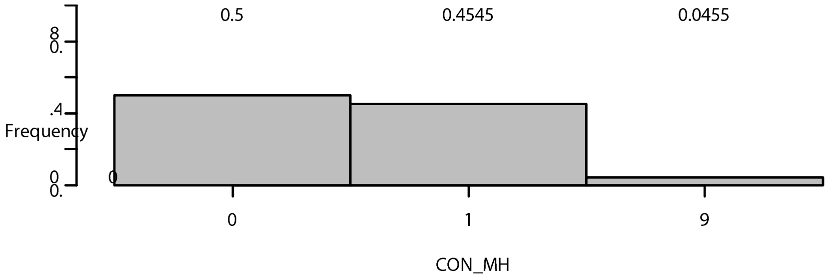

0.6
0.3
0.1
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

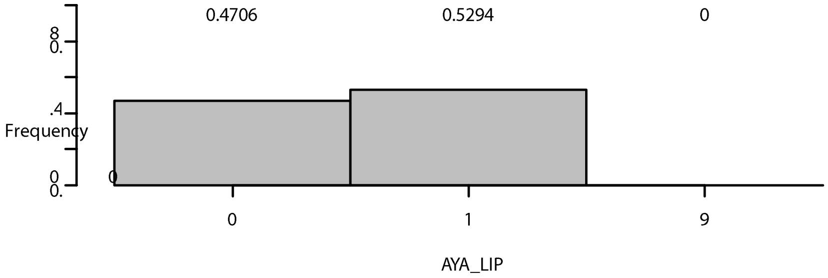

0.7778
0.2222
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

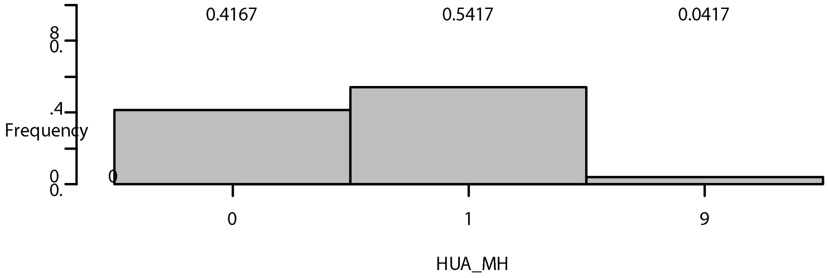

0.3065
0.6935
0
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

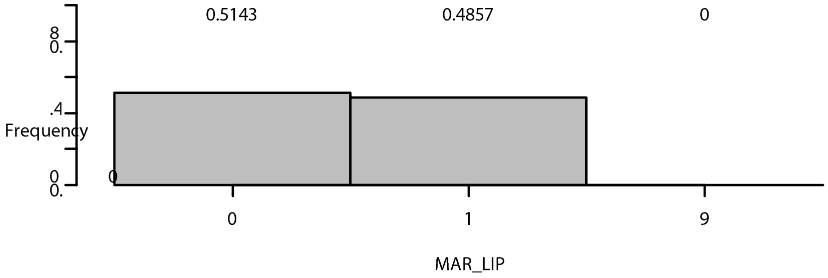

0.3273
0.6727
0
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

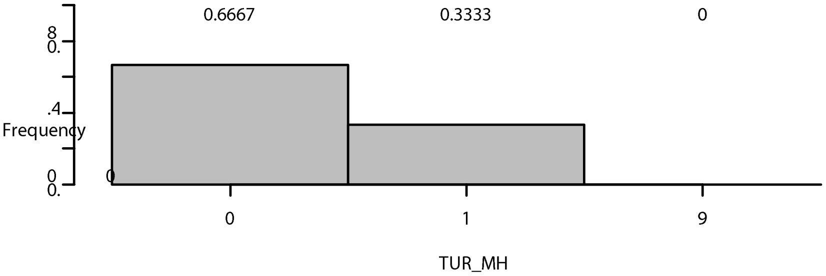
Trait 3 Presence of Supraorbital foramen

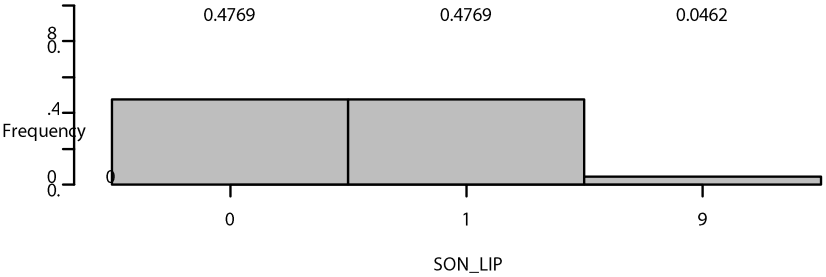


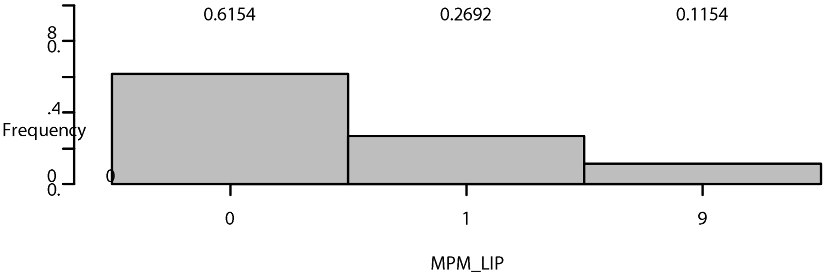


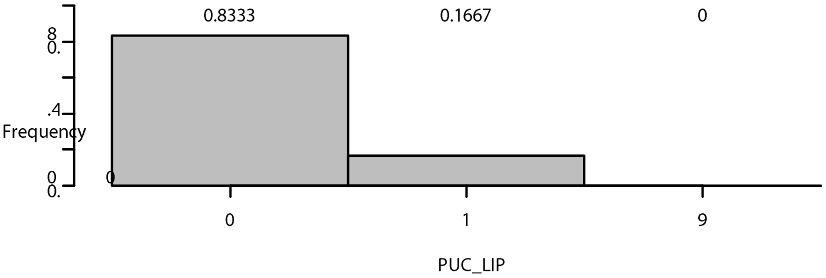


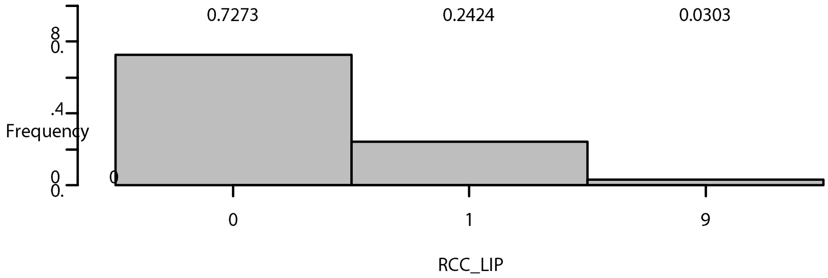


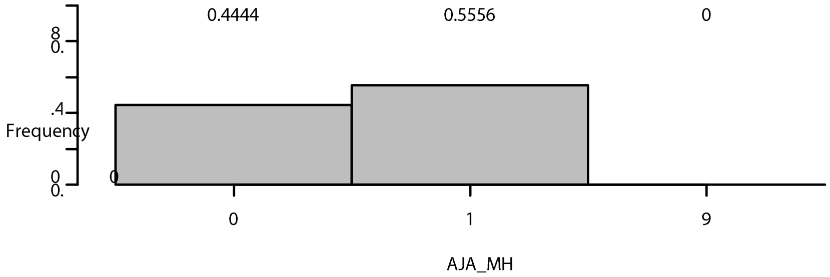

0.6667
0.3333
0
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

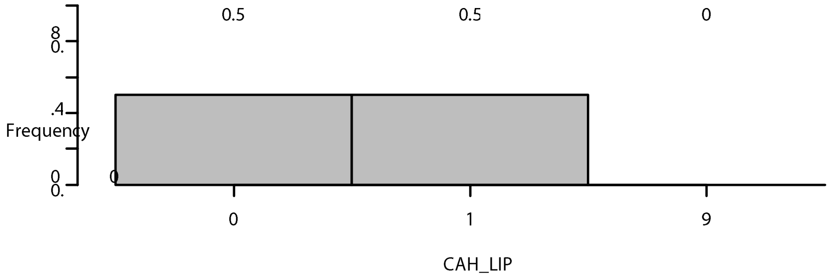

0.4769
0.4769
0.0462
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

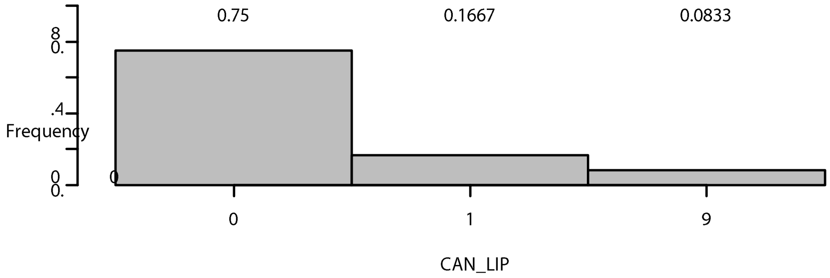

0.6154
0.2692
0.1154
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

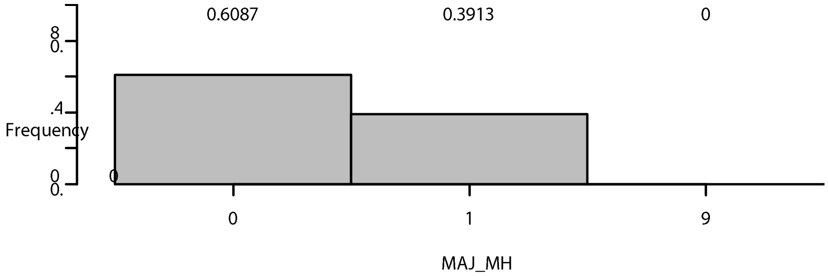

0.8333
0.1667
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

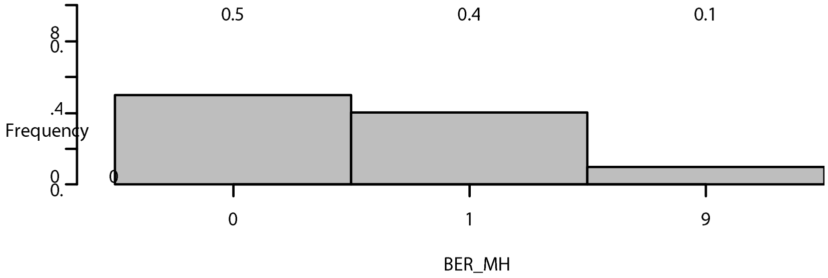

0.7273
0.2424
0.0303
0.8
.4
Frequency
0.0
0
0
1
9
RCC_LIP

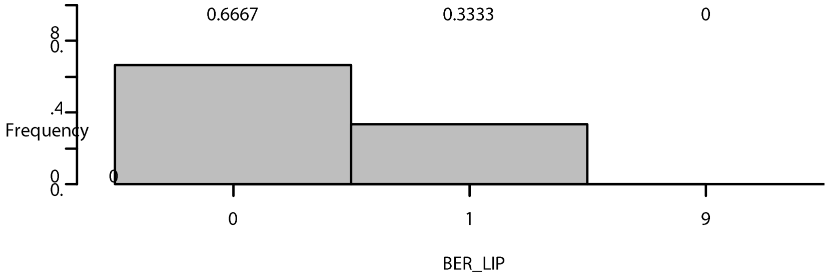

0.4444
0.5556
0
0.8
.4
Frequency
0.0
0
0
1
9
AJA_MH

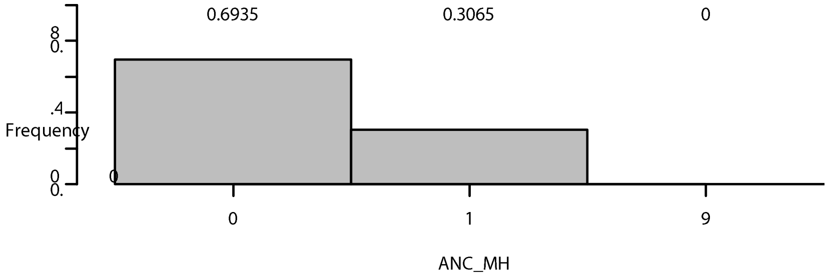

0.5
0.5
0
0.8
.4
Frequency
0.0
0
0
1
9
CAH_LIP

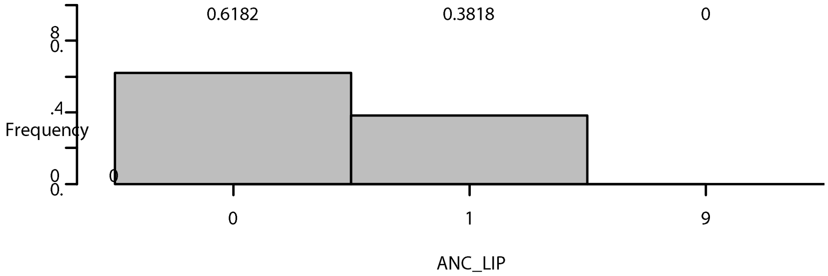

0.75
0.1667
0.0833
0.8
.4
Frequency
0.0
0
0
1
9
CAN_LIP


0.6087
0.3913
0
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

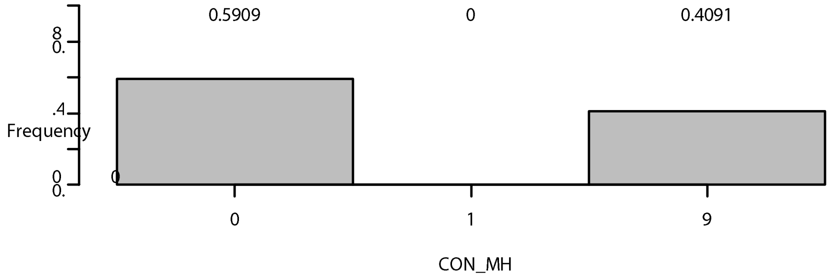

0.5
0.4
0.1
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

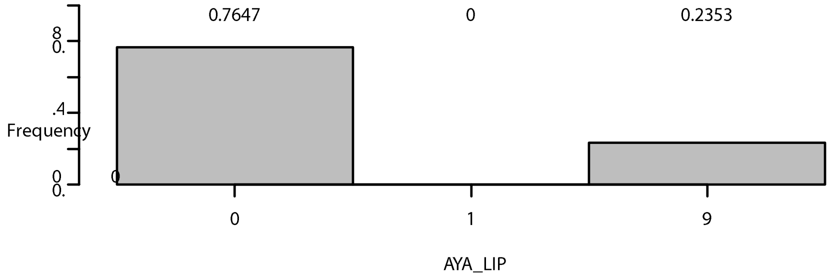

0.6667
0.3333
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

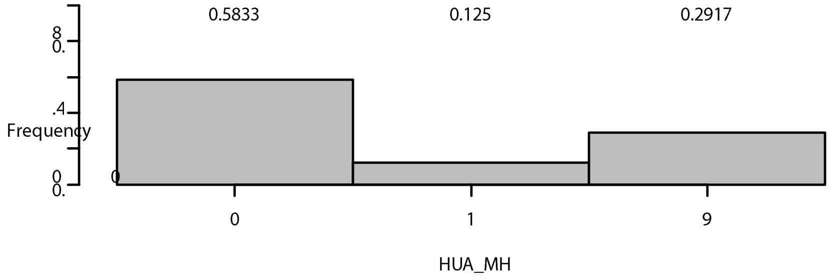

0.6935
0.3065
0
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

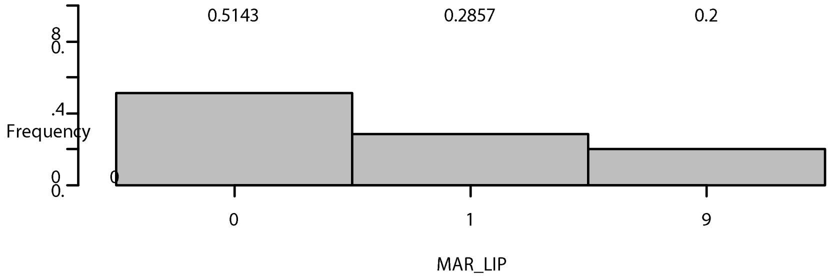

0.6182
0.3818
0
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

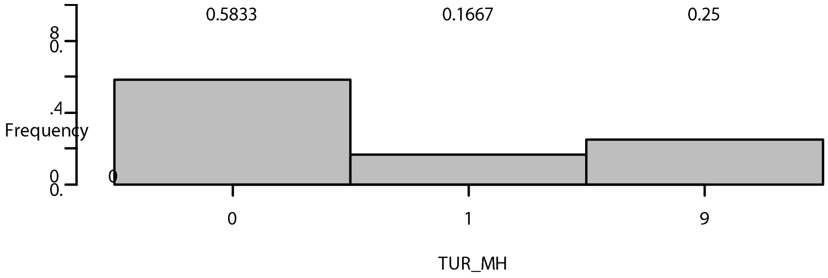
Trait 5 Multiple infraorbital foramina

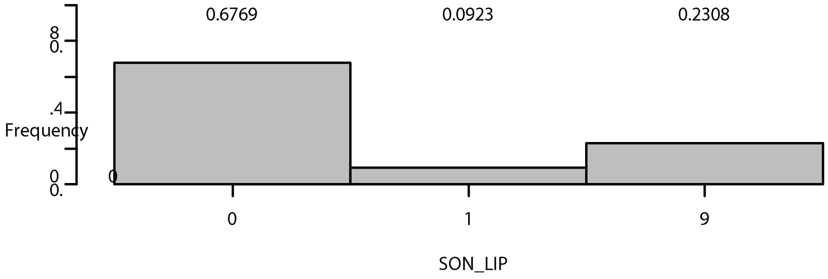


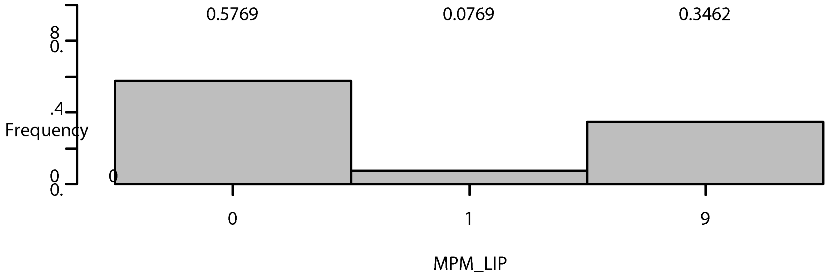


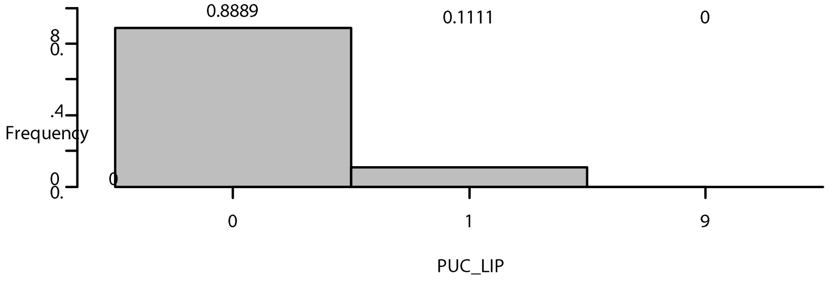


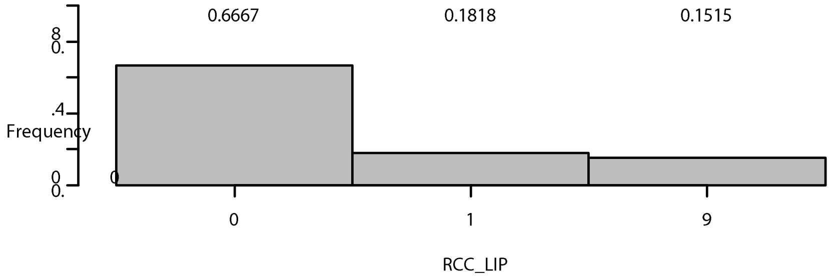


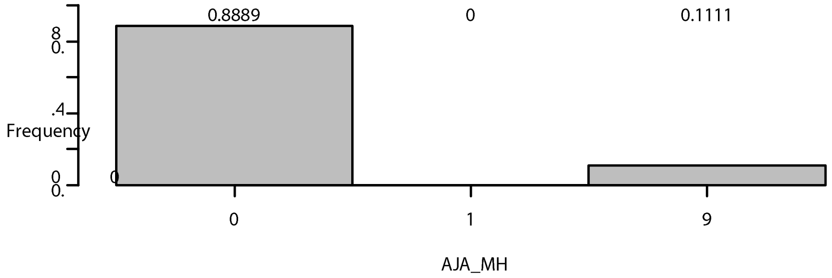

0.5833
0.1667
0.25
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

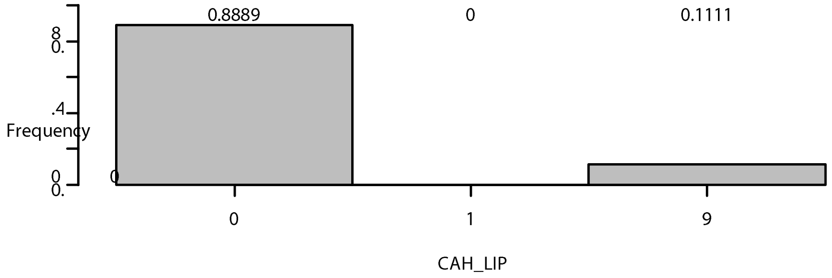

0.6769
0.0923
0.2308
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

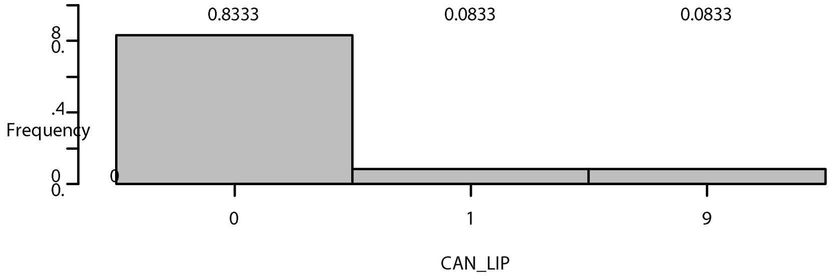

0.5769
0.0769
0.3462
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

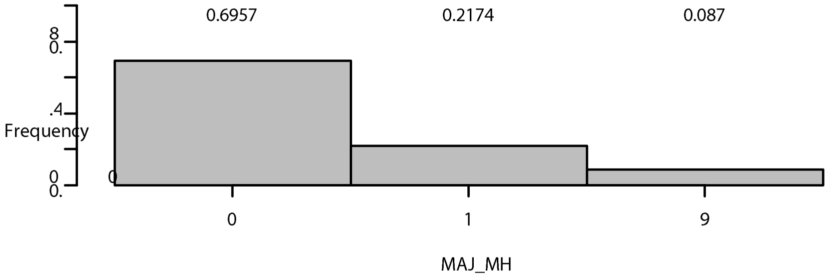

0.8889
0.1111
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

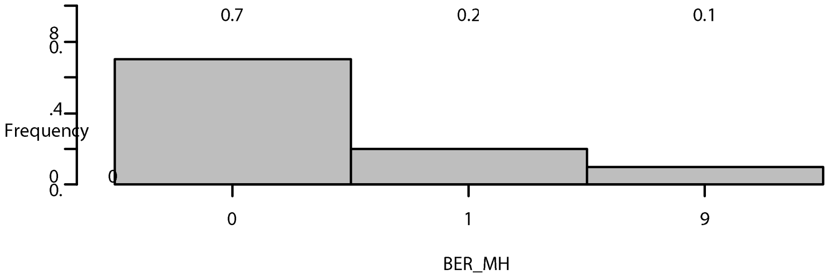

0.6667
0.1818
0.1515
0.8
.4
Frequency
0.0
0
0
1
9
RCC_LIP

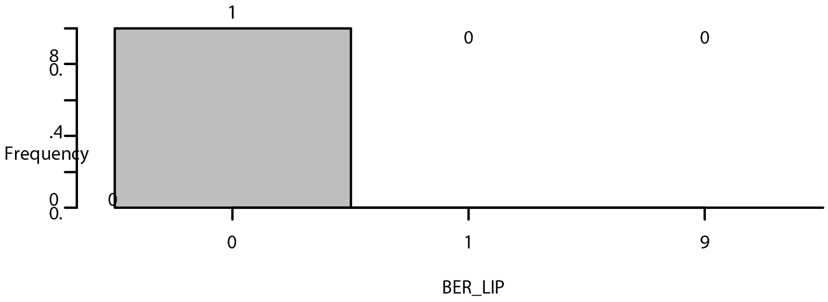

0.8889
0
0.1111
0.8
.4
Frequency
0.0
0
0
1
9
AJA_MH

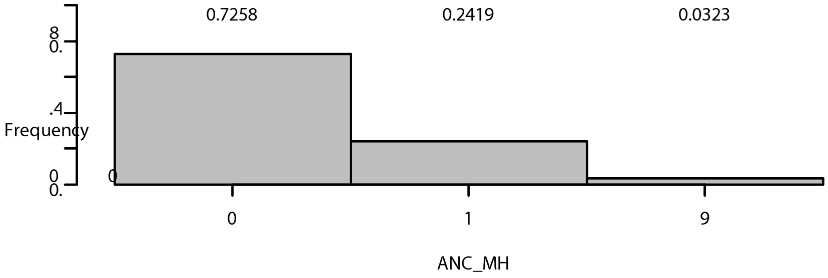

0.8889
0
0.1111
0.8
.4
Frequency
0.0
0
0
1
9
CAH_LIP

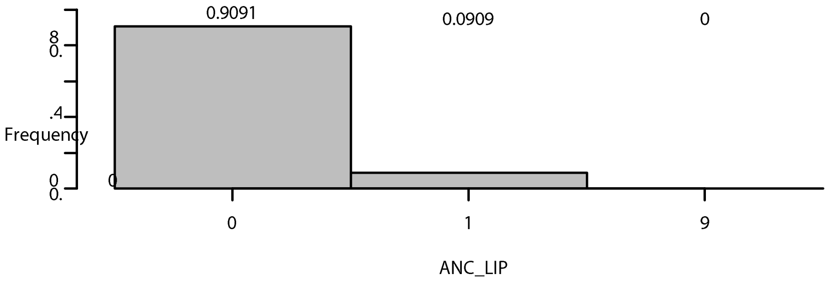

0.8333
0.0833
0.0833
0.8
.4
Frequency
0.0
0
0
1
9
CAN_LIP


0.6957
0.2174
0.087
0.8
.4
Frequency
0.0
0
1
9
MAJ_MH

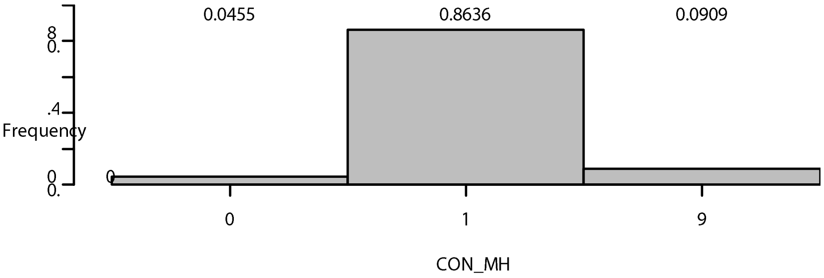

0.7
0.2
0.1
0.8
.4
Frequency
0.0
0
1
9
BER_MH

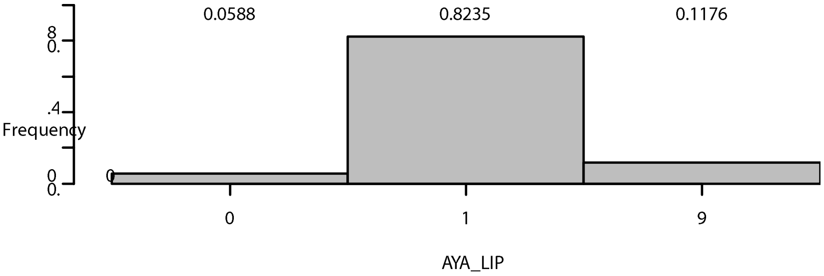

1
0
0
0.8
.4
Frequency
0.0
0
1
9
BER_LIP

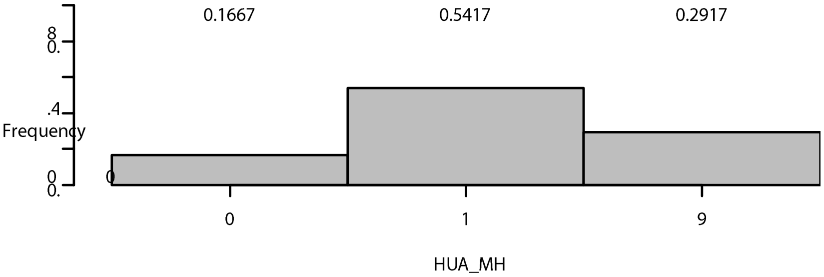

0.7258
0.2419
0.0323
0.8
.4
Frequency
0.0
0
1
9
ANC_MH

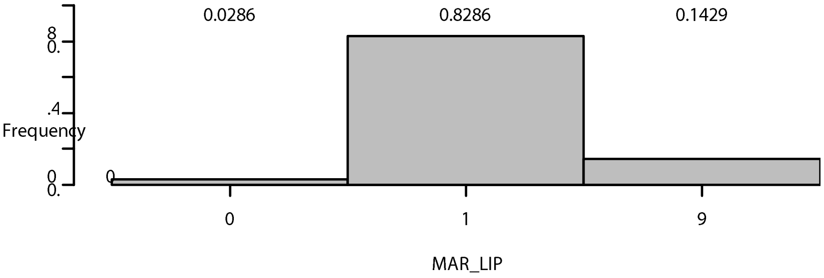

0.9091
0.0909
0
0.8
.4
Frequency
0.0
0
1
9
ANC_LIP

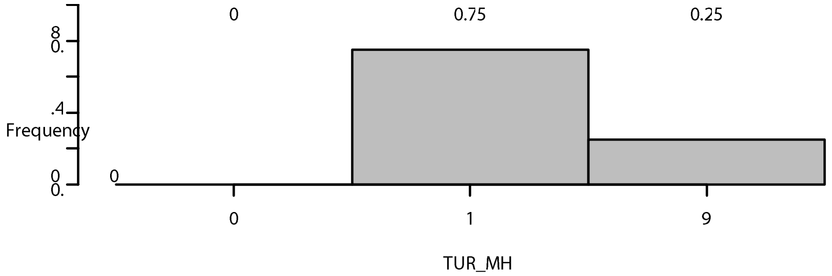
Trait 6 Multiple zygomatico-facial foramina

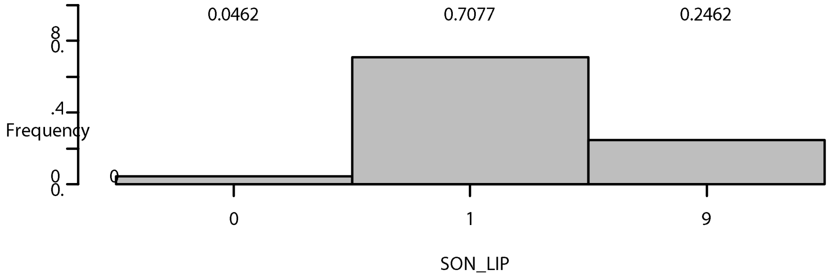


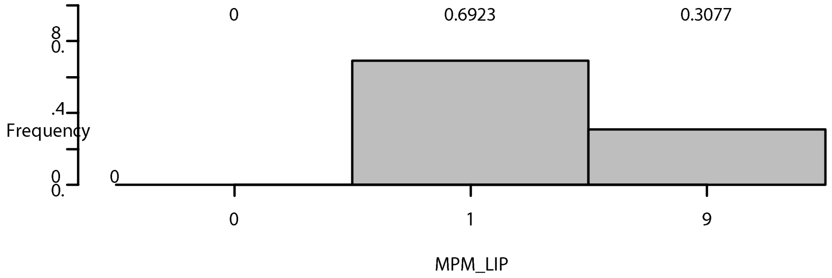


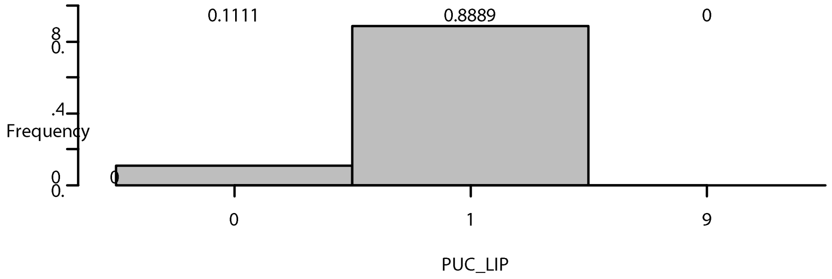


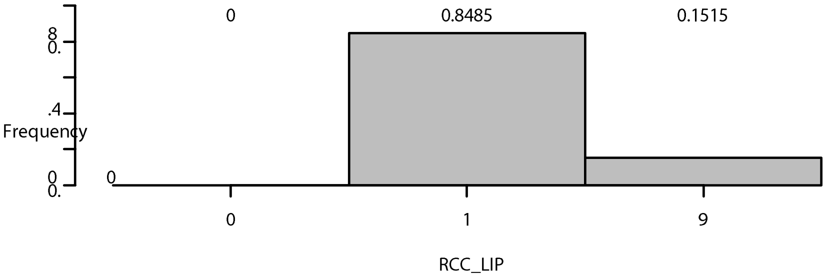


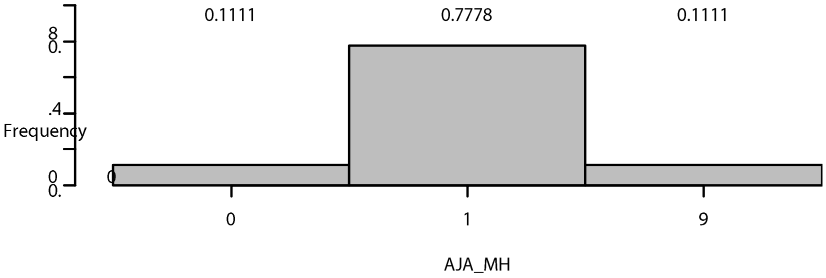

0
0.75
0.25
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

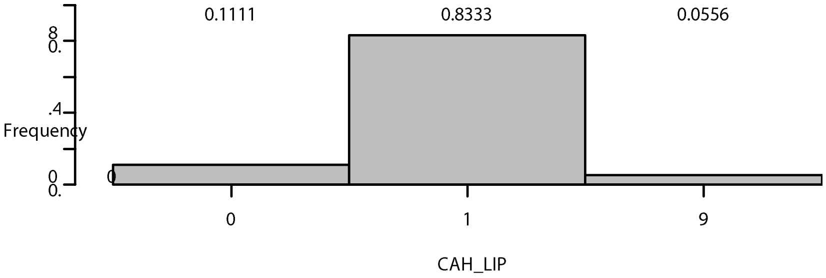

0.0462
0.7077
0.2462
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

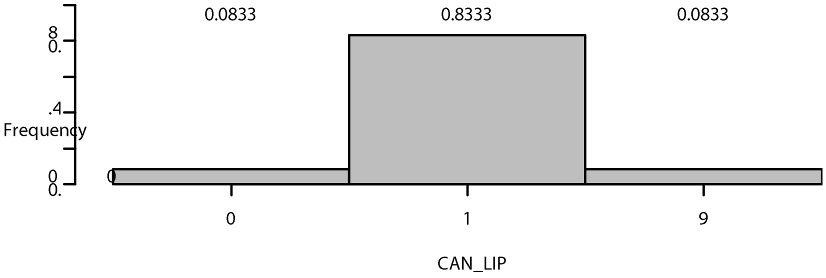

0
0.6923
0.3077
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

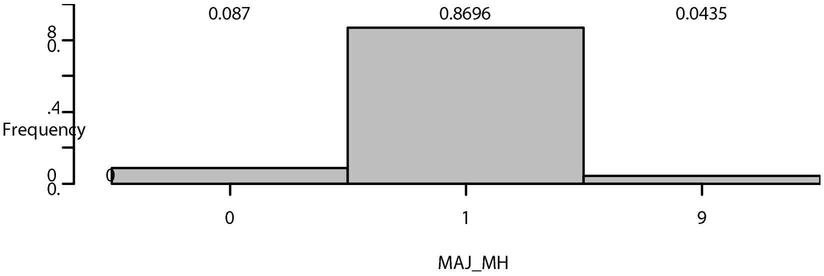

0.1111
0.8889
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

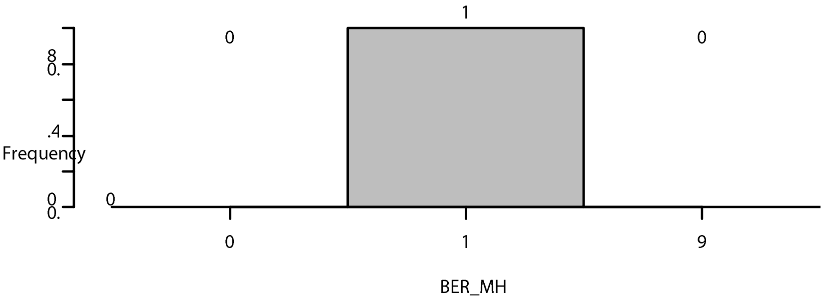

0
0.8485
0.1515
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

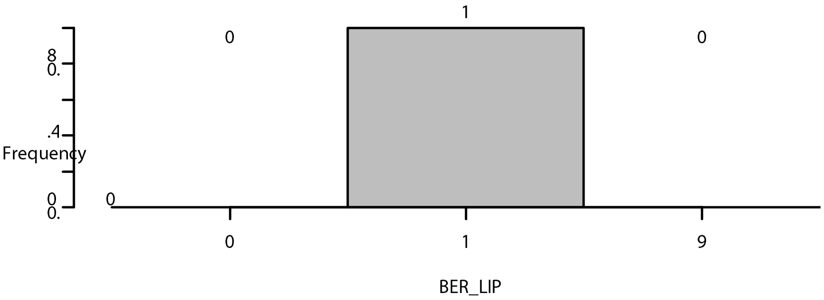

0.1111
0.7778
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

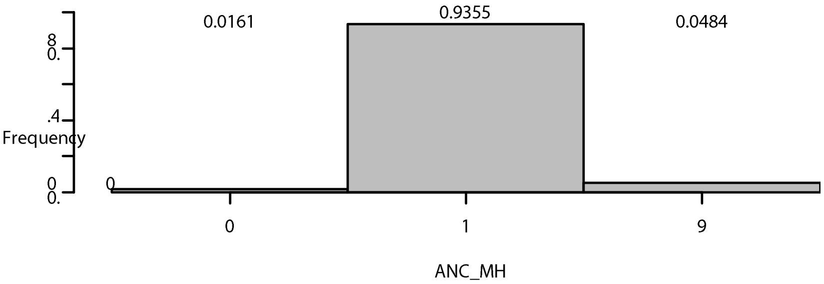

0.1111
0.8333
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

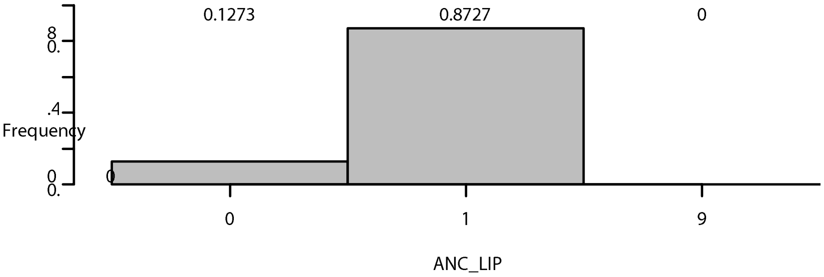

0.0833
0.8333
0.0833
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.087
0.8696
0.0435
0.8
0.4
Frequency
0.0
0
0
1
9
MAJ_MH

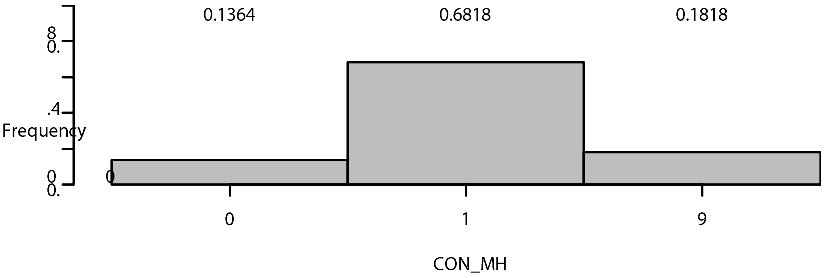

0
1
0
0.8
0.4
Frequency
0.0
0
0
1
9
BER_MH

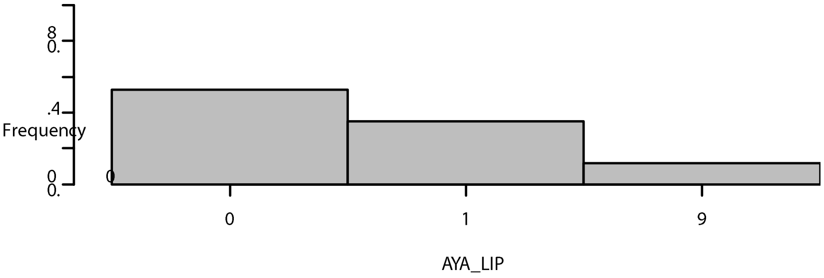

0
1
0
0.8
0.4
Frequency
0.0
0
0
1
9
BER_LIP

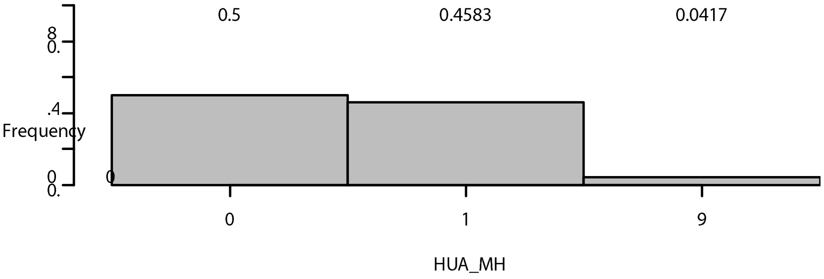

0.0161
0.9355
0.0484
0.8
0.4
Frequency
0.0
0
0
1
9
ANC_MH

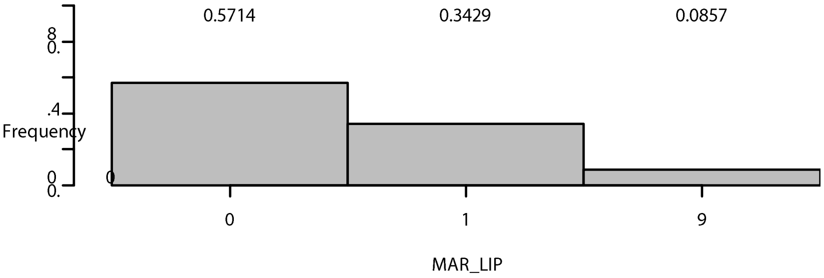

0.1273
0.8727
0
0.8
0.4
Frequency
0.0
0
0
1
9
ANC_LIP

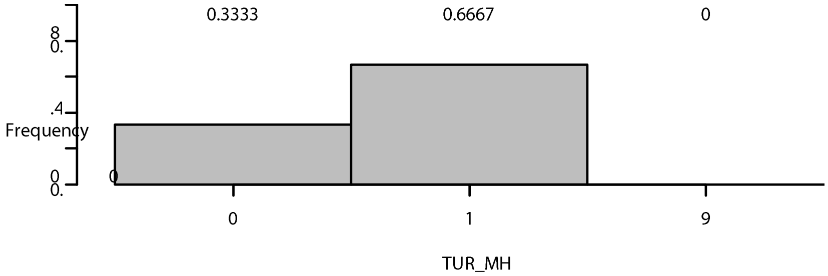
Trait 7 Parietal foramen

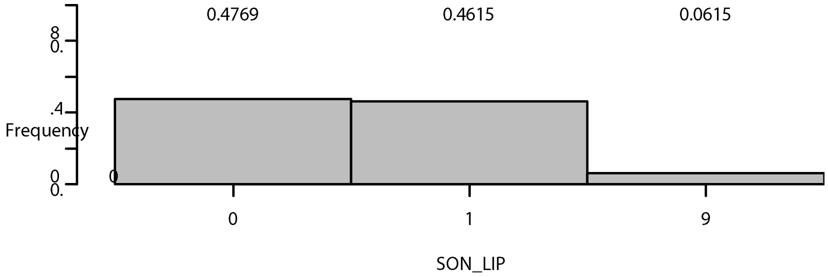


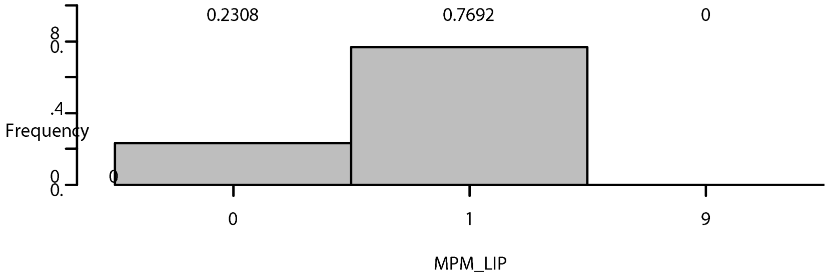


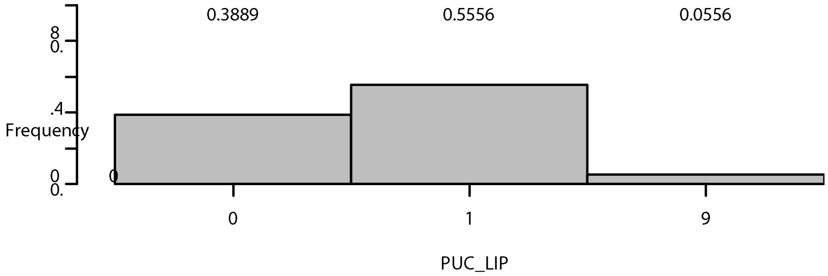


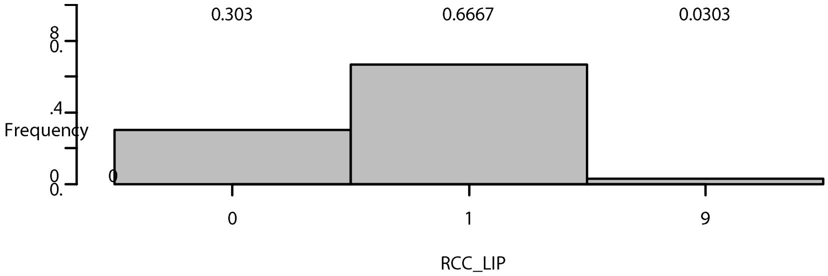


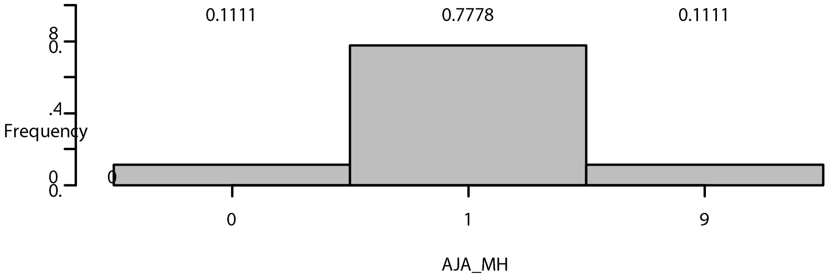

0.3333
0.6667
0
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

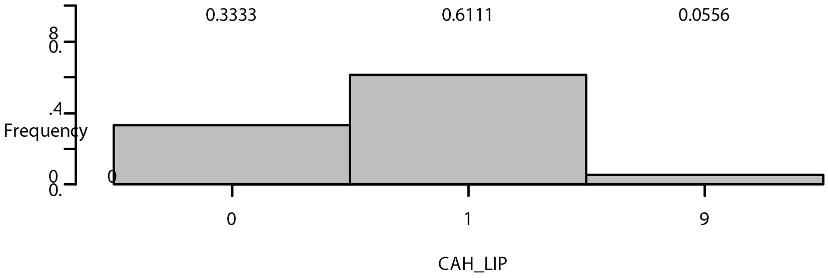

0.4769
0.4615
0.0615
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

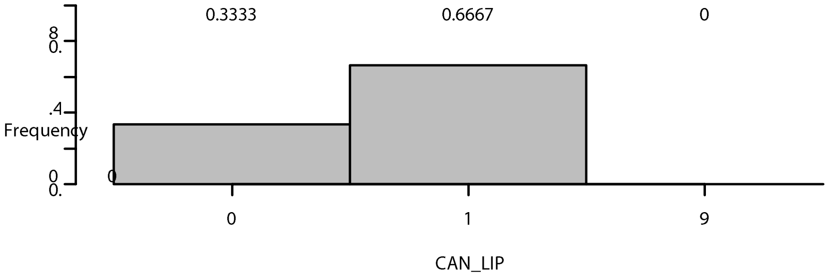

0.2308
0.7692
0
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

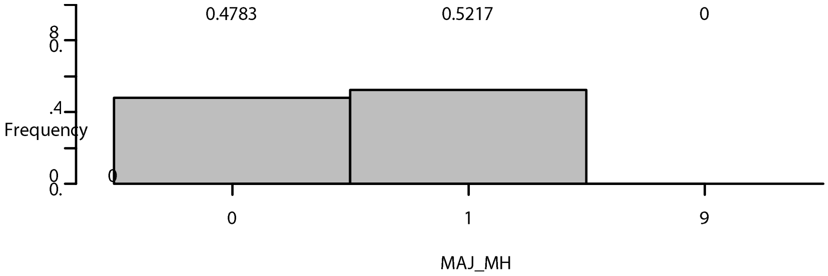

0.3889
0.5556
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

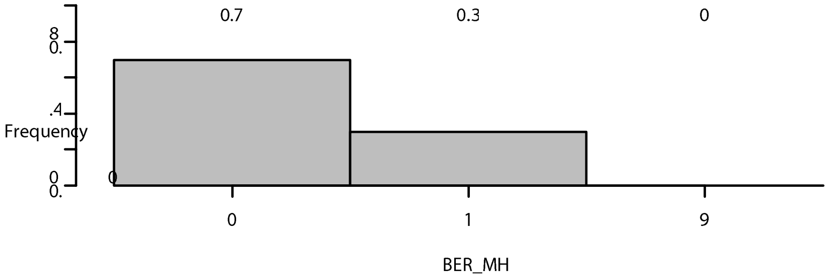

0.303
0.6667
0.0303
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

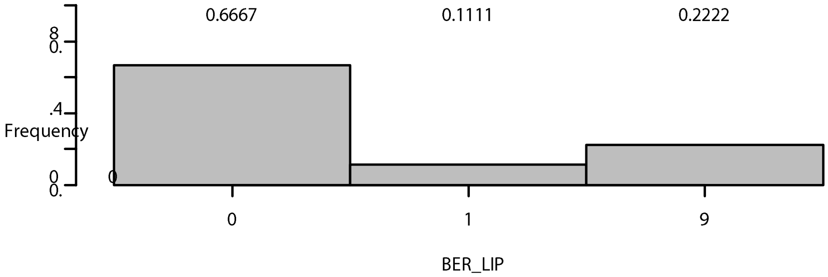

0.1111
0.7778
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

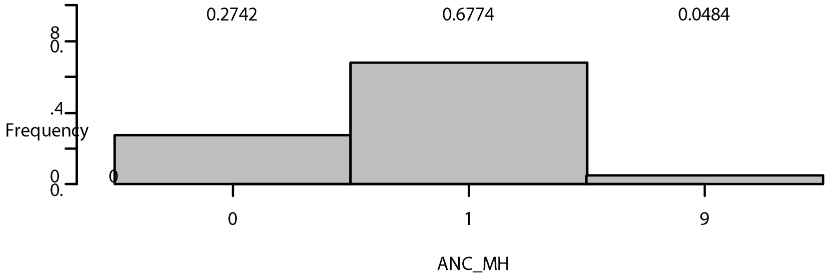

0.3333
0.6111
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

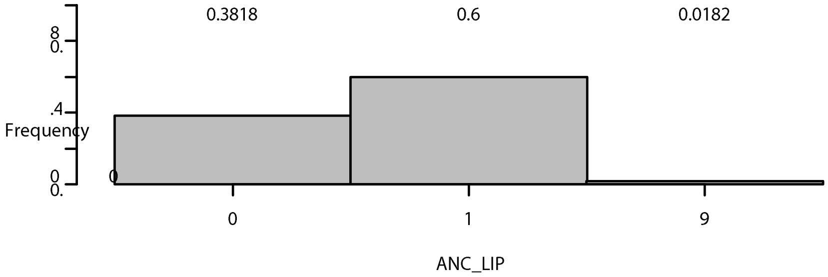

0.3333
0.6667
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.4783
0.5217
0
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

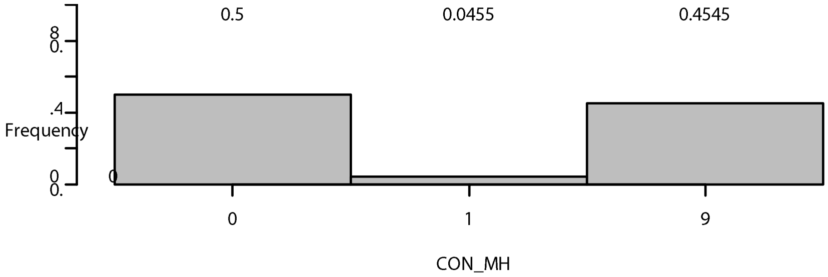

0.7
0.3
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

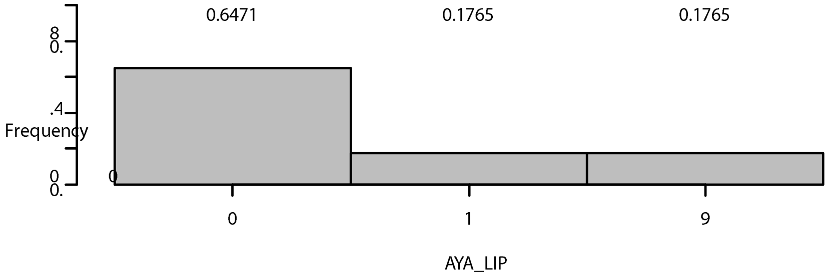

0.6667
0.1111
0.2222
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

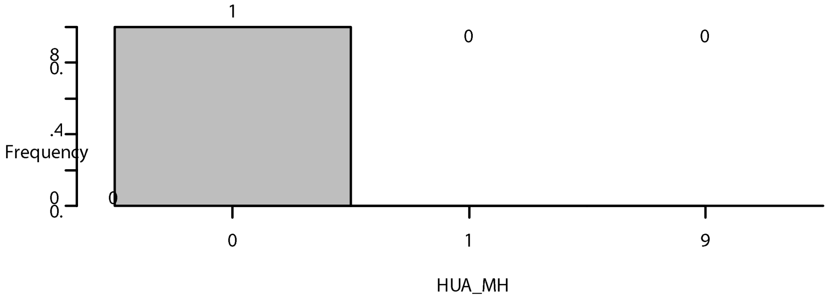

0.2742
0.6774
0.0484
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

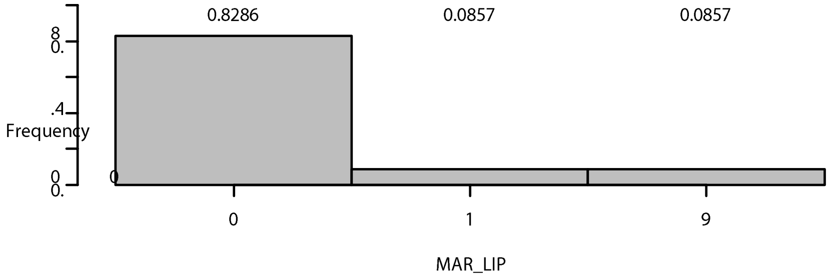

0.3818
0.6
0.0182
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

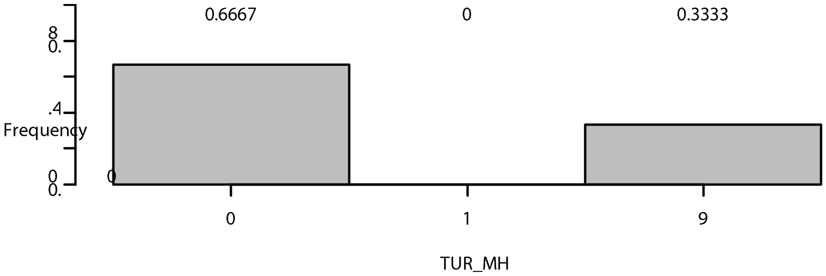
Trait 8 Epiteric bone

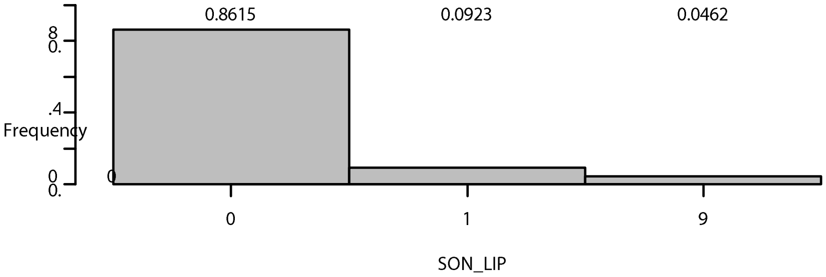


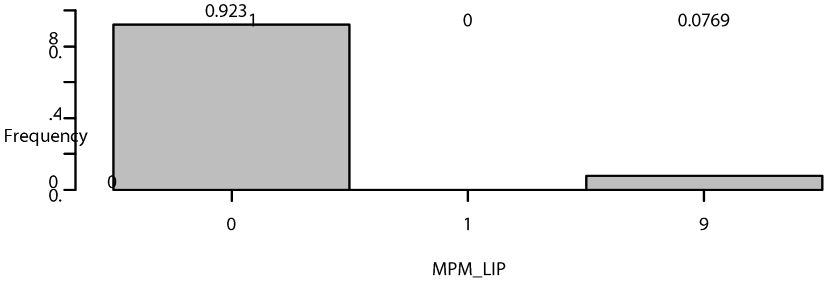


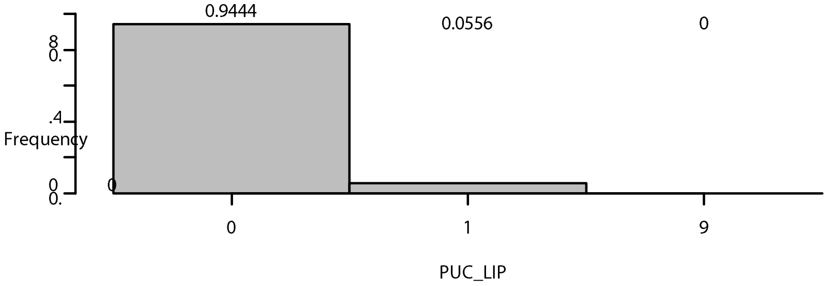


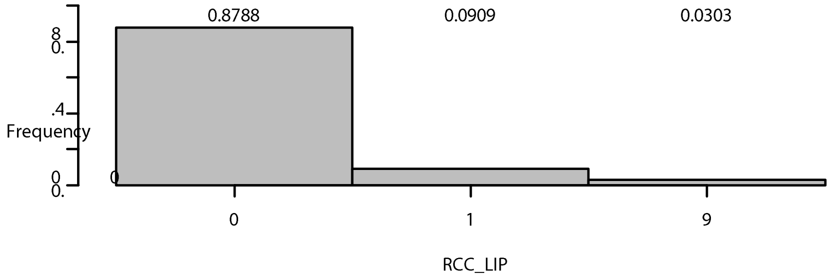


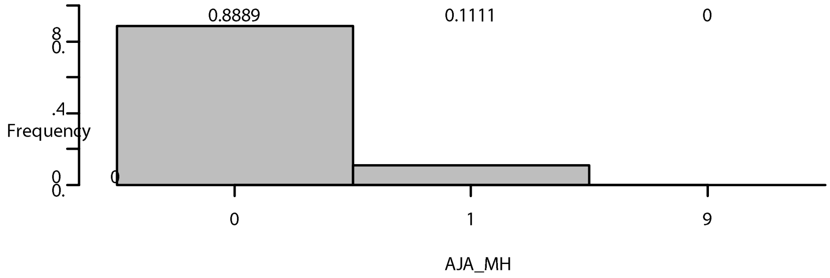

0.6667
0
0.3333
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

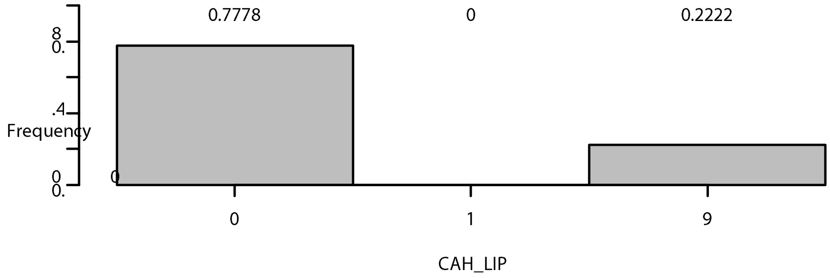

0.8615
0.0923
0.0462
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

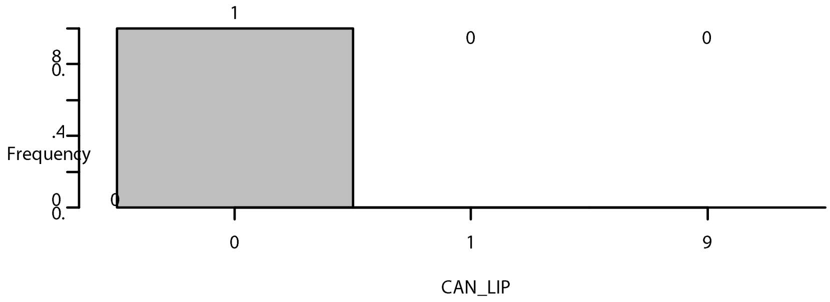

0.923
1
0
0.0769
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

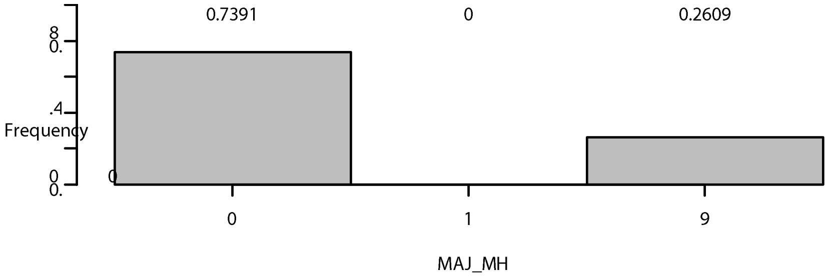

0.9444
0.0556
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

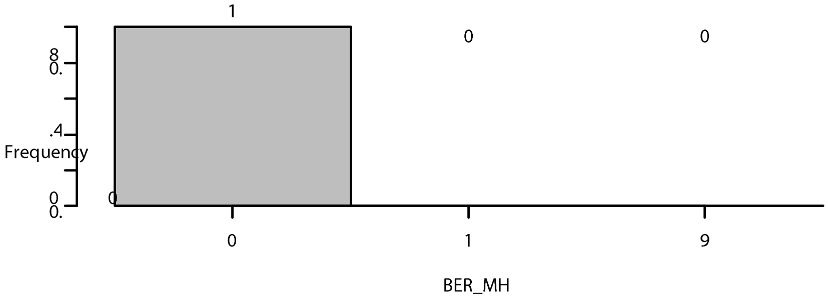

0.8788
0.0909
0.0303
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

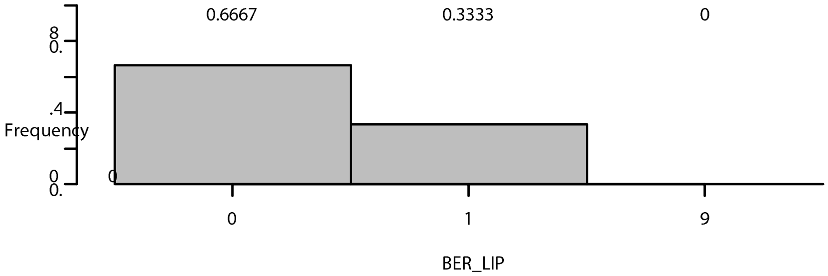

0.8889
0.1111
0
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

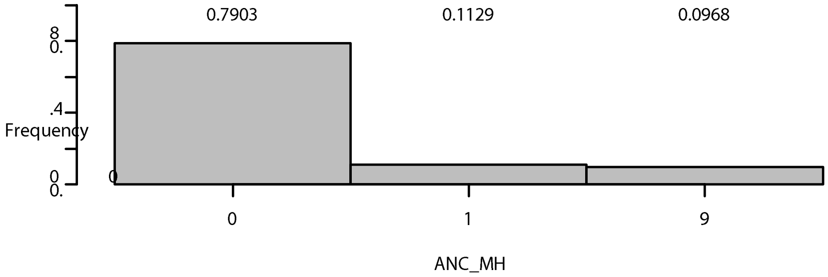

0.7778
0
0.2222
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

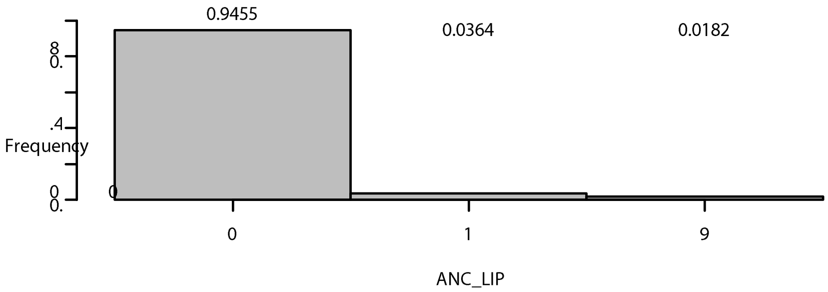

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.7391
0
0.2609
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

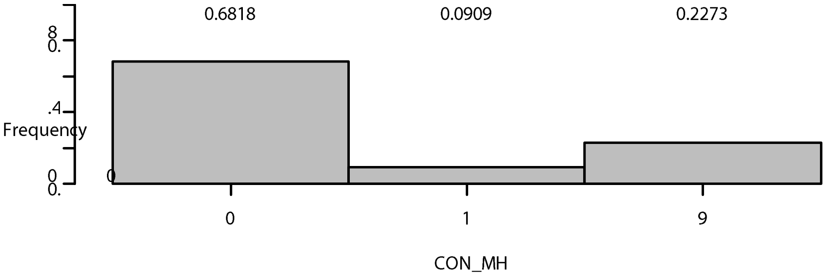

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

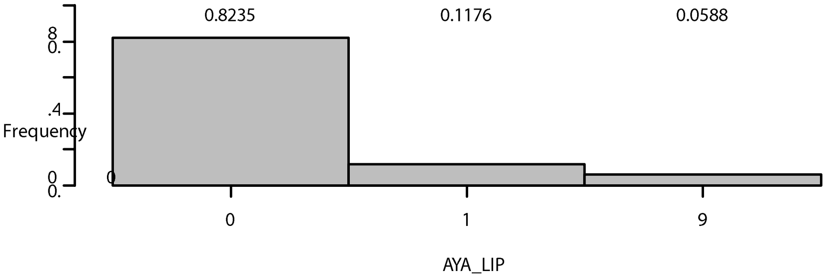

0.6667
0.3333
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

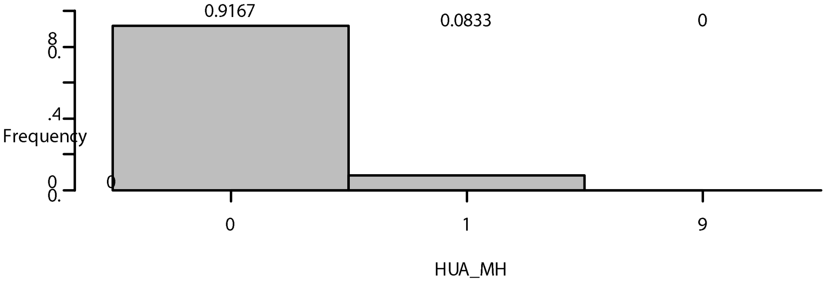

0.7903
0.1129
0.0968
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

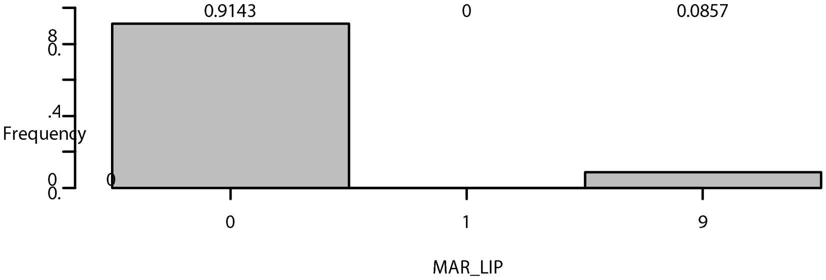

0.9455
0.0364
0.0182
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

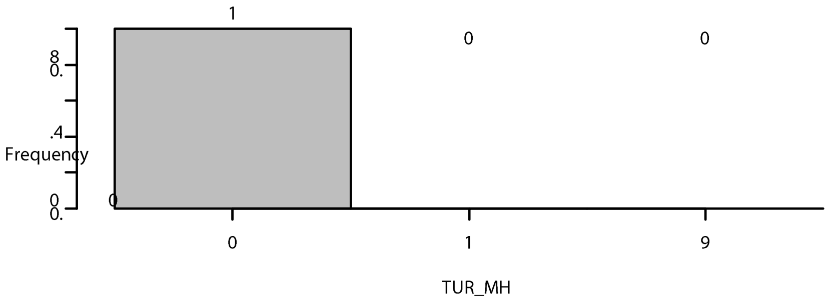
Trait 9 Coronal ossicle

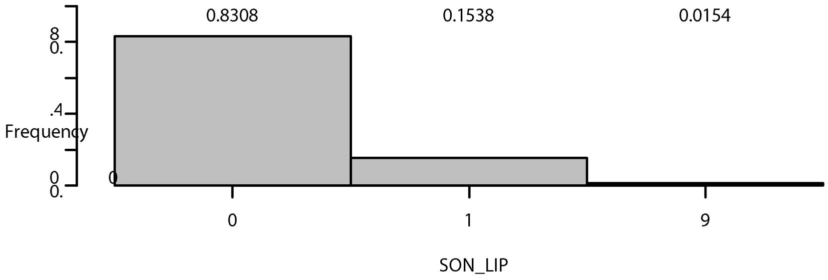


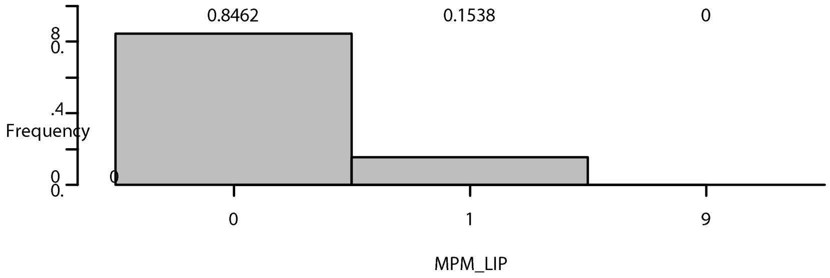


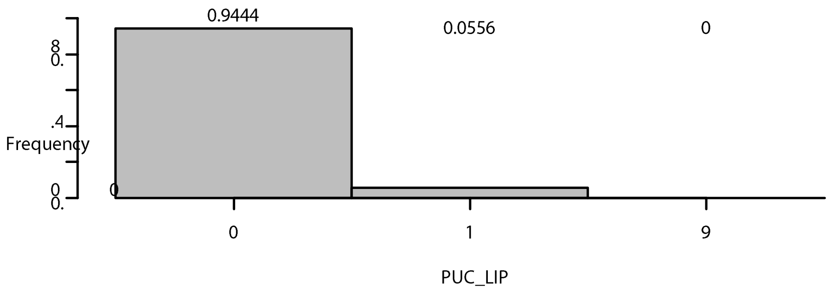


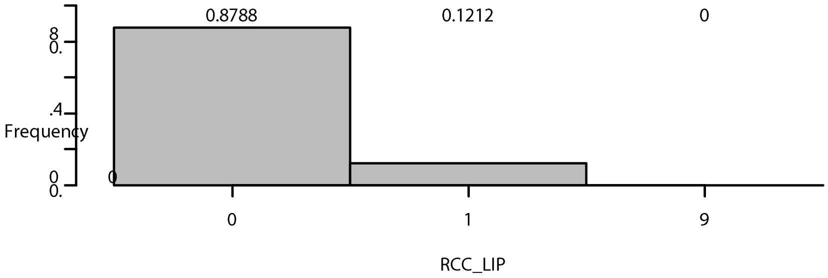


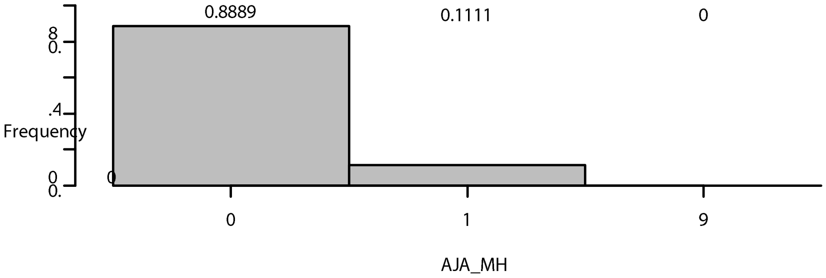

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

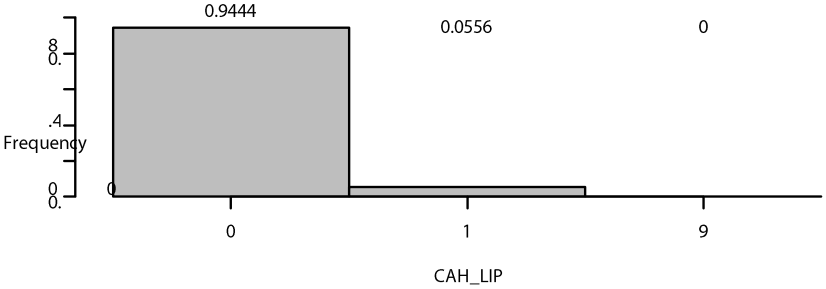

0.8308
0.1538
0.0154
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

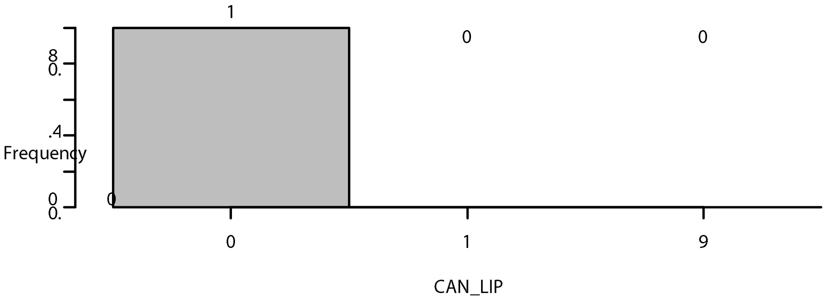

0.8462
0.1538
0
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

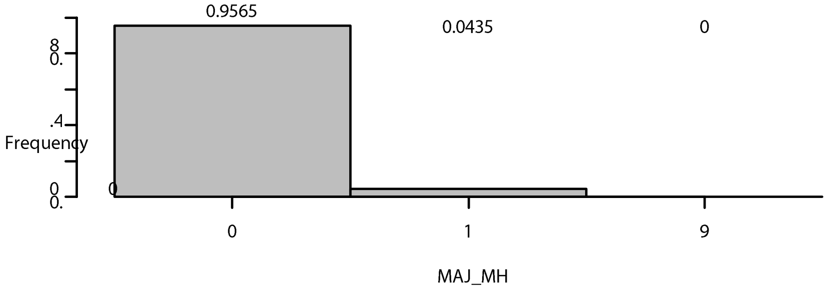

0.9444
0.0556
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

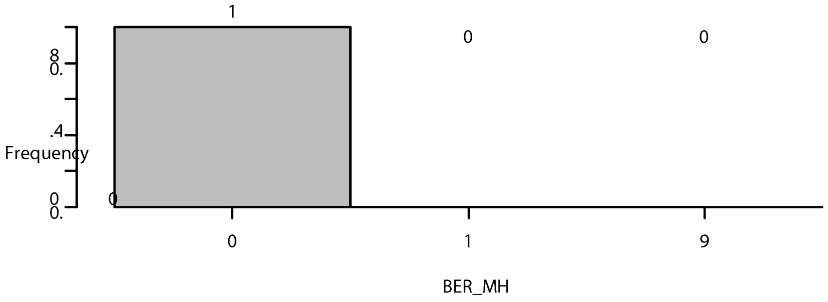

0.8788
0.1212
0
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

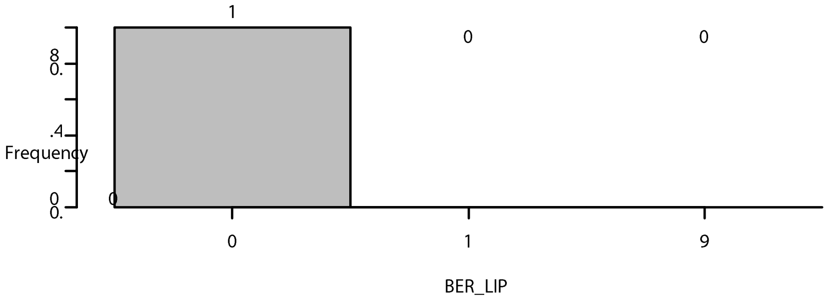

0.8889
0.1111
0
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

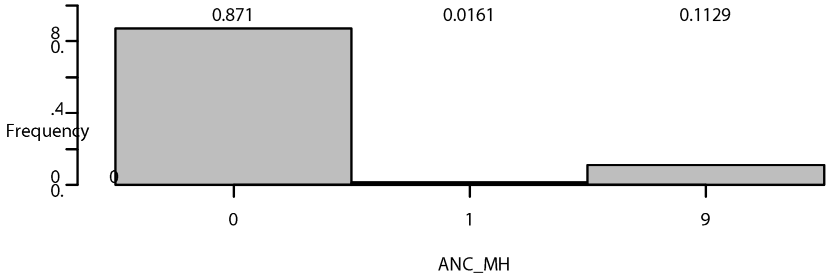

0.9444
0.0556
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

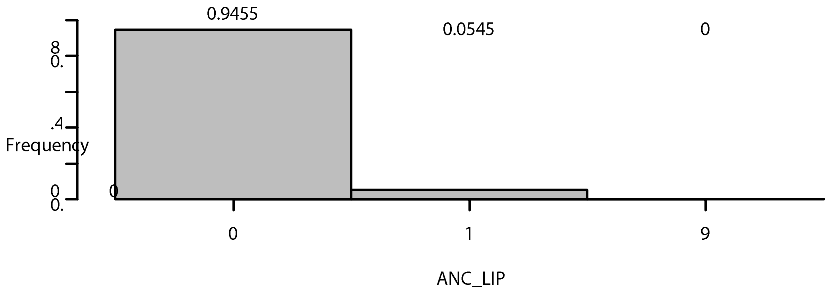

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.9565
0.0435
0
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

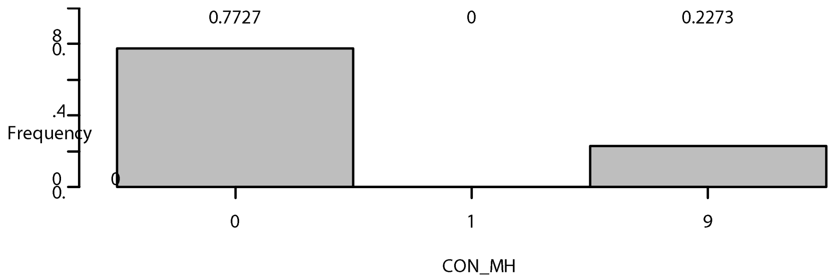

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

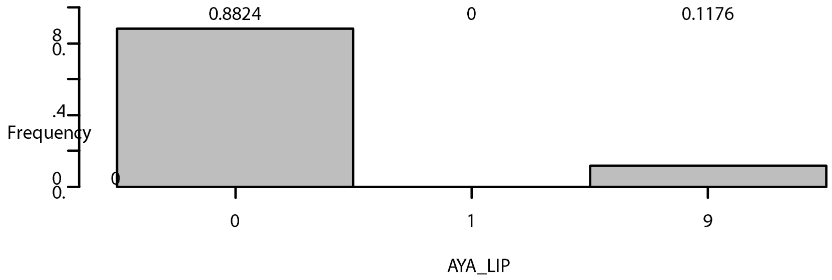

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

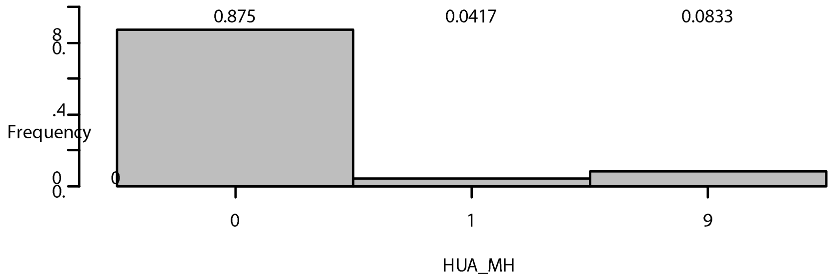

0.871
0.0161
0.1129
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

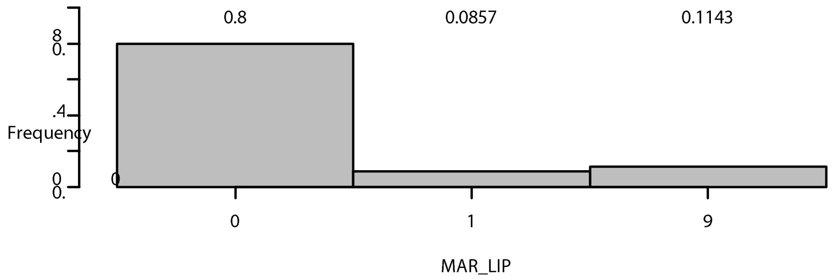

0.9455
0.0545
0
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

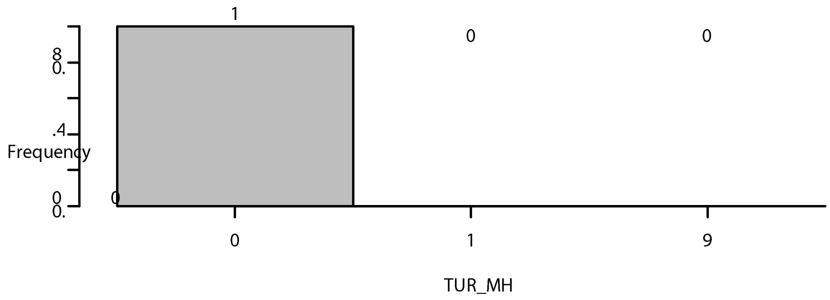
Trait 11 Sagittal ossicle

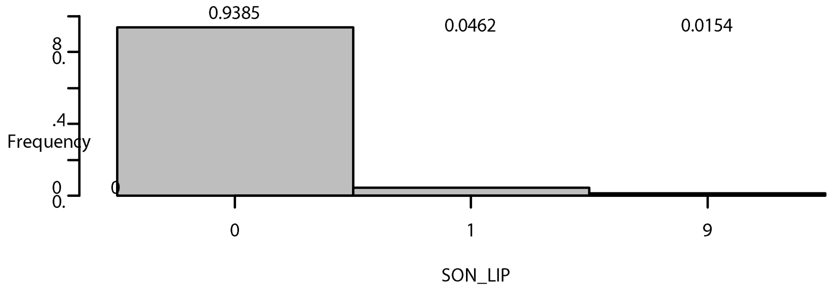


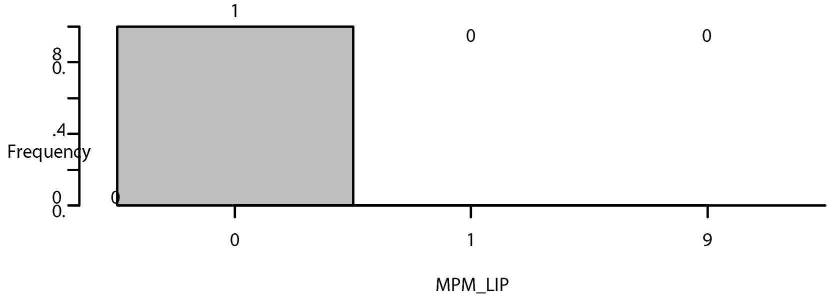


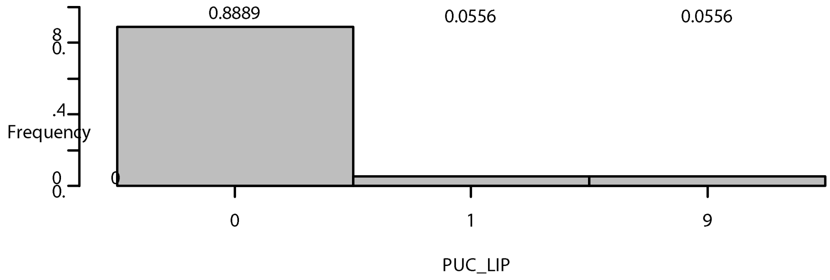


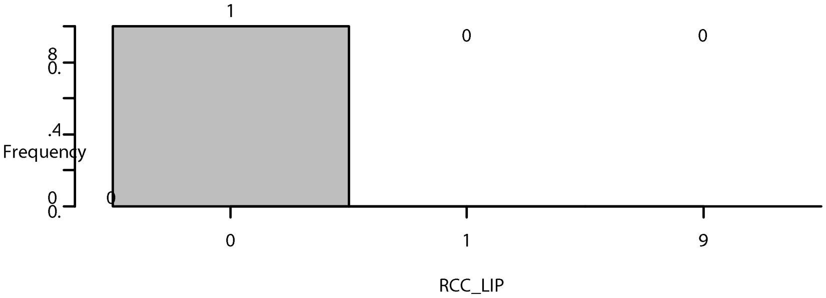


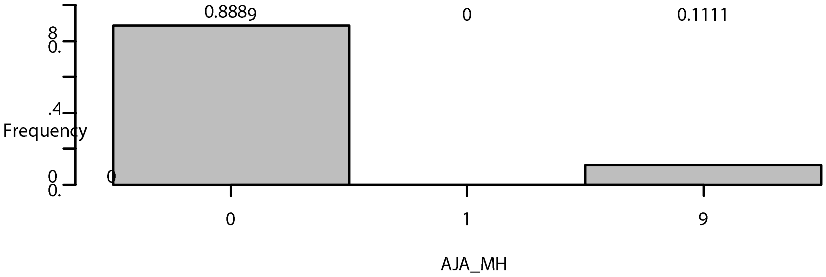

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

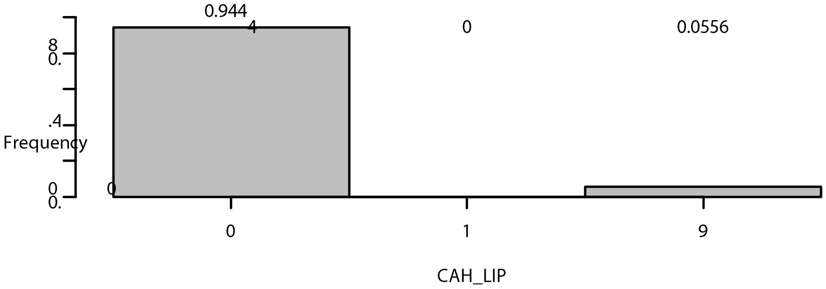

0.9385
0.0462
0.0154
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

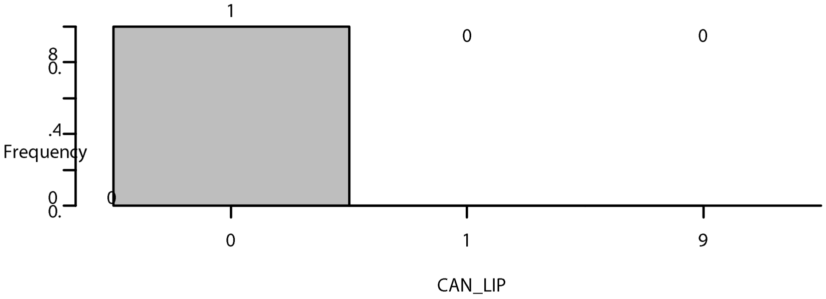

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

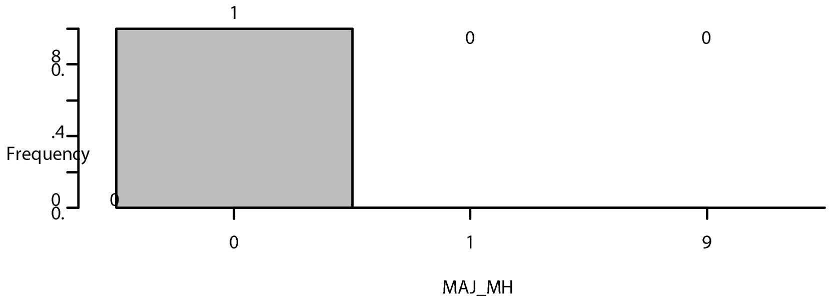

0.8889
0.0556
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

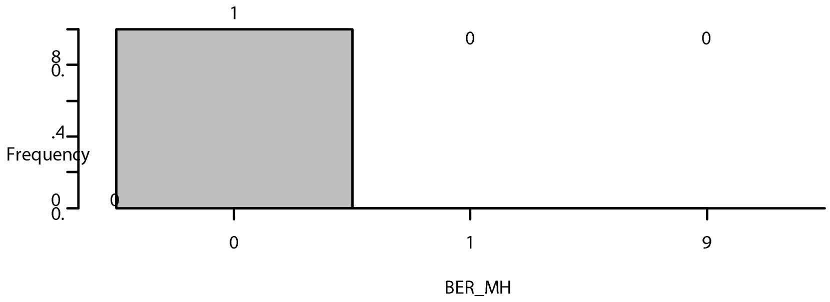

1
0
0
0.8
0.4
Frequency
0.0
0
0
1
9
RCC_LIP

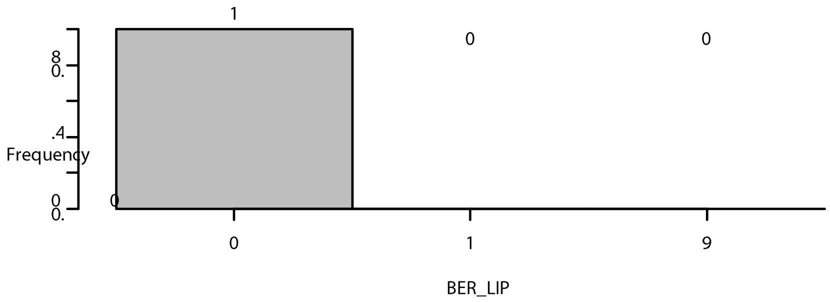

0.8889
0
0.1111
0.8
0.4
Frequency
0.0
0
0
1
9
AJA_MH

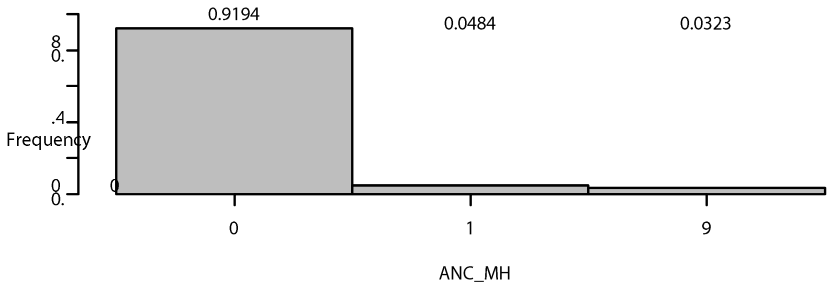

0.9444
0
0.0556
0.8
0.4
Frequency
0.0
0
0
1
9
CAH_LIP

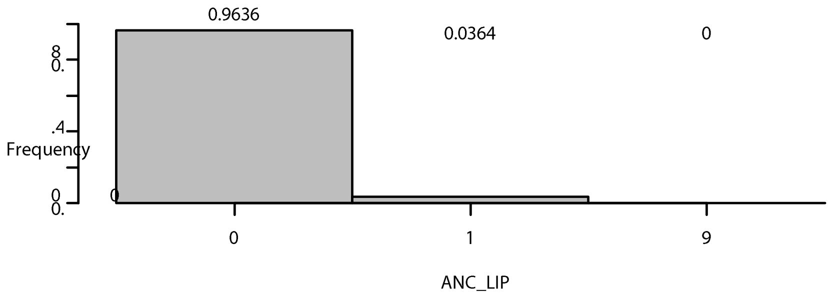

1
0
0
0.8
0.4
Frequency
0.0
0
0
1
9
CAN_LIP


1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

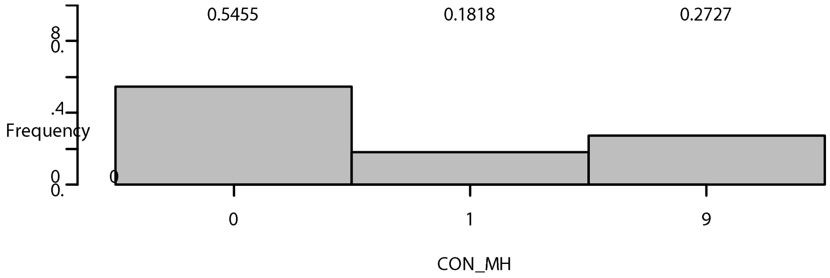

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

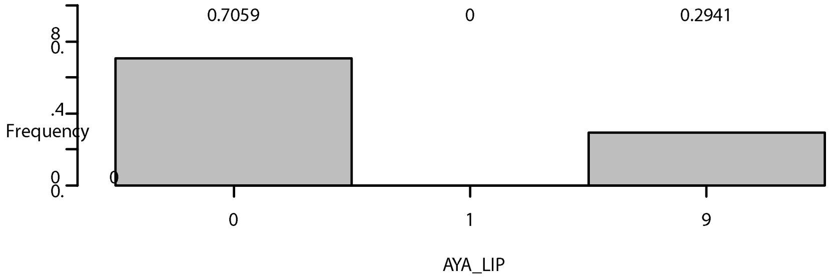

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

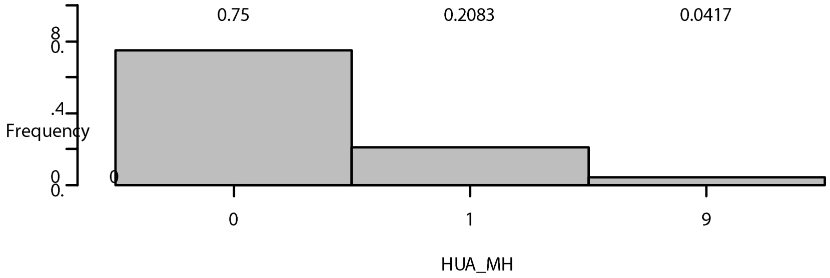

0.9194
0.0484
0.0323
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

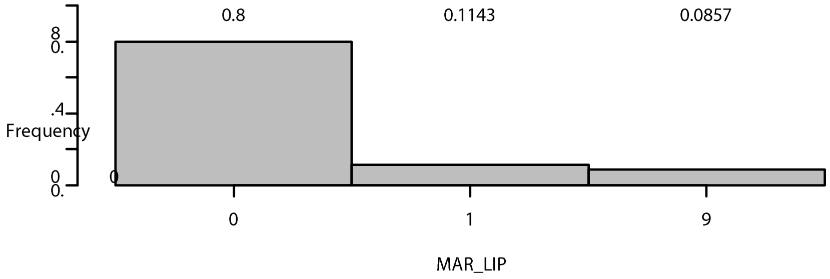

0.9636
0.0364
0
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

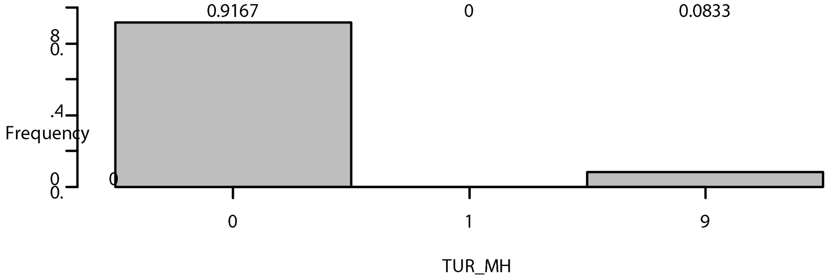
Trait 12 Apical bone

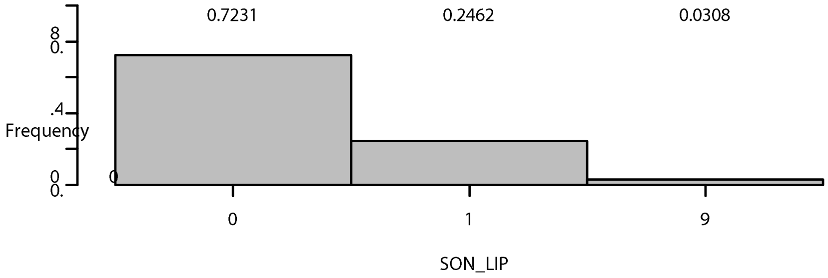


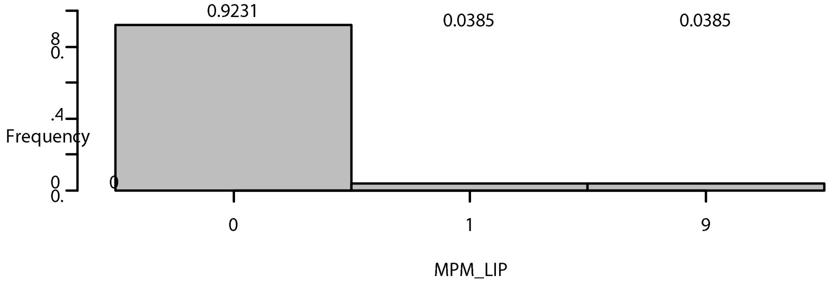


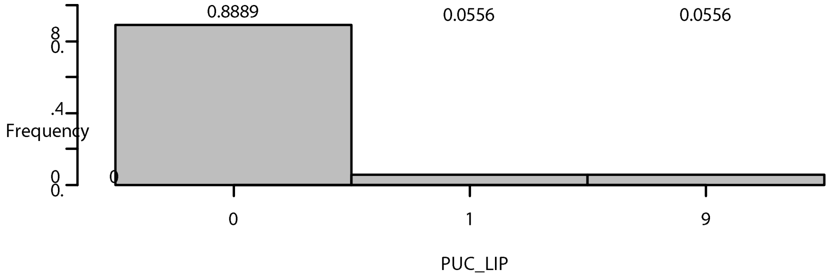


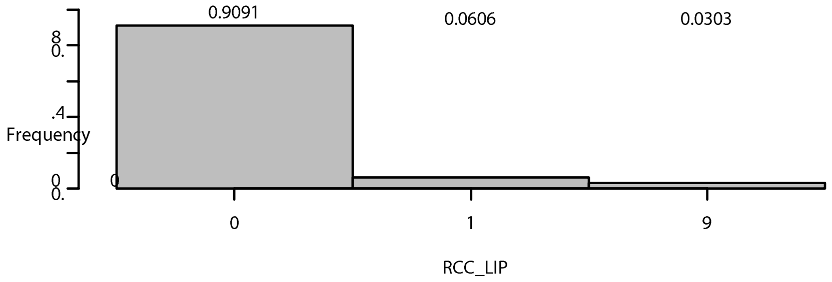


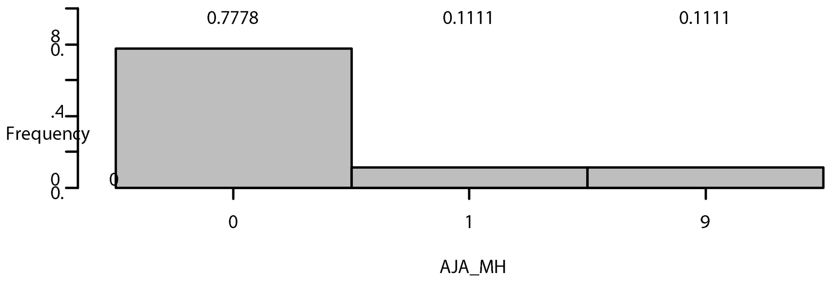

0.9167
0
0.0833
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

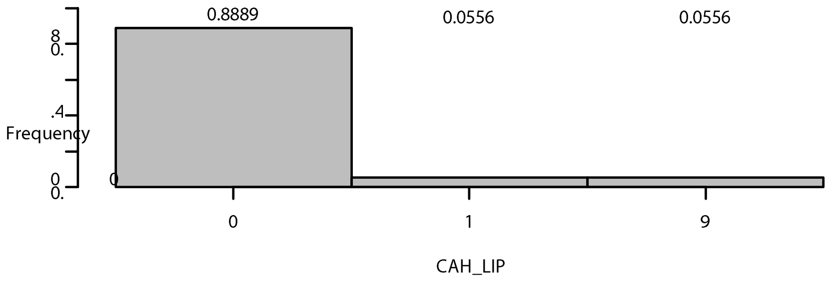

0.7231
0.2462
0.0308
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

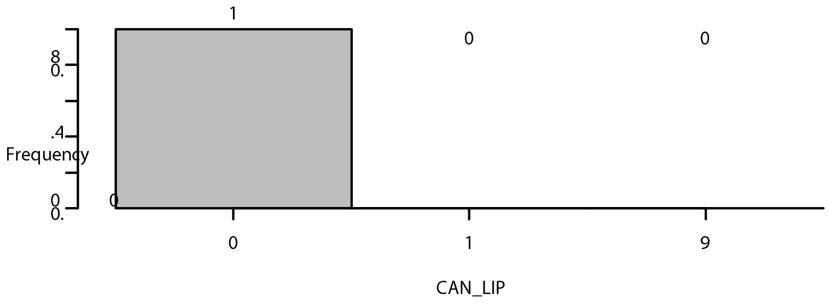

0.9231
0.0385
0.0385
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

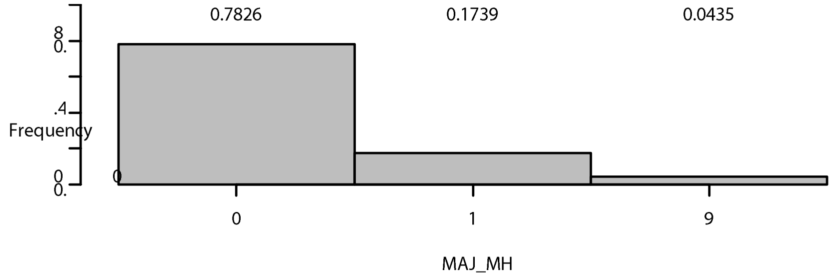

0.8889
0.0556
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

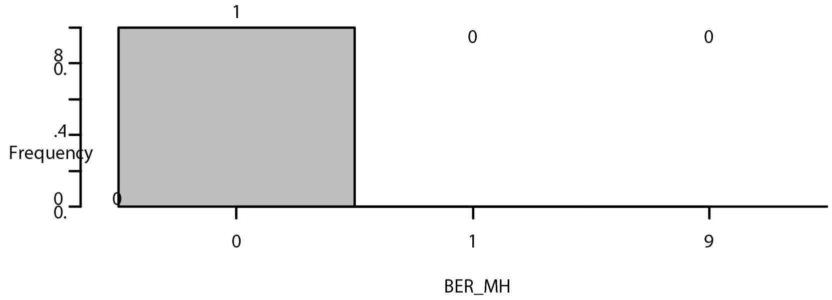

0.9091
0.0606
0.0303
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

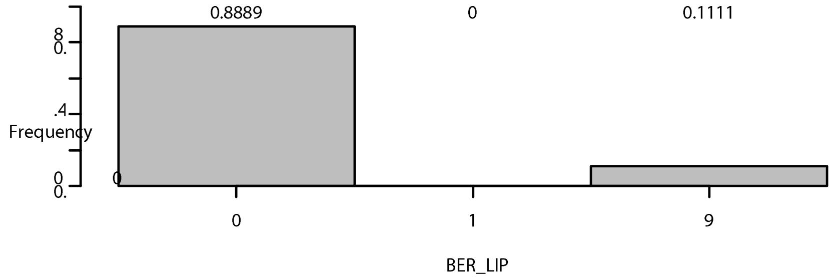

0.7778
0.1111
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

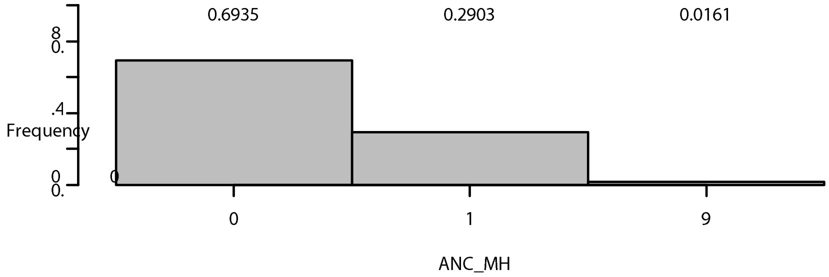

0.8889
0.0556
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

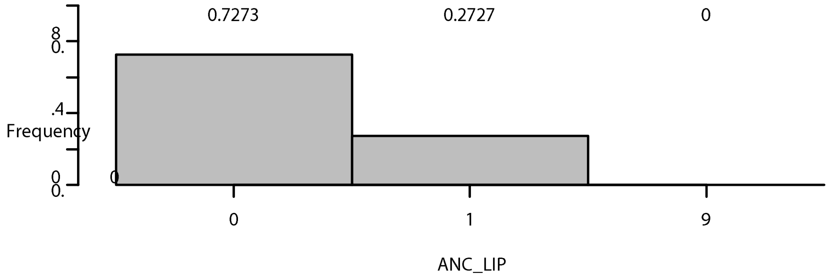

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.7826
0.1739
0.0435
0.8
.4
Frequency
0.0
0
0
1
9
MAJ_MH

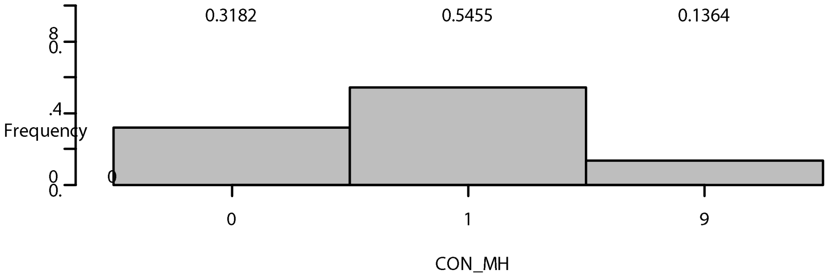

1
0
0
0.8
.4
Frequency
0.0
0
0
1
9
BER_MH

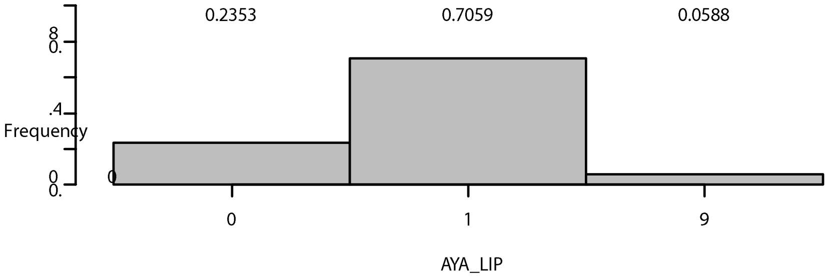

0.8889
0
0.1111
0.8
.4
Frequency
0.0
0
0
1
9
BER_LIP

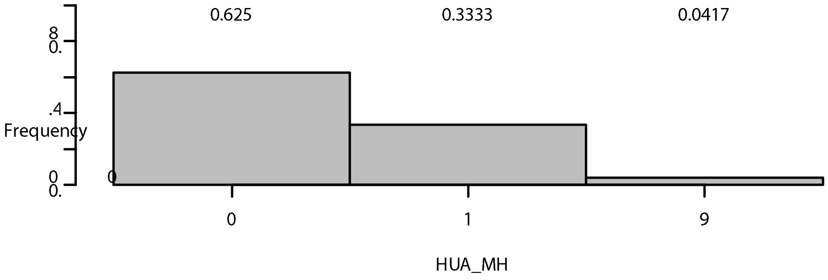

0.6935
0.2903
0.0161
0.8
.4
Frequency
0.0
0
0
1
9
ANC_MH

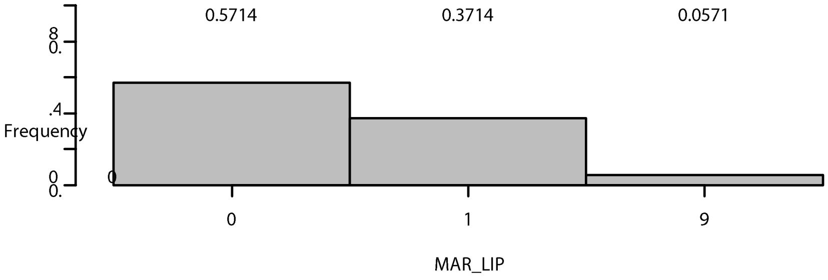

0.7273
0.2727
0
0.8
.4
Frequency
0.0
0
0
1
9
ANC_LIP

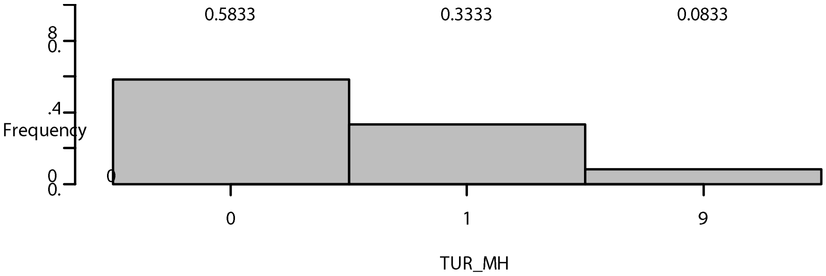
Trait 13 Lambdoid ossicle

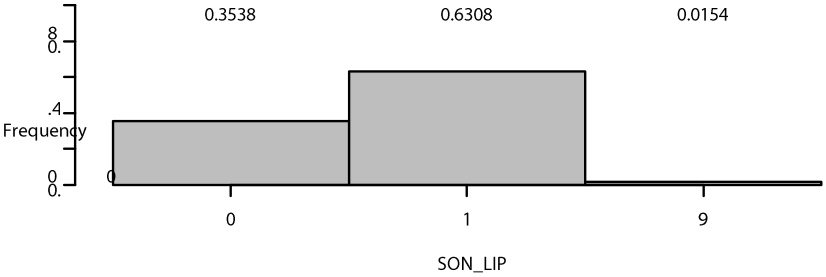


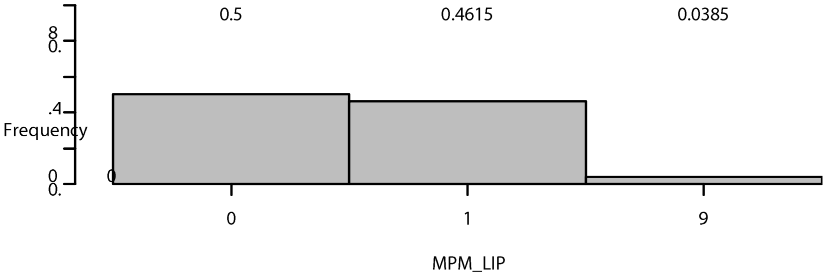


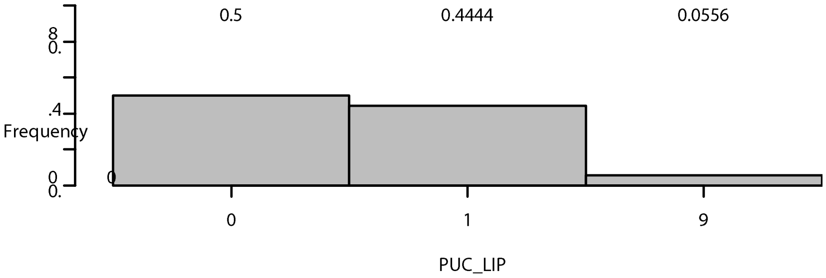


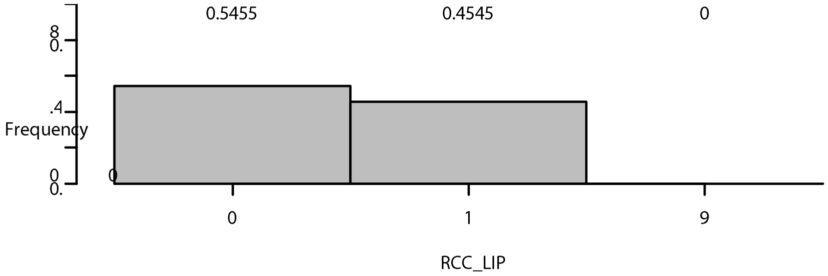


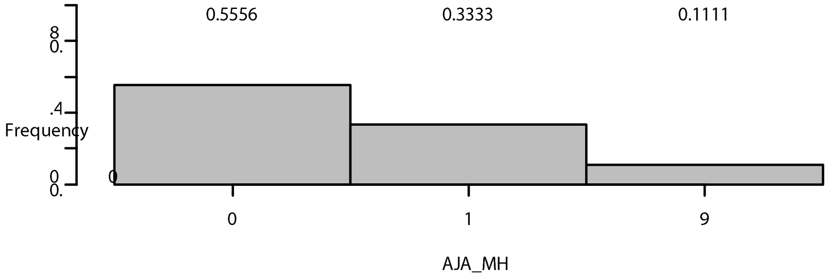

0.5833
0.3333
0.0833
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

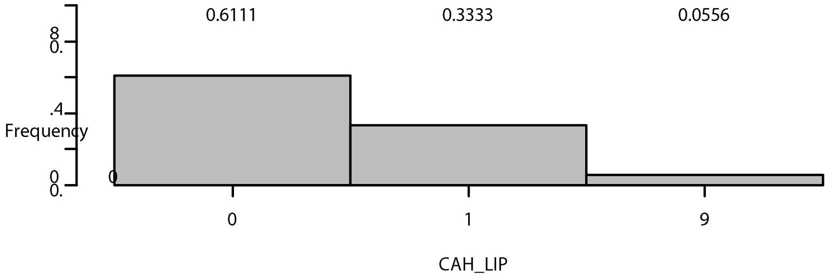

0.3538
0.6308
0.0154
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

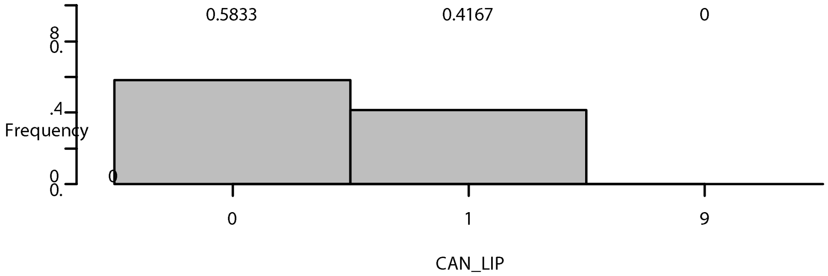

0.5
0.4615
0.0385
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

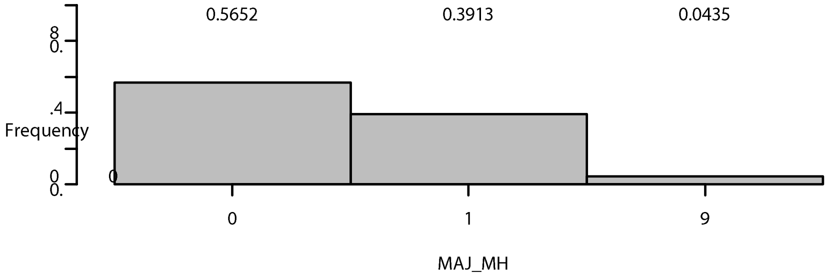

0.5
0.4444
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

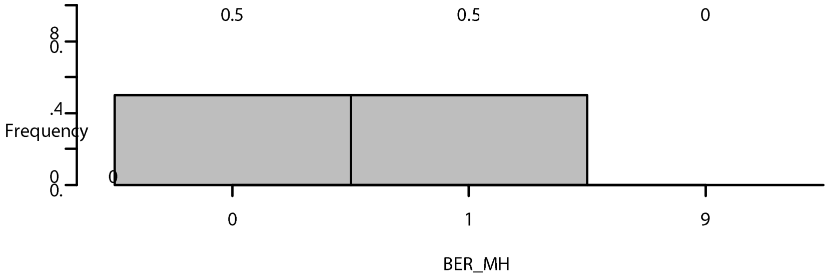

0.5455
0.4545
0
0.8
.4
Frequency
0.0
0
0
1
9
RCC_LIP

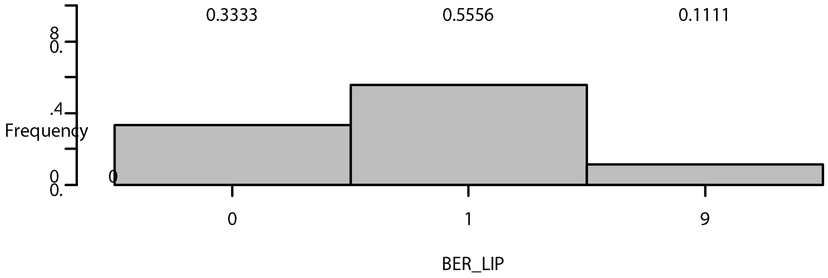

0.5556
0.3333
0.1111
0.8
.4
Frequency
0.0
0
0
1
9
AJA_MH

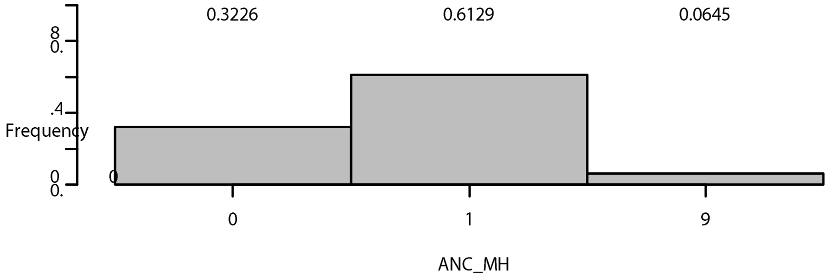

0.6111
0.3333
0.0556
0.8
.4
Frequency
0.0
0
0
1
9
CAH_LIP

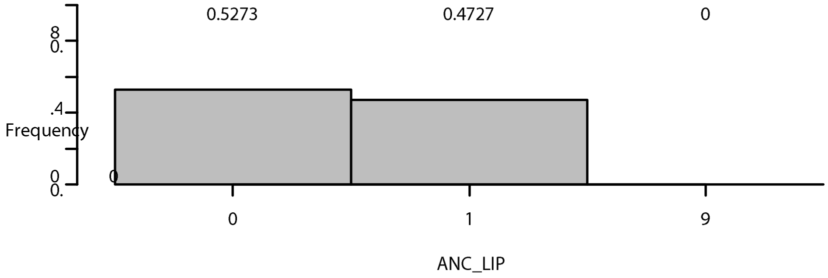

0.5833
0.4167
0
0.8
.4
Frequency
0.0
0
0
1
9
CAN_LIP


0.5652
0.3913
0.0435
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

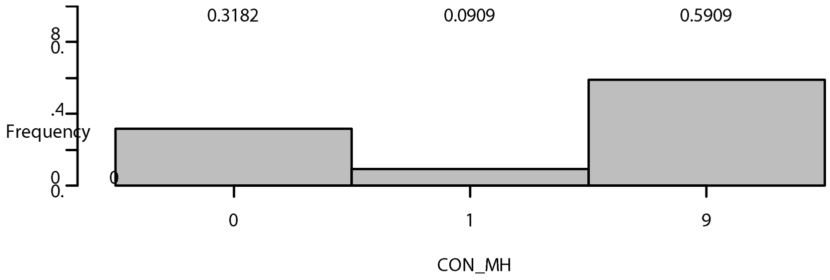

0.5
0.5
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

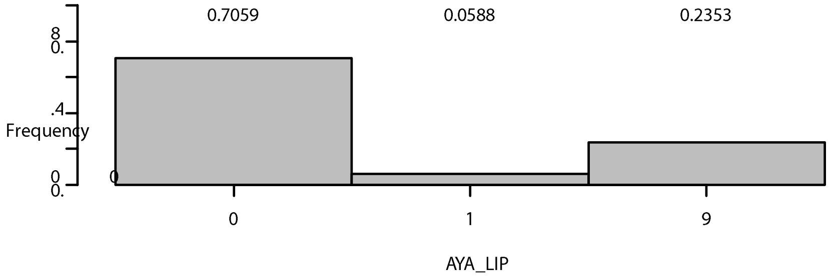

0.3333
0.5556
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

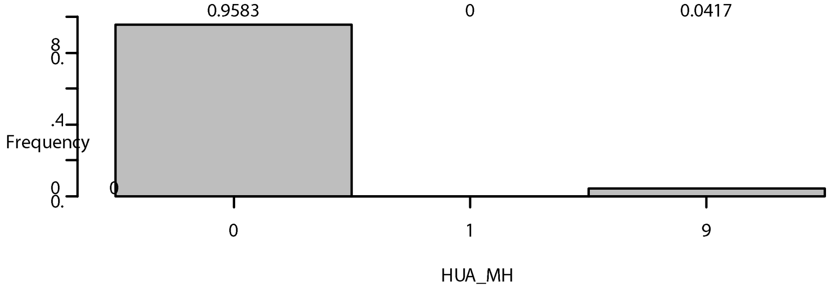

0.3226
0.6129
0.0645
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

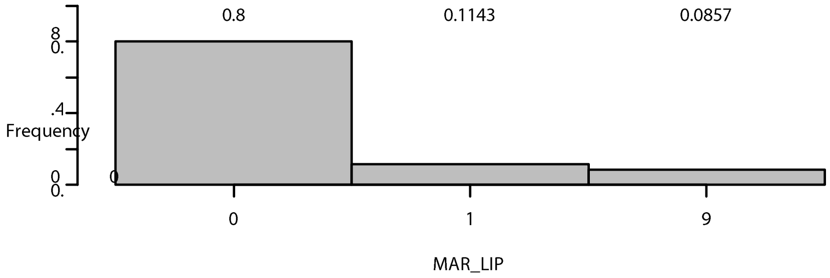

0.5273
0.4727
0
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

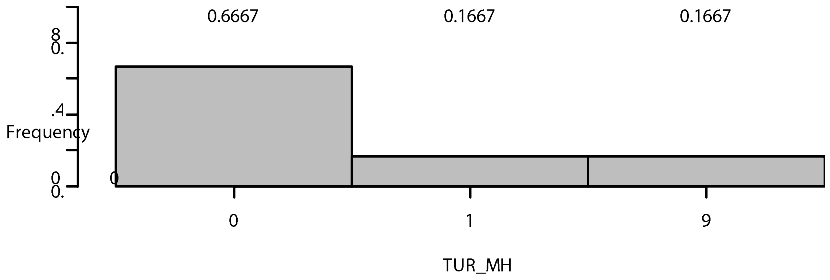
Trait 14 Asterionic bone

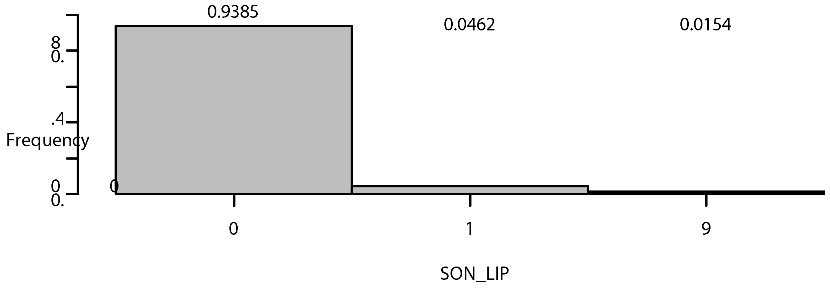


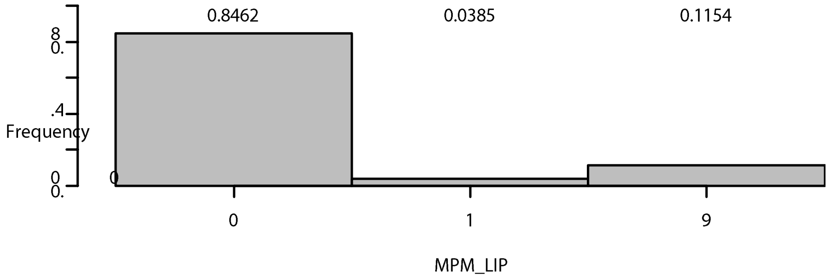


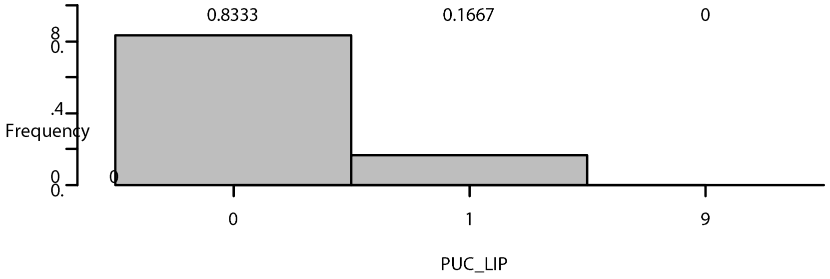


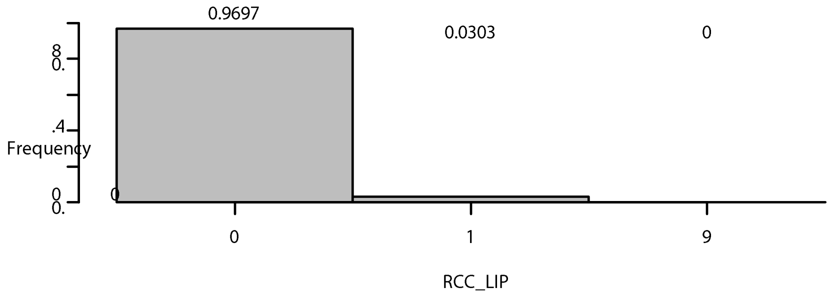


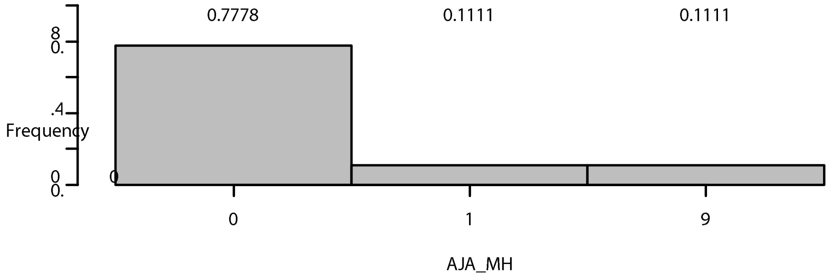

0.6667
0.1667
0.1667
0.8
.4
Frequency
0.0
0
0
1
9
TUR_MH

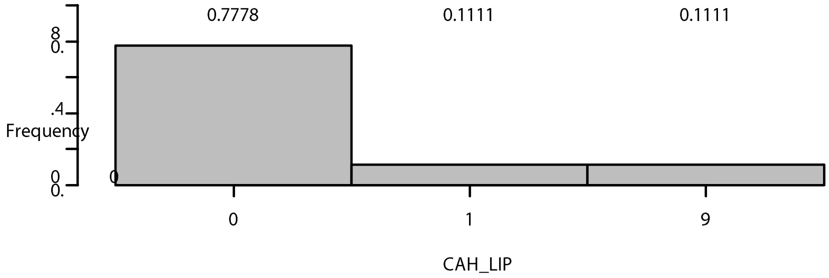

0.9385
0.0462
0.0154
0.8
.4
Frequency
0.0
0
0
1
9
SON_LIP

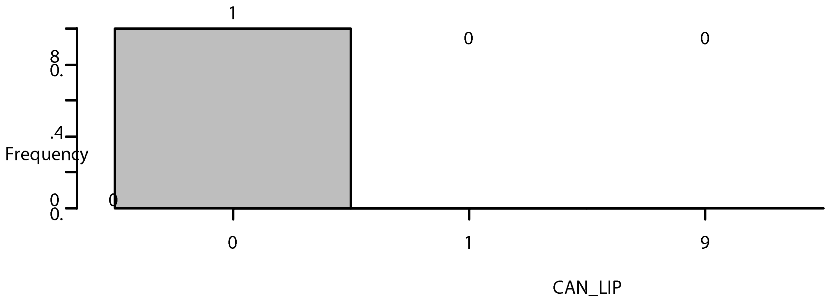

0.8462
0.0385
0.1154
0.8
.4
Frequency
0.0
0
0
1
9
MPM_LIP

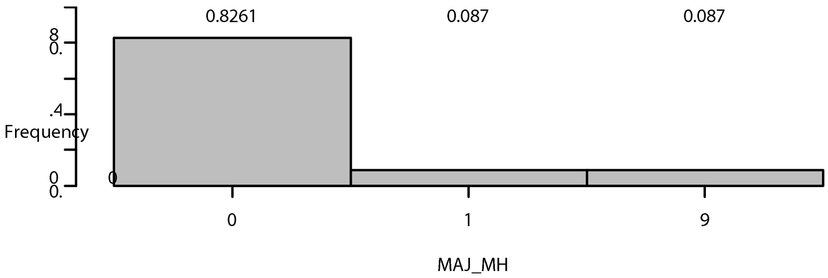

0.8333
0.1667
0
0.8
.4
Frequency
0.0
0
0
1
9
PUC_LIP

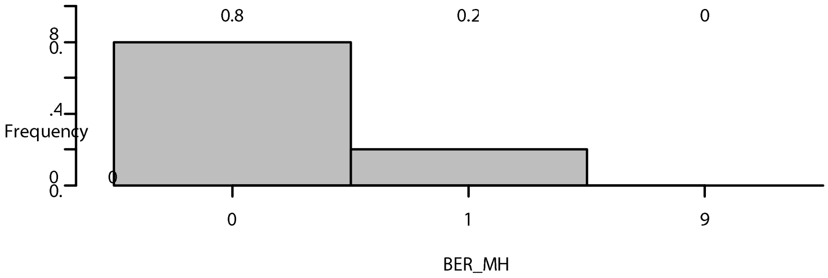

0.9697
0.0303
0
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

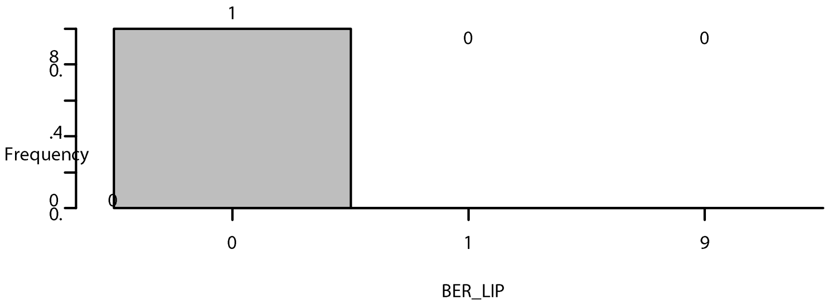

0.7778
0.1111
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

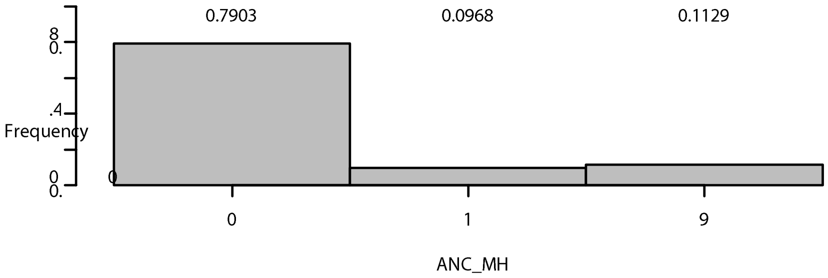

0.7778
0.1111
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

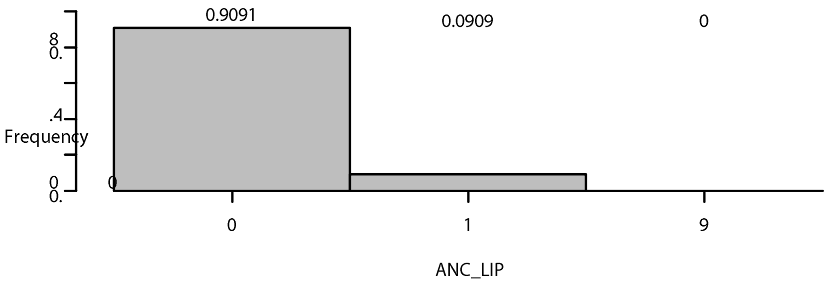

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.8261
0.087
0.087
0.8
0.4
Frequency
0.0
0
0
1
9
MAJ_MH

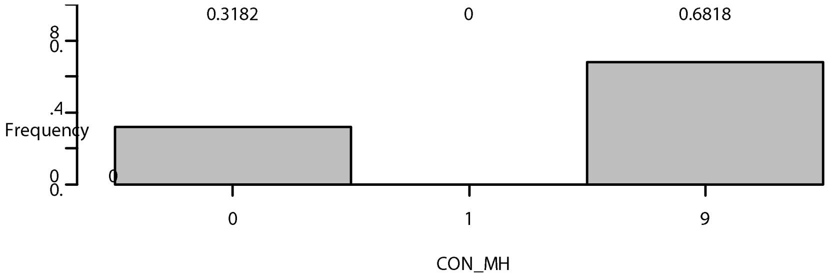

0.8
0.2
0
0.8
0.4
Frequency
0.0
0
0
1
9
BER_MH

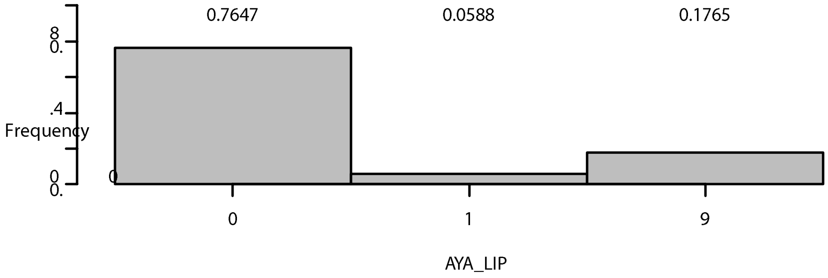

1
0
0
0.8
0.4
Frequency
0.0
0
0
1
9
BER_LIP

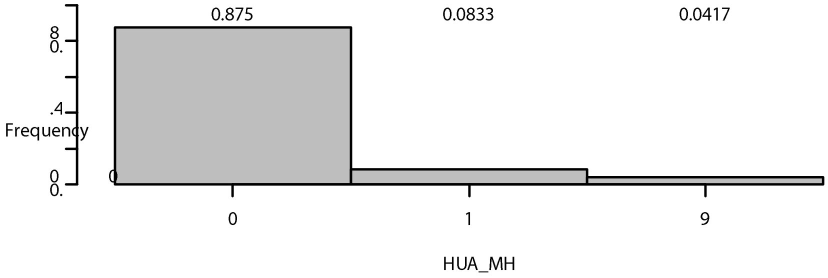

0.7903
0.0968
0.1129
0.8
0.4
Frequency
0.0
0
0
1
9
ANC_MH

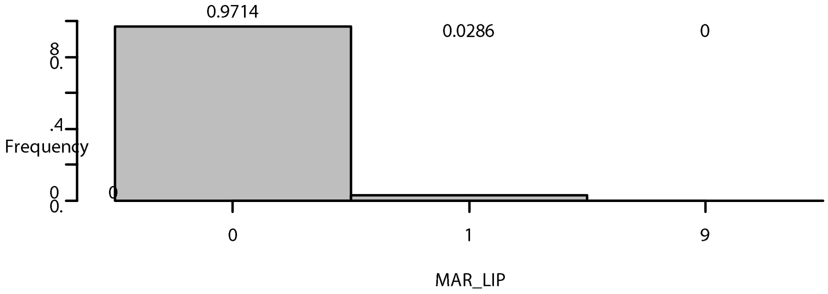

0.9091
0.0909
0
0.8
0.4
Frequency
0.0
0
0
1
9
ANC_LIP

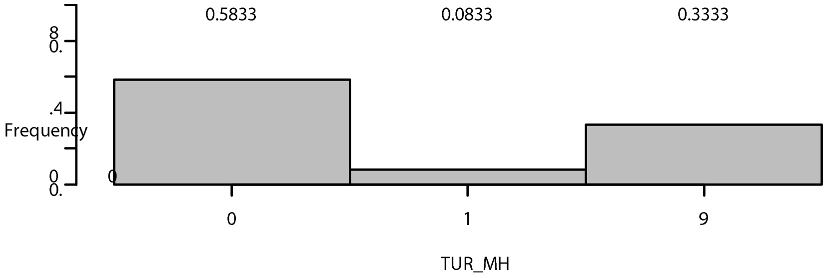
Trait 15 Ossicle in occipito-mastoid suture

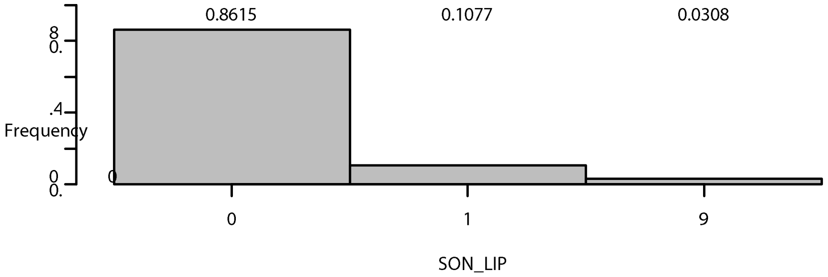


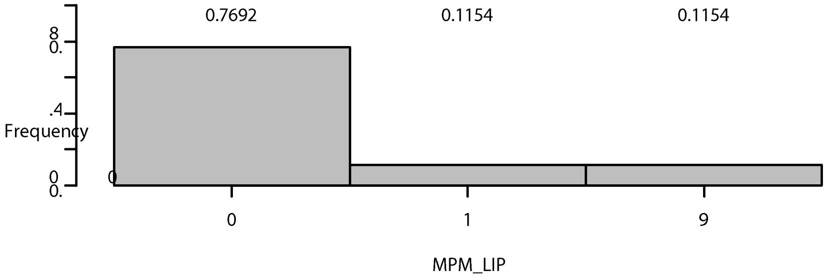


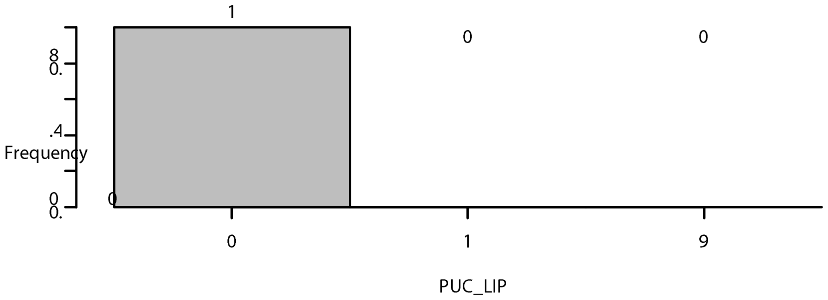


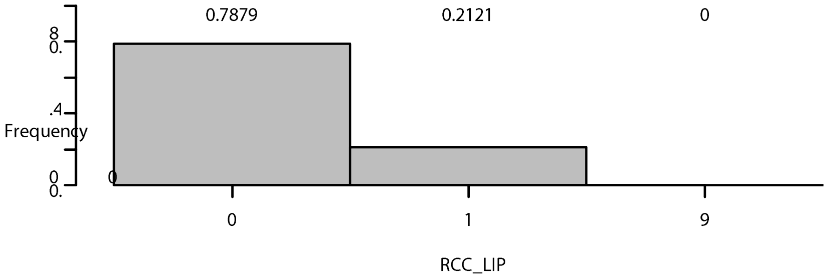


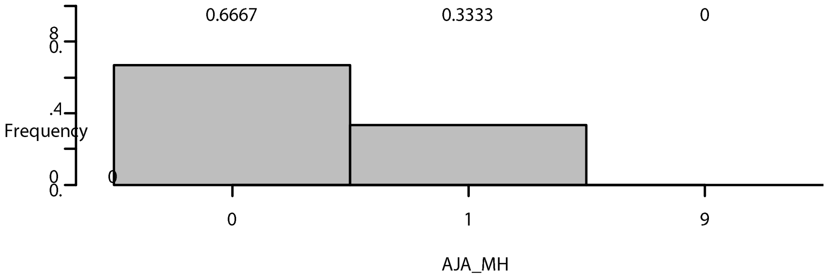

0.5833
0.0833
0.3333
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

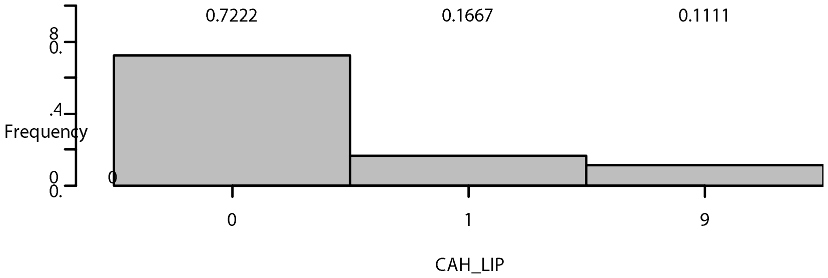

0.8615
0.1077
0.0308
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

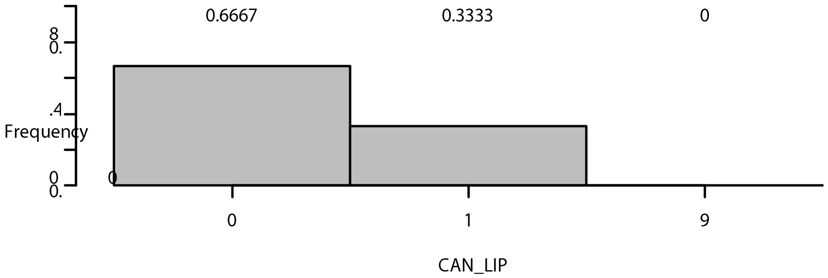

0.7692
0.1154
0.1154
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

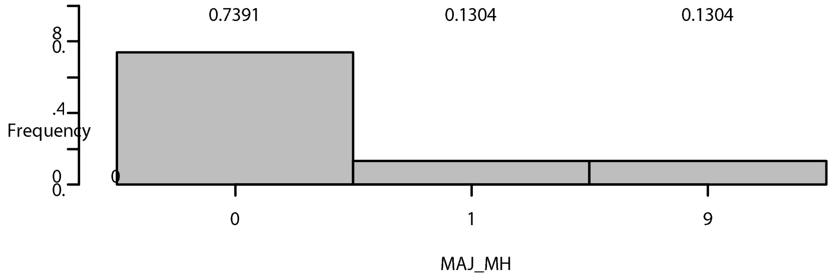

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

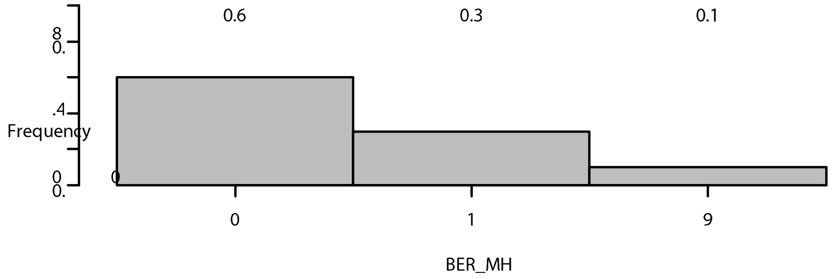

0.7879
0.2121
0
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

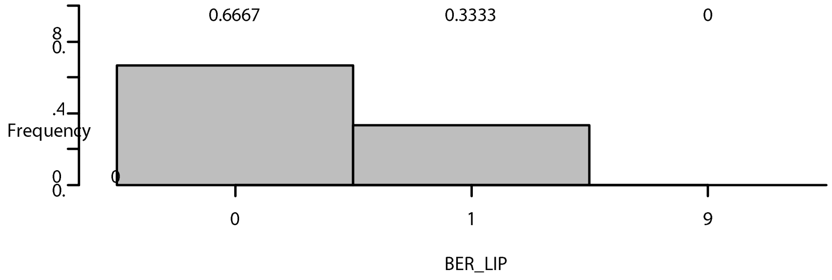

0.6667
0.3333
0
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

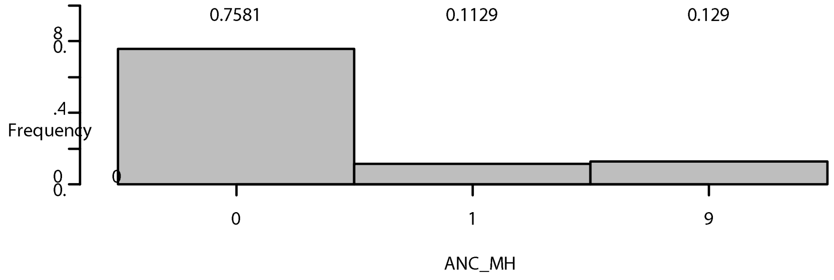

0.7222
0.1667
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

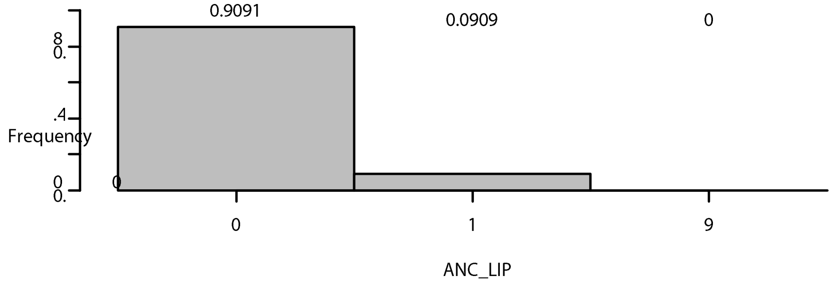

0.6667
0.3333
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.7391
0.1304
0.1304
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

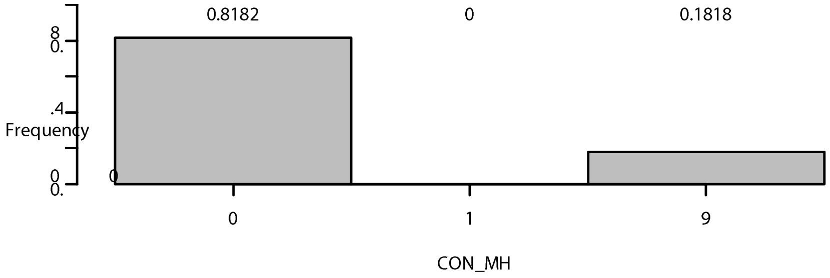

0.6
0.3
0.1
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

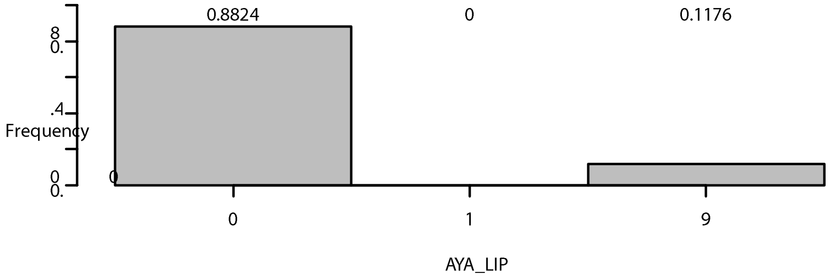

0.6667
0.3333
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

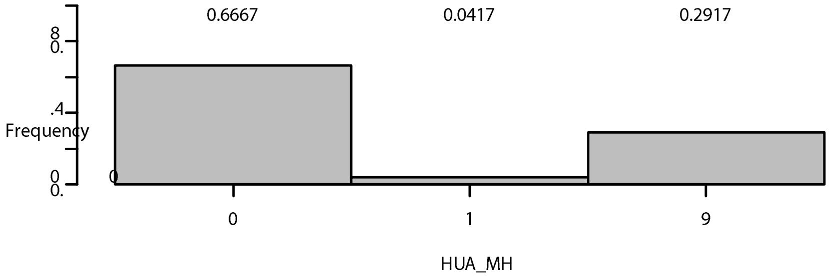

0.7581
0.1129
0.129
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

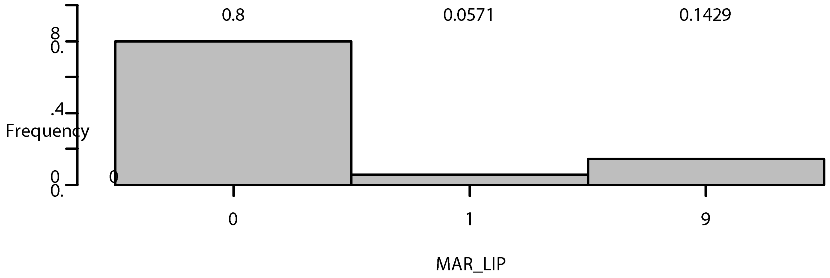

0.9091
0.0909
0
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

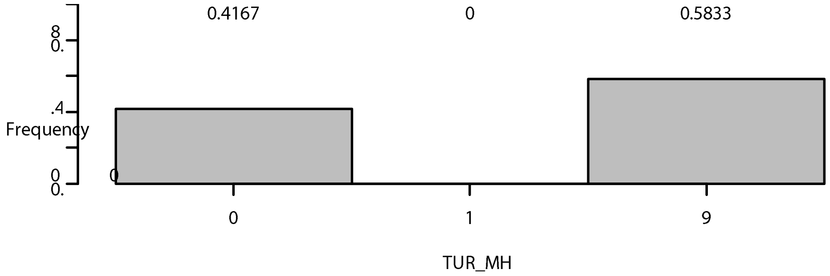
Trait 18 Os japonicum

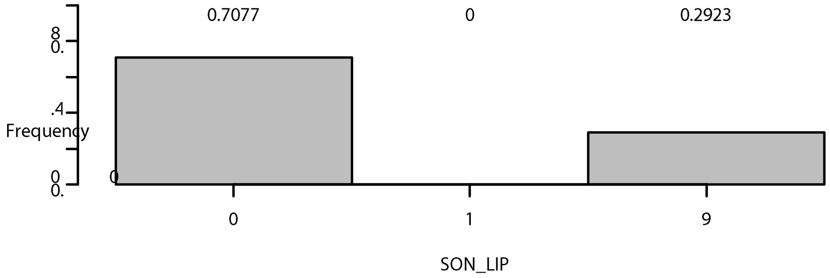


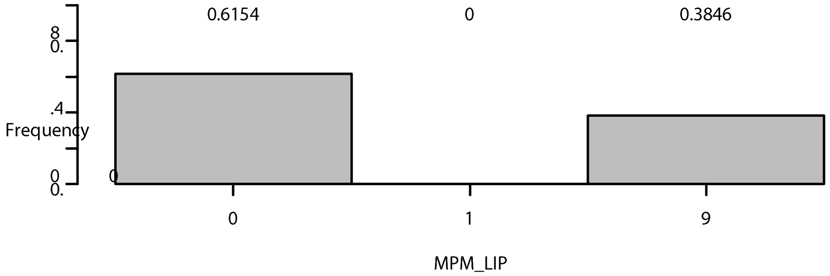


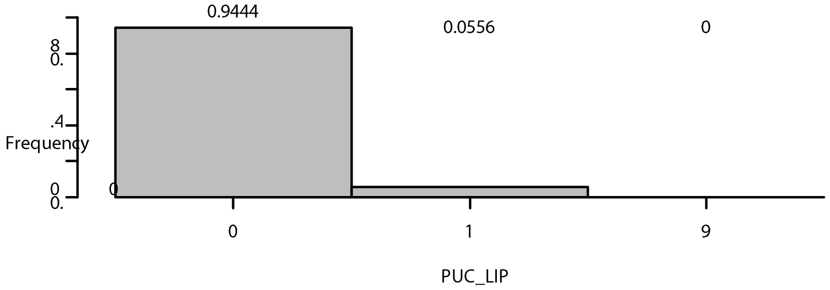


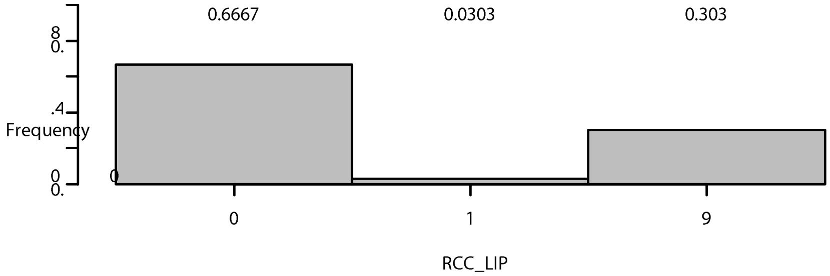


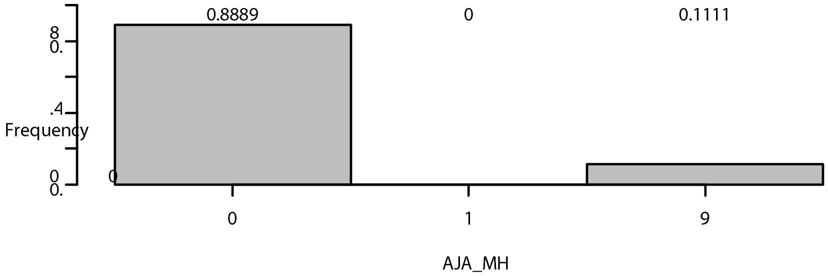

0.4167
0
0.5833
0.8
.4
Frequency
0.0
0
0
1
9
TUR_MH

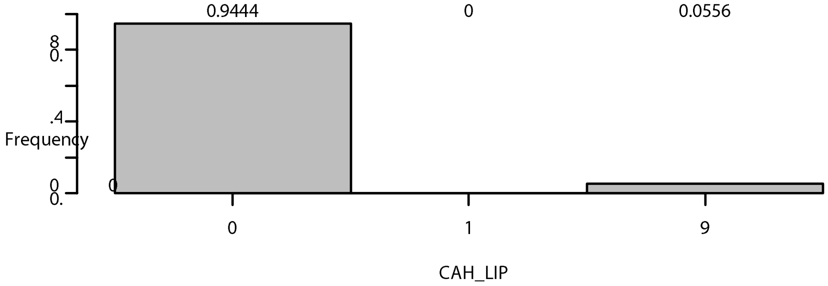

0.7077
0
0.2923
0.8
.4
Frequency
0.0
0
0
1
9
SON_LIP

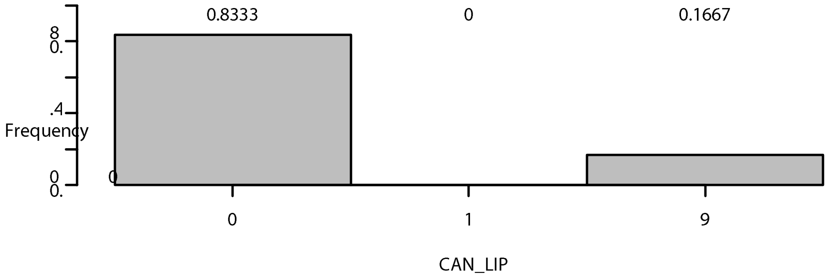

0.6154
0
0.3846
0.8
.4
Frequency
0.0
0
0
1
9
MPM_LIP

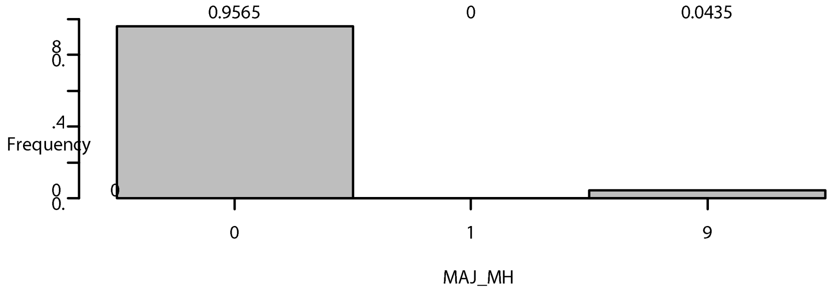

0.9444
0.0556
0
0.8
.4
Frequency
0.0
0
0
1
9
PUC_LIP

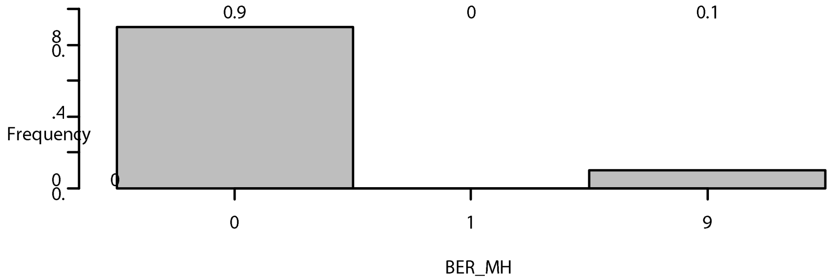

0.6667
0.0303
0.303
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

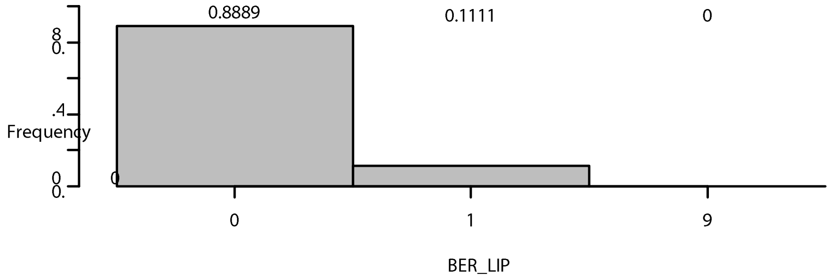

0.8889
0
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

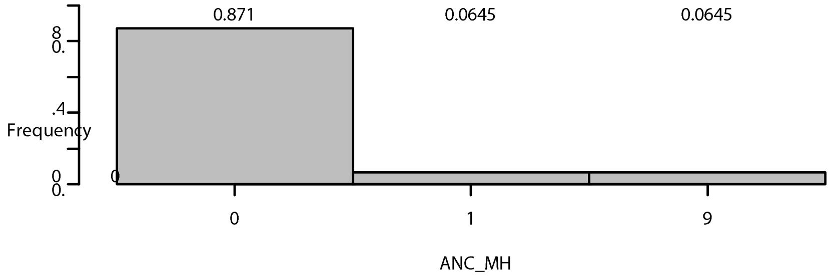

0.9444
0
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

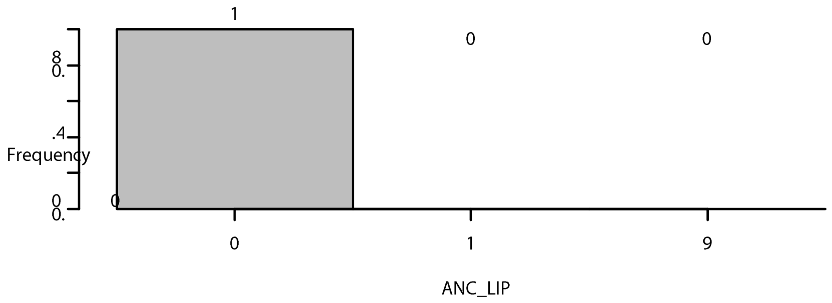

0.8333
0
0.1667
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.9565
0
0.0435
0.8
0.4
Frequency
0.0
0
0
1
9
MAJ_MH

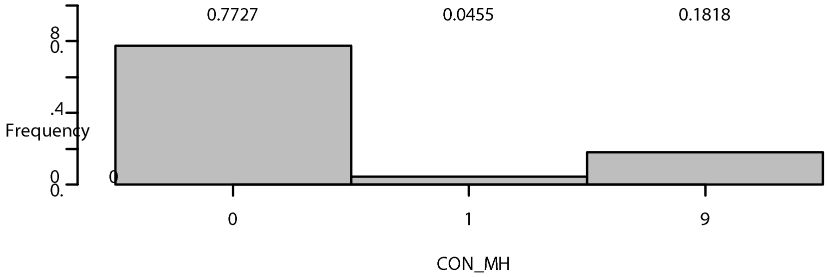

0.9
0
0.1
0.8
0.4
Frequency
0.0
0
0
1
9
BER_MH

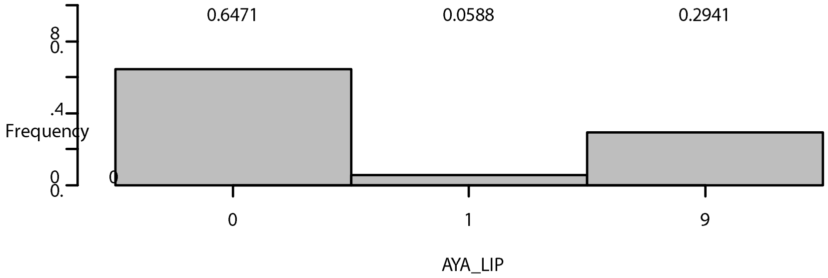

0.8889
0.1111
0
0.8
0.4
Frequency
0.0
0
0
1
9
BER_LIP

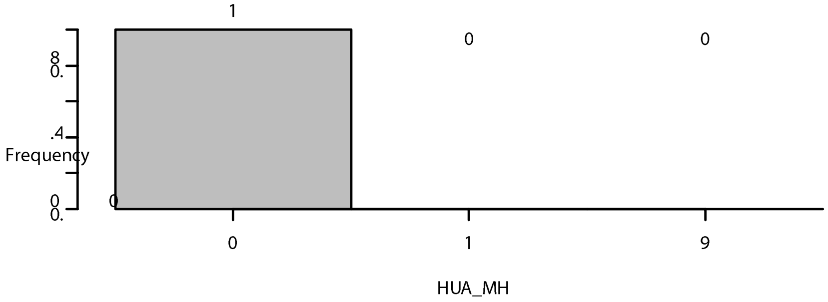

0.871
0.0645
0.0645
0.8
0.4
Frequency
0.0
0
0
1
9
ANC_MH

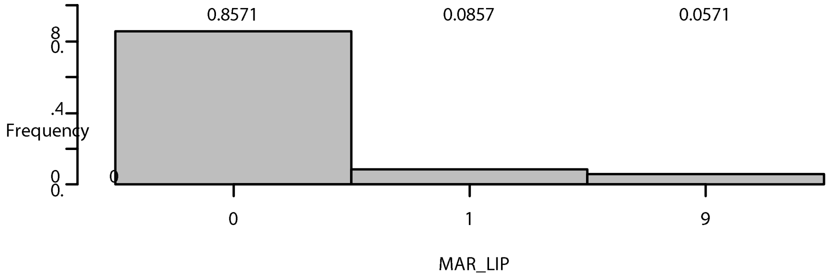

1
0
0
0.8
0.4
Frequency
0.0
0
0
1
9
ANC_LIP

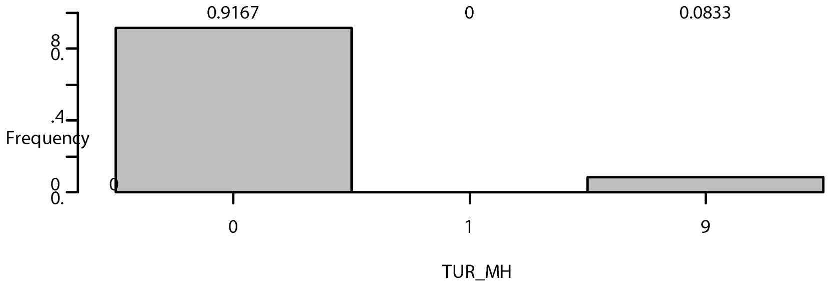
Trait 19 Inca bone

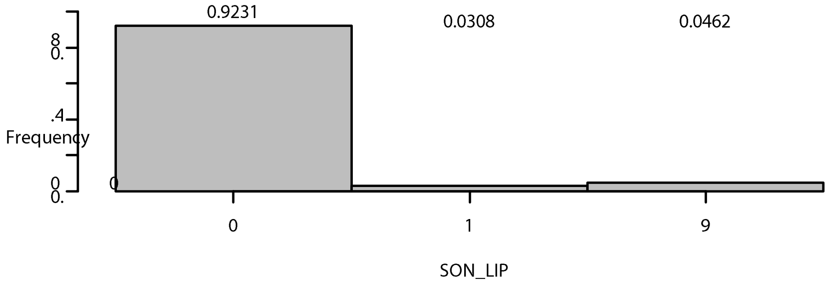


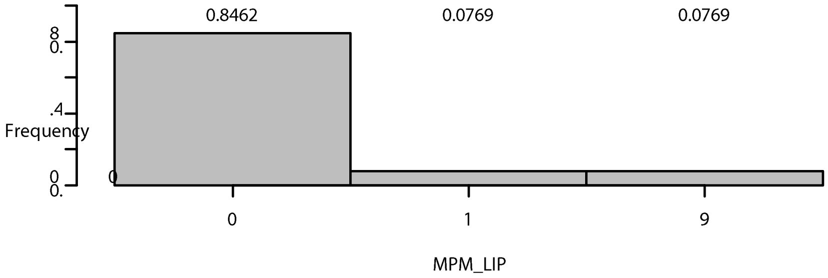


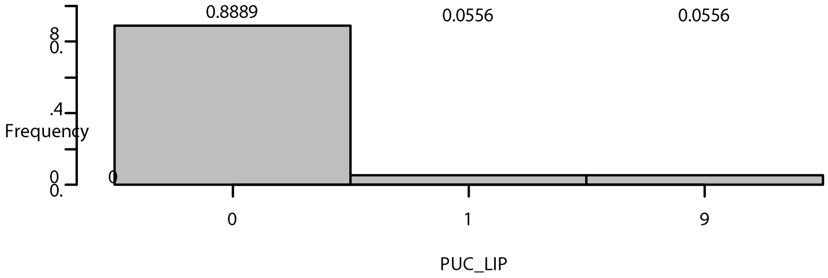


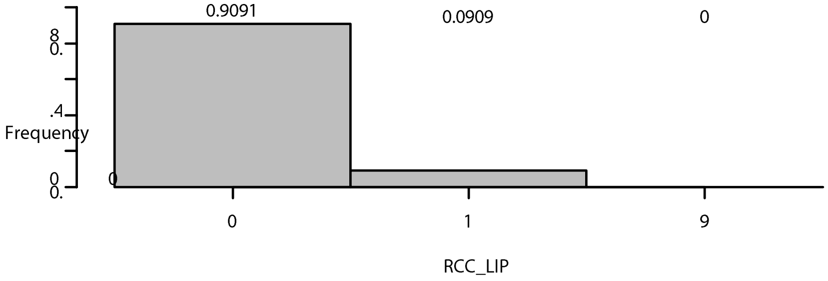


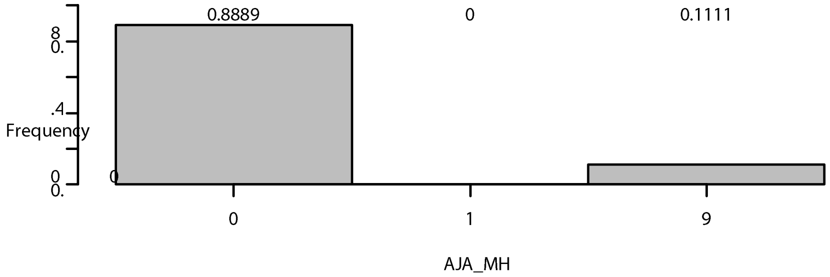

0.9167
0
0.0833
0.8
0.4
0.0
Frequency
0
1
9
TUR_MH

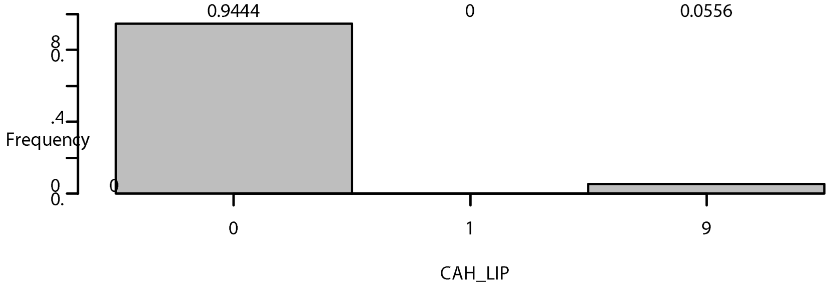

0.9231
0.0308
0.0462
0.8
0.4
0.0
Frequency
0
1
9
SON_LIP

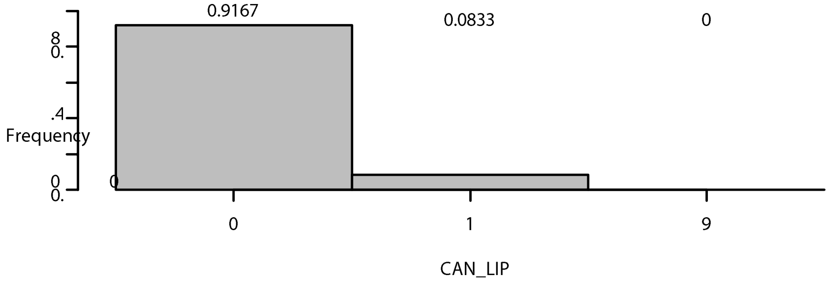

0.8462
0.0769
0.0769
0.8
0.4
0.0
Frequency
0
1
9
MPM_LIP

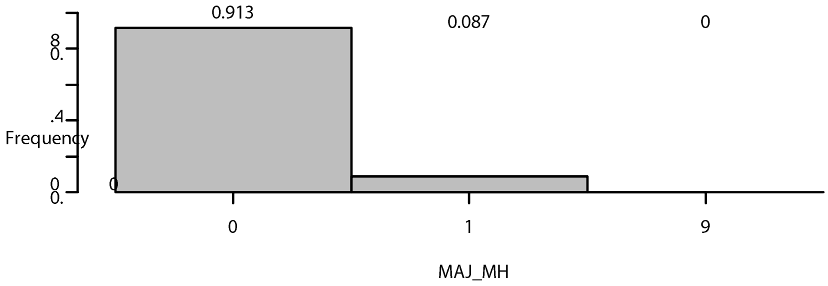

0.8889
0.0556
0.0556
0.8
0.4
0.0
Frequency
0
1
9
PUC_LIP

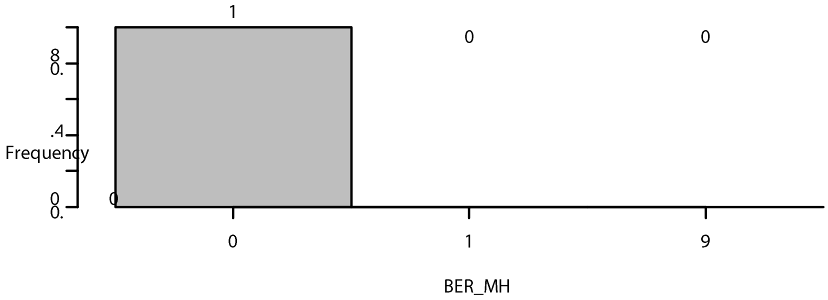

0.9091
0.0909
0
0.8
0.4
Frequency
0.0
0
1
9
RCC_LIP

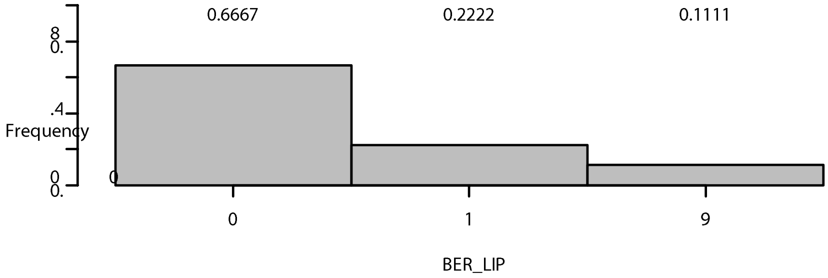

0.8889
0
0.1111
0.8
0.4
Frequency
0.0
0
1
9
AJA_MH

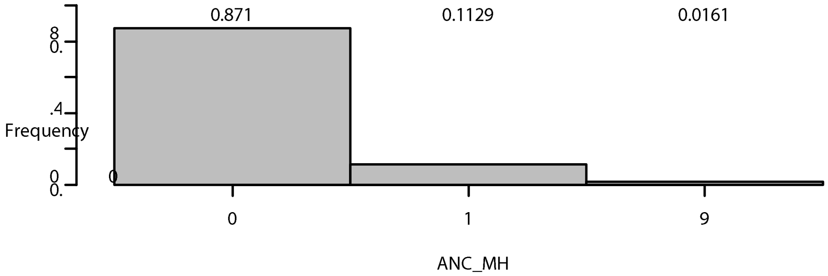

0.9444
0
0.0556
0.8
0.4
Frequency
0.0
0
1
9
CAH_LIP

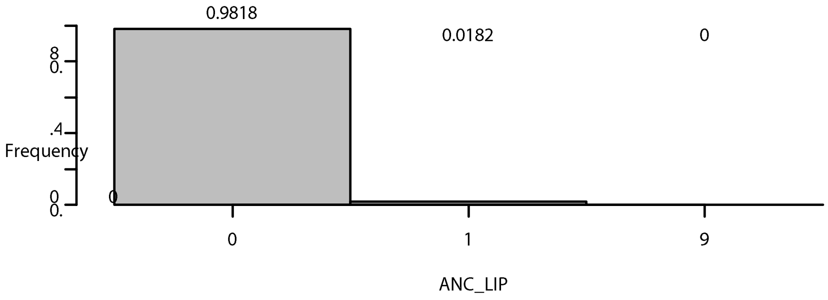

0.9167
0.0833
0
0.8
0.4
Frequency
0.0
0
1
9
CAN_LIP


0.913
0.087
0
Frequency
0
1
9
MAJ_MH

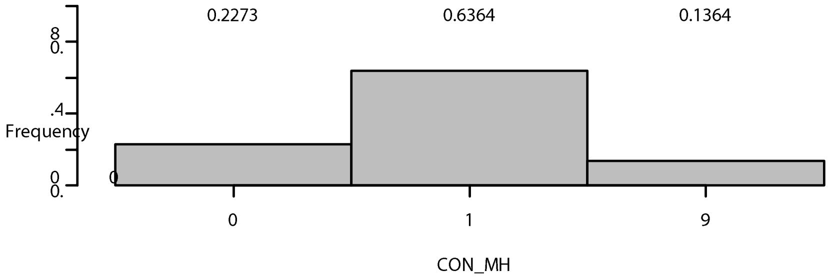

1
0
0
Frequency
0
1
9
BER_MH

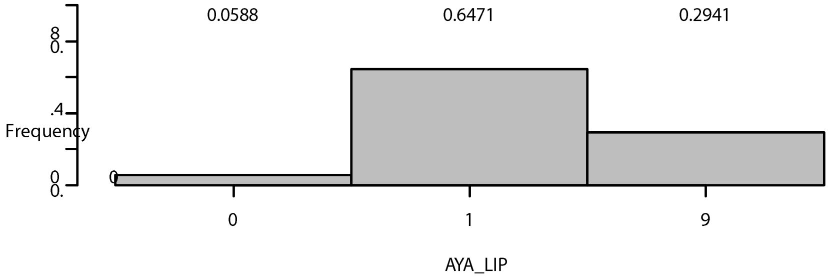

0.6667
0.2222
0.1111
Frequency
0
1
9
BER_LIP

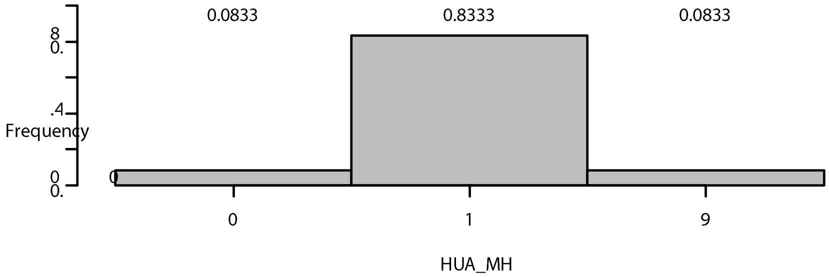

0.871
0.1129
0.0161
Frequency
0
1
9
ANC_MH

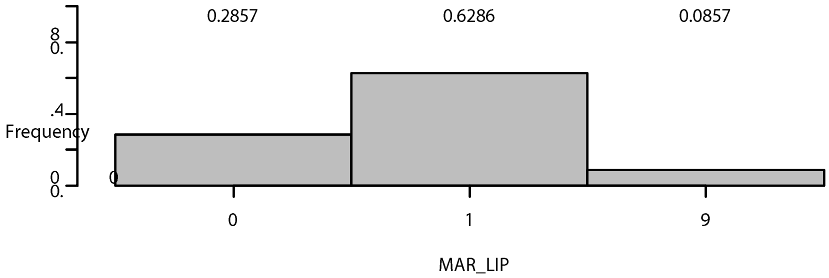

0.9818
0.0182
0
Frequency
0
1
9
ANC_LIP

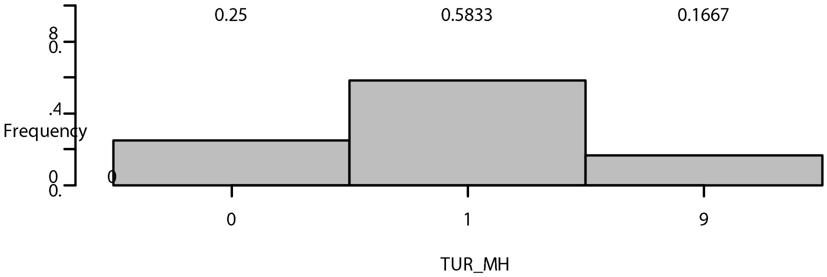
Trait 20 Condylar canal patent

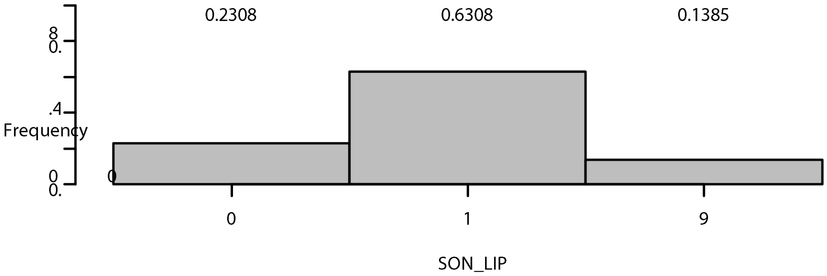


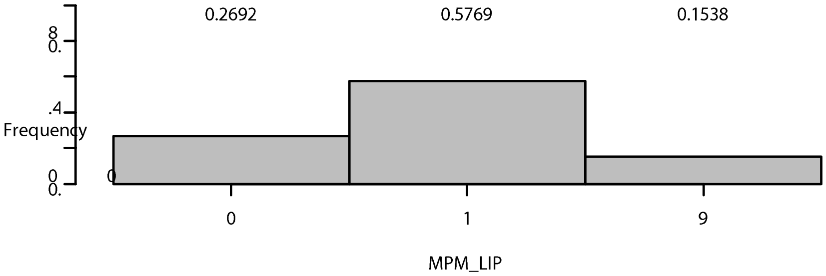


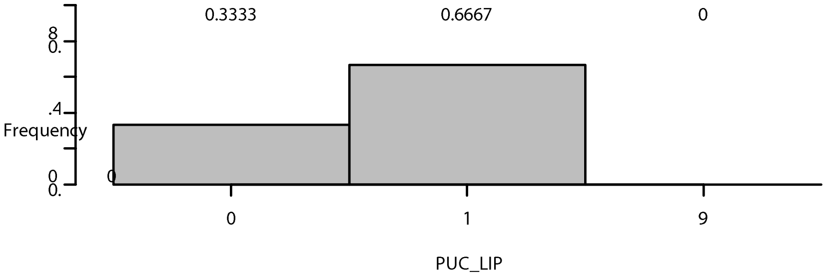


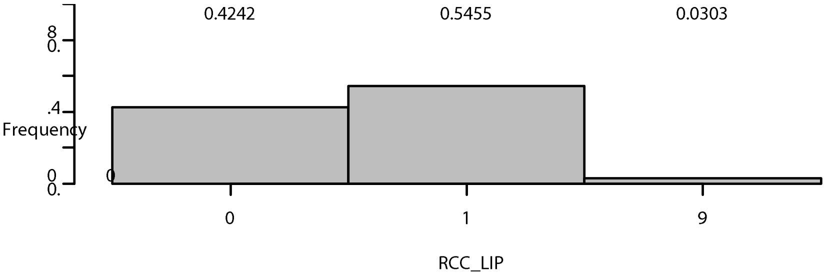


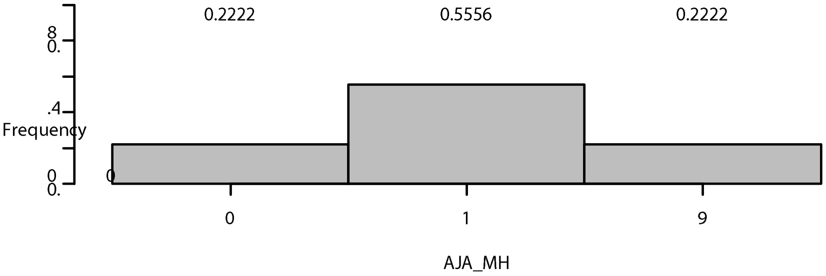

0.25
0.5833
0.1667
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

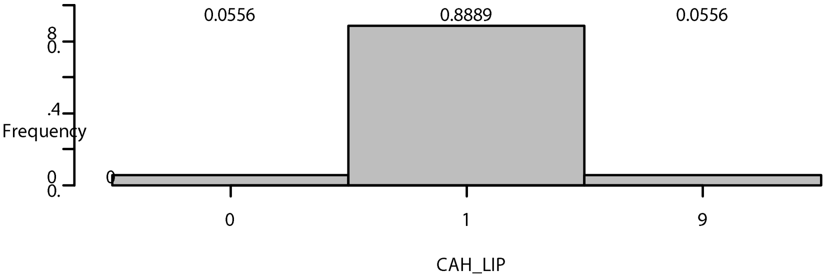

0.2308
0.6308
0.1385
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

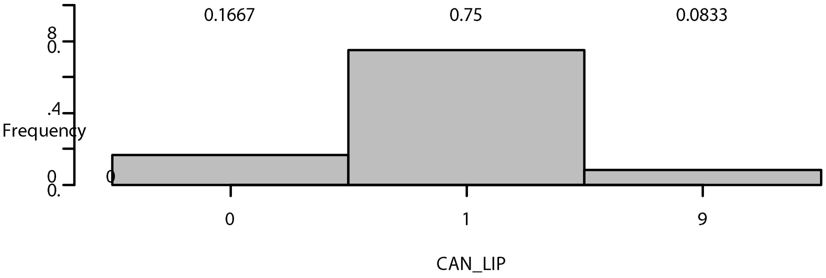

0.2692
0.5769
0.1538
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

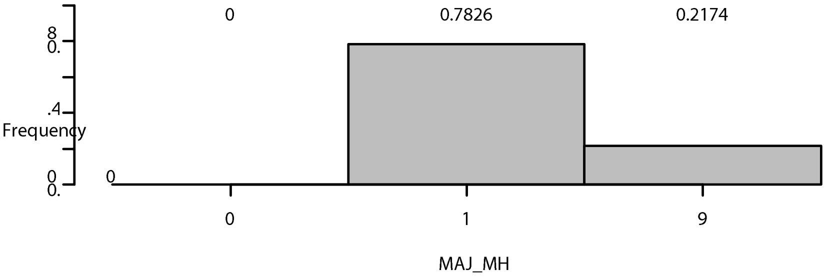

0.3333
0.6667
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

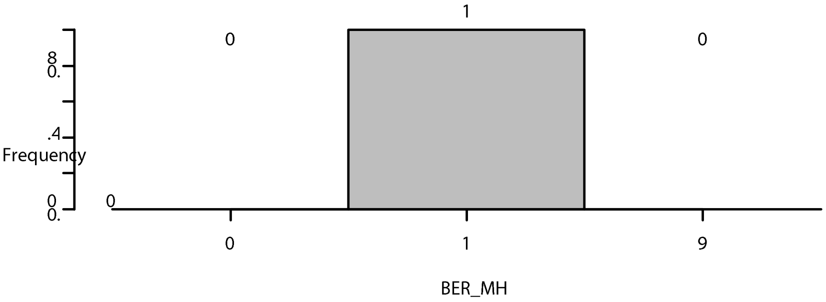

0.4242
0.5455
0.0303
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

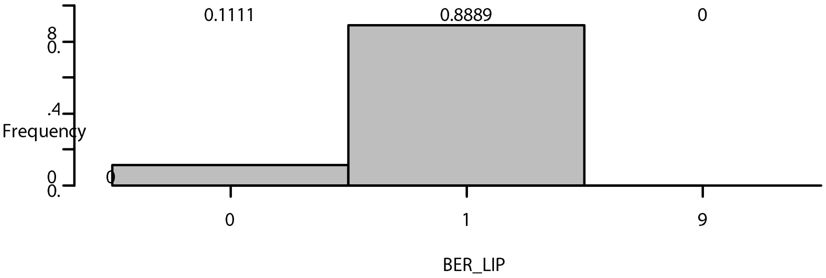

0.2222
0.5556
0.2222
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

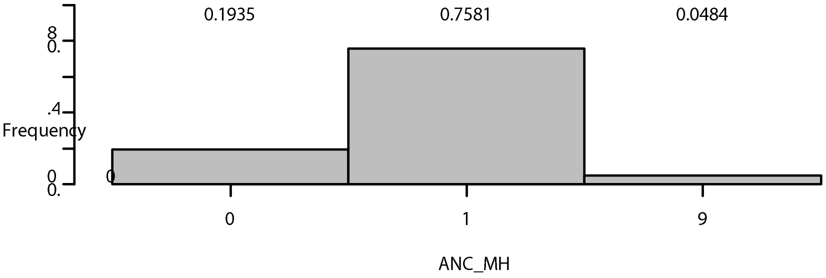

0.0556
0.8889
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

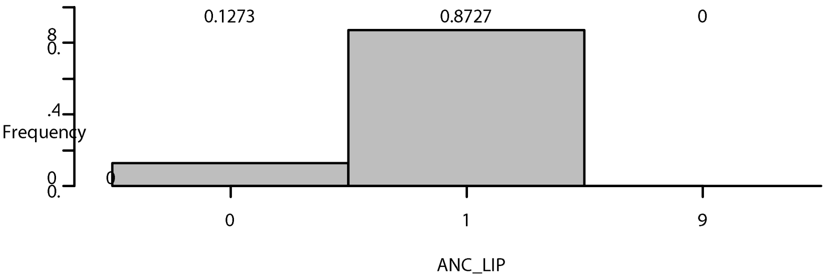

0.1667
0.75
0.0833
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0
0.7826
0.2174
0.8
.4
Frequency
0.0
0
0
1
9
MAJ_MH

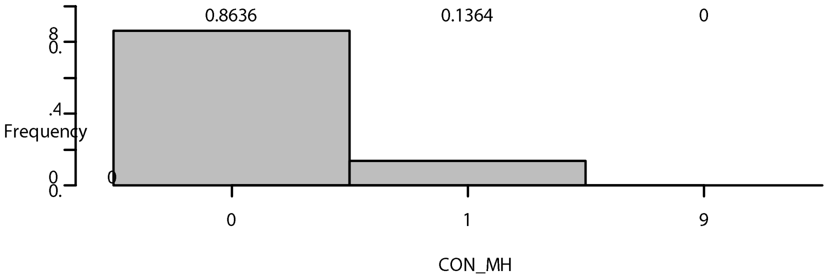

1
0
0
0.8
.4
Frequency
0.0
0
0
1
9
BER_MH

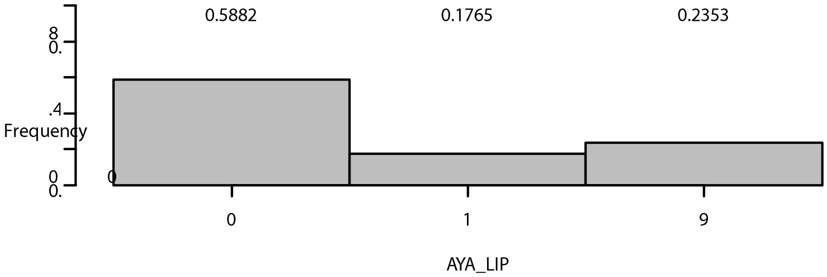

0.1111
0.8889
0
0.8
.4
Frequency
0.0
0
0
1
9
BER_LIP

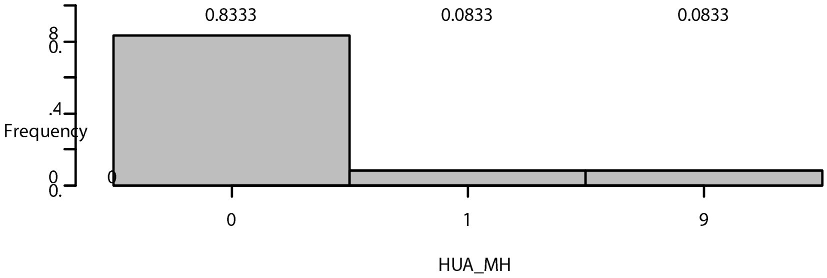

0.1935
0.7581
0.0484
0.8
.4
Frequency
0.0
0
0
1
9
ANC_MH

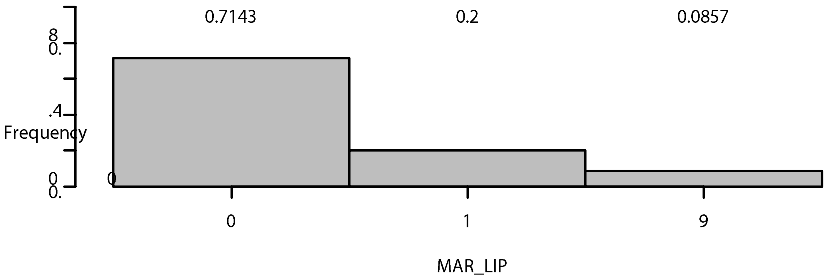

0.1273
0.8727
0
0.8
.4
Frequency
0.0
0
0
1
9
ANC_LIP

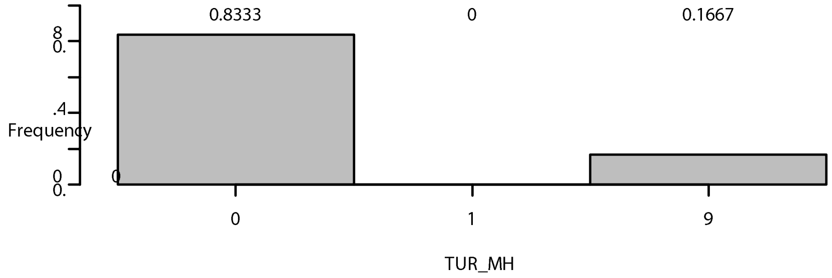
Trait 21 Divided hypoglossal canal

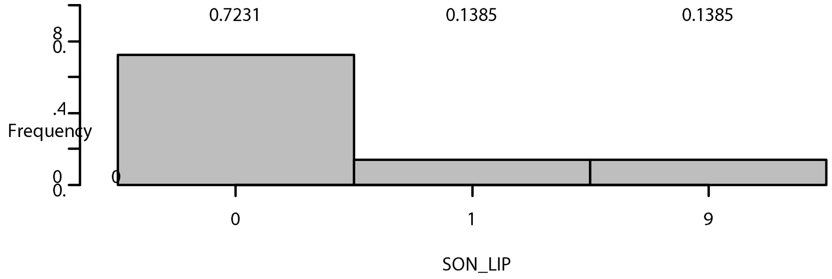


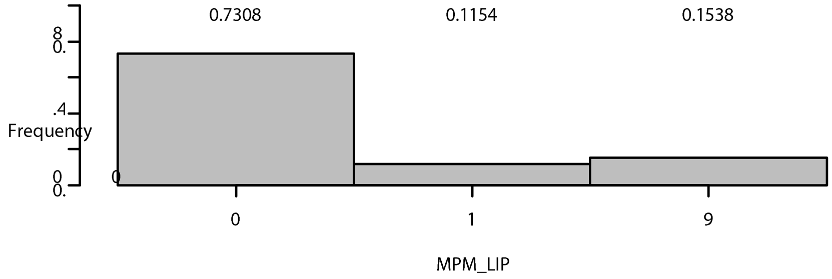


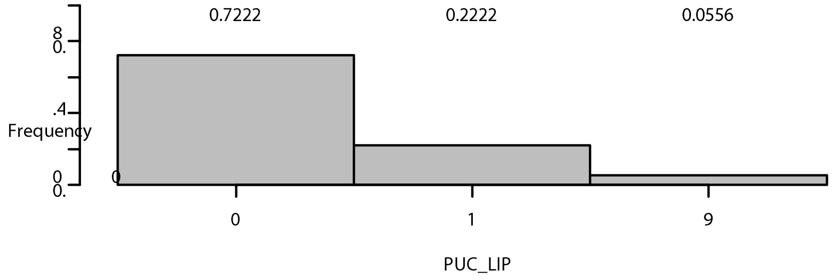


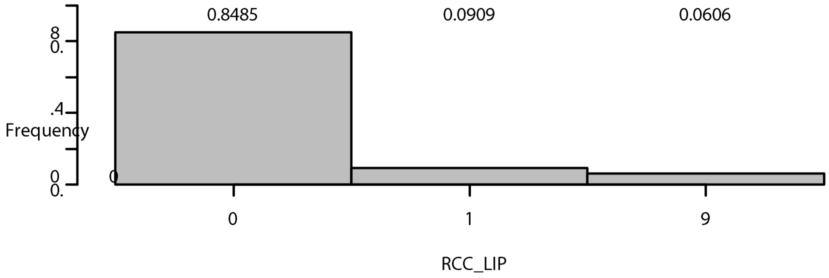


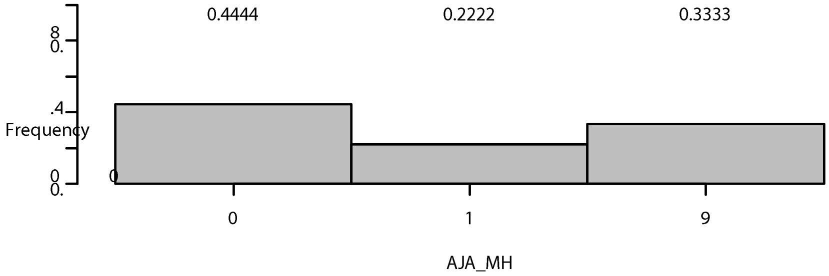

0.8333
0
0.1667
Frequency
0.8
.4
0.0
0
0
1
9
TUR_MH

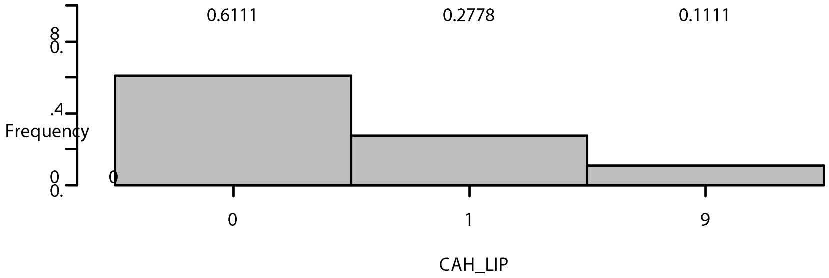

0.7231
0.1385
0.1385
Frequency
0.8
.4
0.0
0
0
1
9
SON_LIP

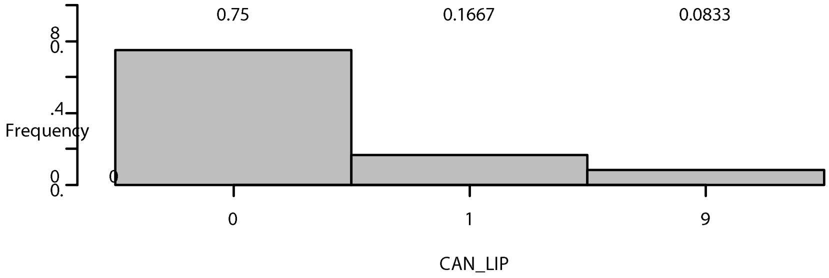

0.7308
0.1154
0.1538
Frequency
0.8
.4
0.0
0
0
1
9
MPM_LIP

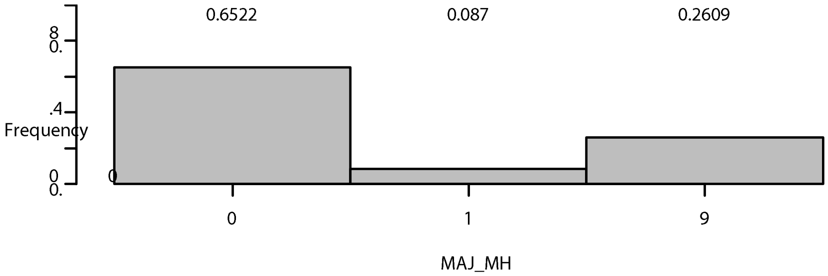

0.7222
0.2222
0.0556
Frequency
0.8
.4
0.0
0
0
1
9
PUC_LIP

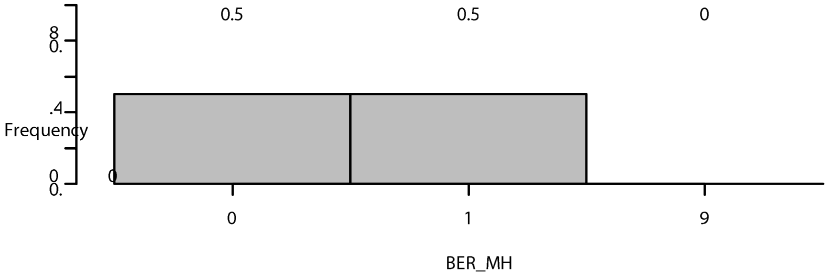

0.8485
0.0909
0.0606
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

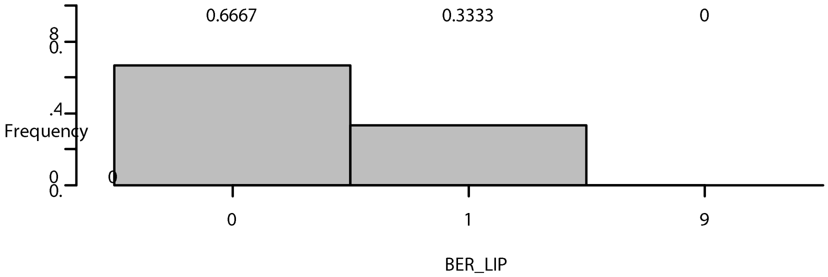

0.4444
0.2222
0.3333
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

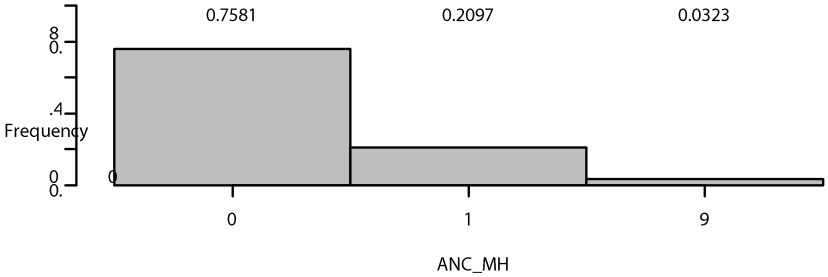

0.6111
0.2778
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

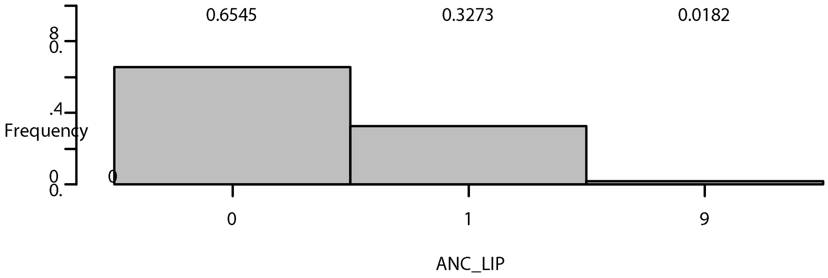

0.75
0.1667
0.0833
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.6522
0.087
0.2609
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

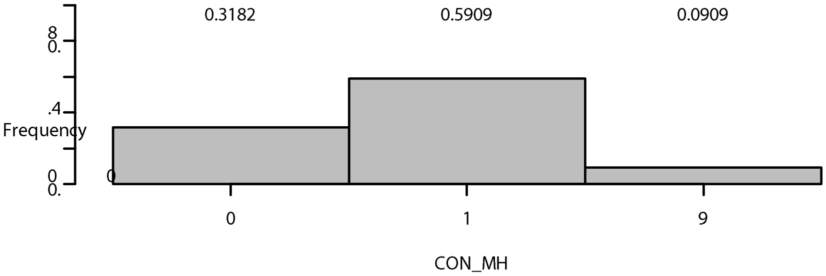

0.5
0.5
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

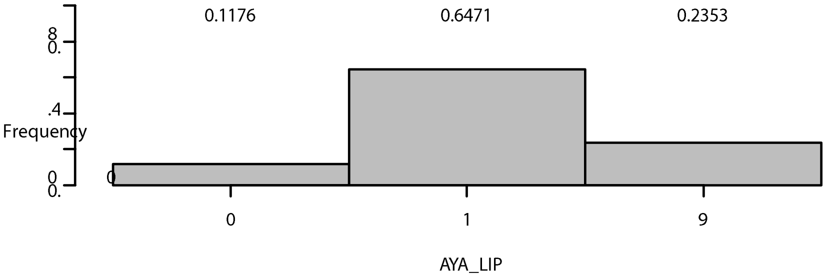

0.6667
0.3333
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

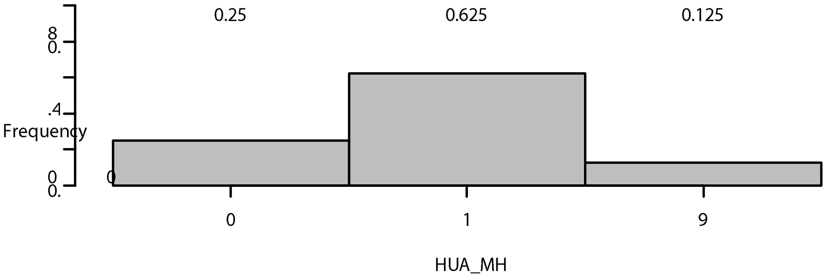

0.7581
0.2097
0.0323
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

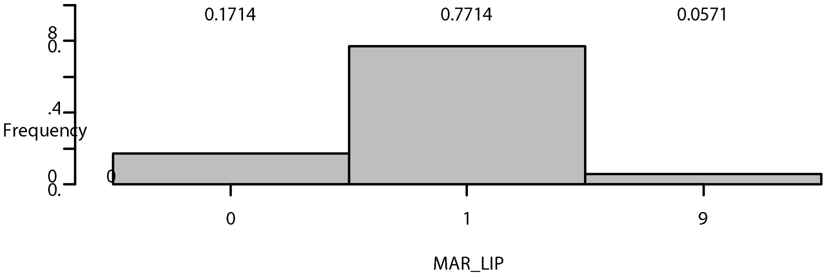

0.6545
0.3273
0.0182
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

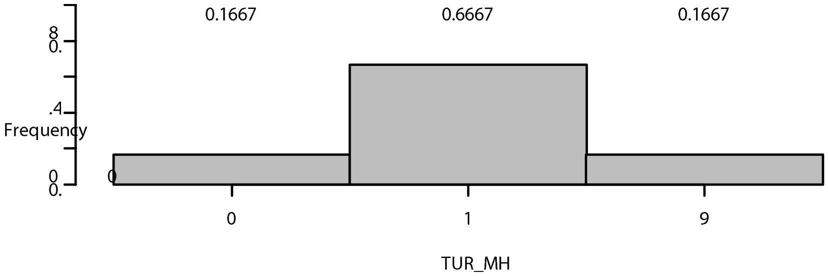
Trait 22 Flexure of superior sagittal sulcus to the right

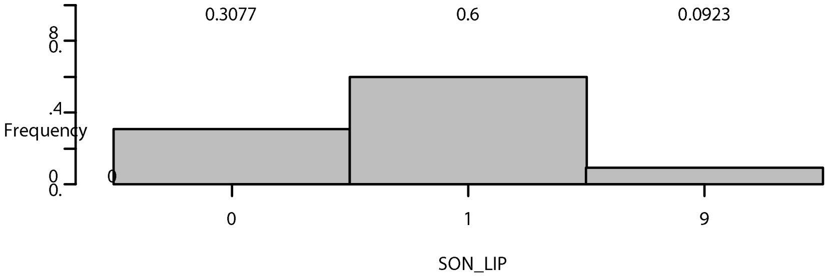


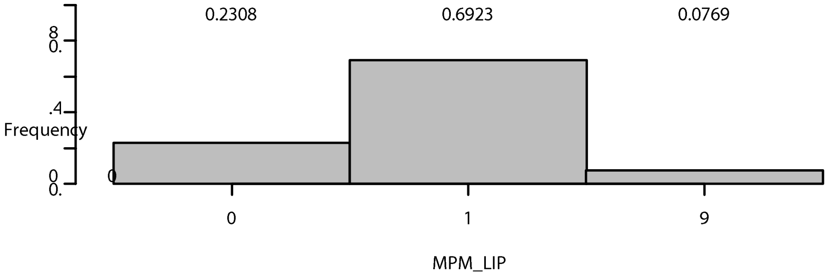


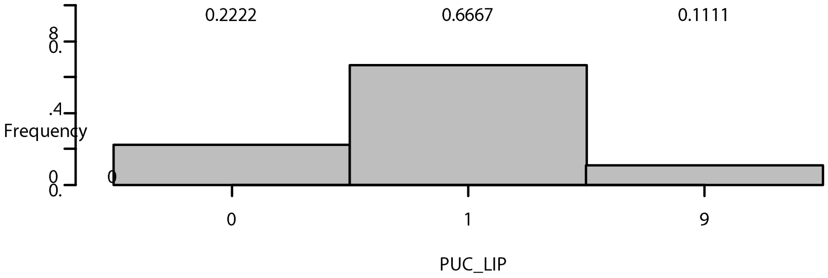


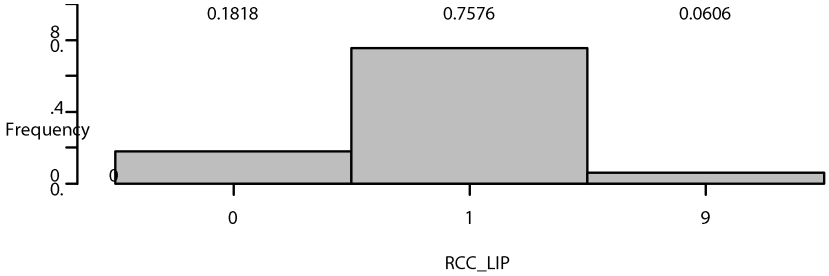


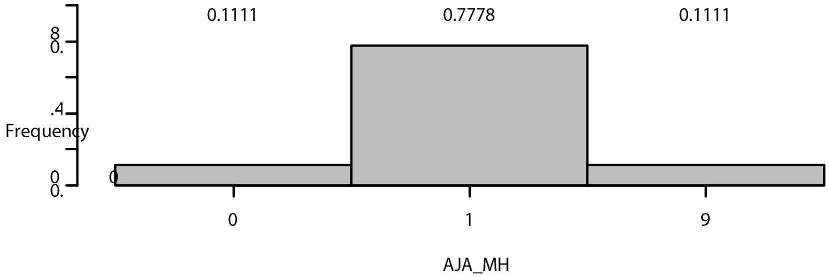

0.1667
0.6667
0.1667
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

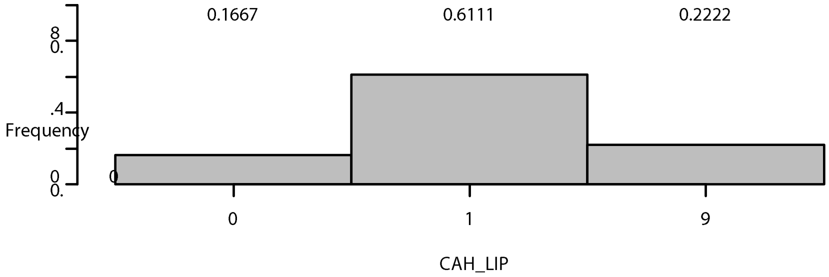

0.3077
0.6
0.0923
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

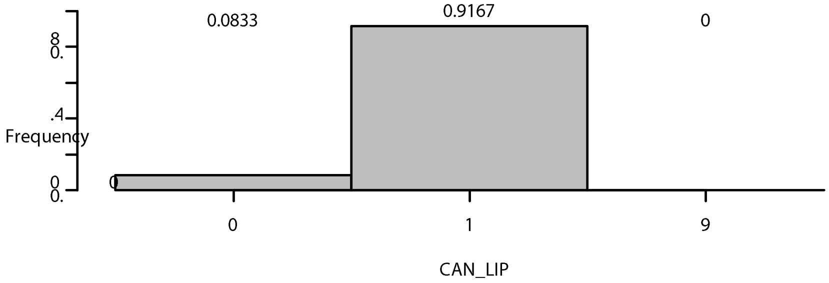

0.2308
0.6923
0.0769
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

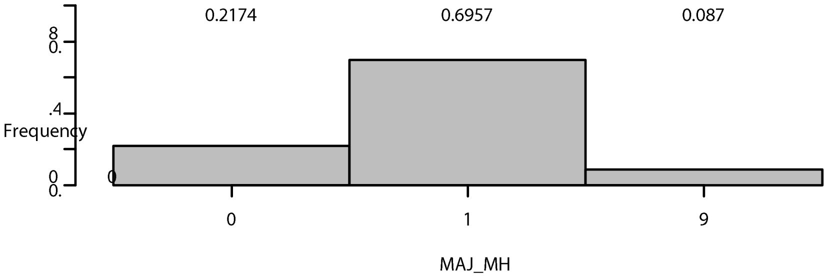

0.2222
0.6667
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

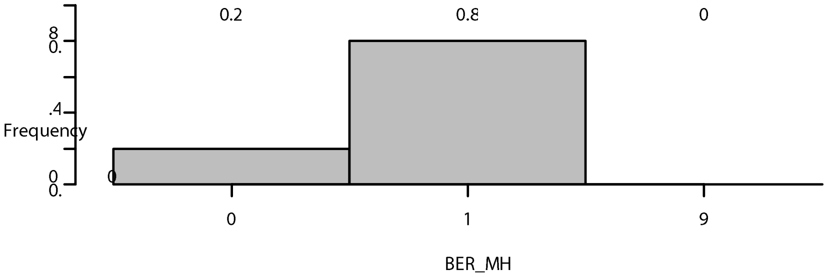

0.1818
0.7576
0.0606
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

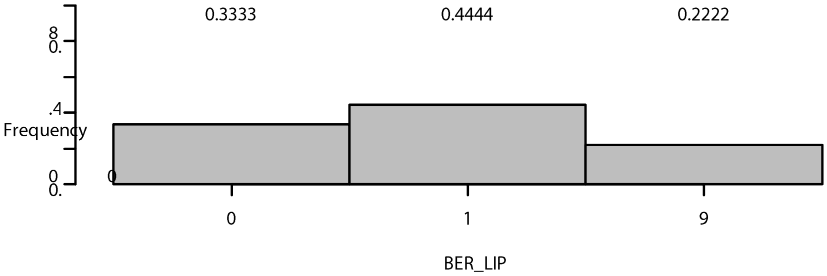

0.1111
0.7778
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

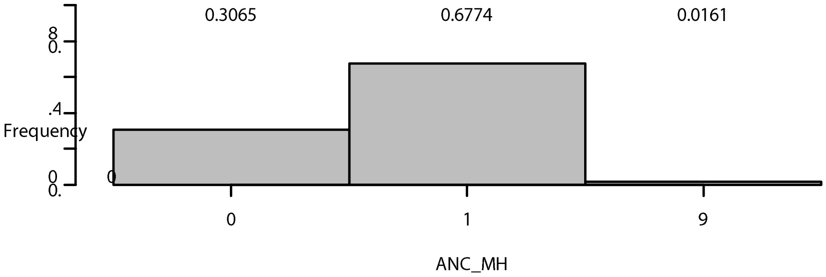

0.1667
0.6111
0.2222
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

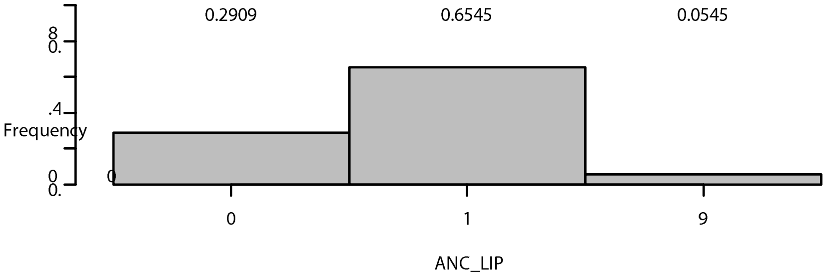

0.0833
0.9167
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.2174
0.6957
0.087
0.8
0.4
Frequency
0.0
0
1
9
MAJ_MH

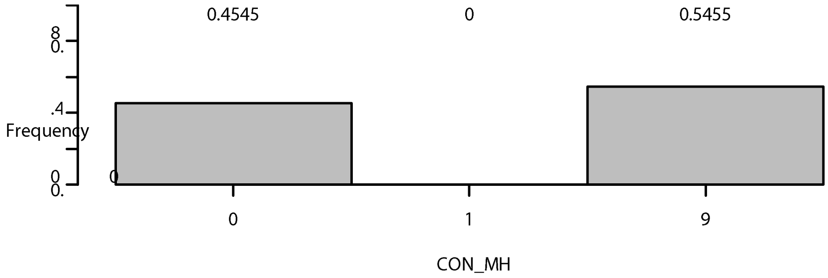

0.2
0.8
0
0.8
0.4
Frequency
0.0
0
1
9
BER_MH

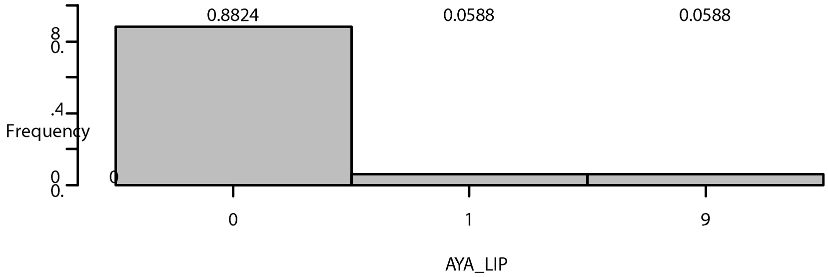

0.3333
0.4444
0.2222
0.8
0.4
Frequency
0.0
0
1
9
BER_LIP

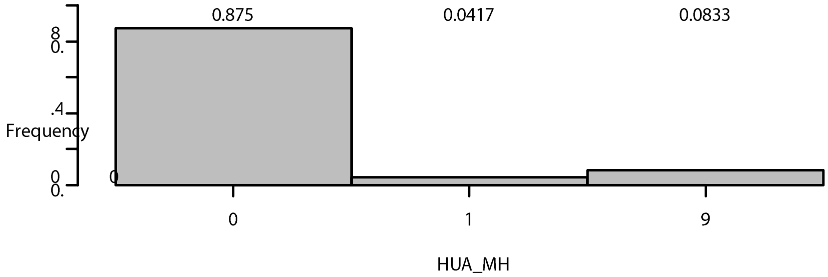

0.3065
0.6774
0.0161
0.8
0.4
Frequency
0.0
0
1
9
ANC_MH

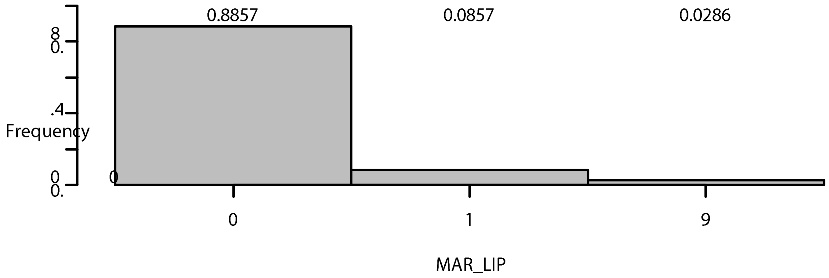

0.2909
0.6545
0.0545
0.8
0.4
Frequency
0.0
0
1
9
ANC_LIP

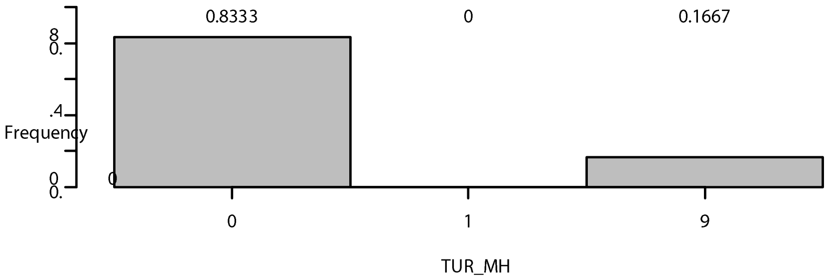
Trait 25 Pterygo-spinous bridge

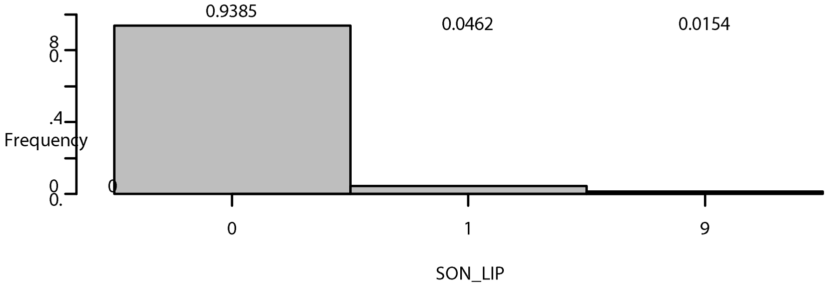


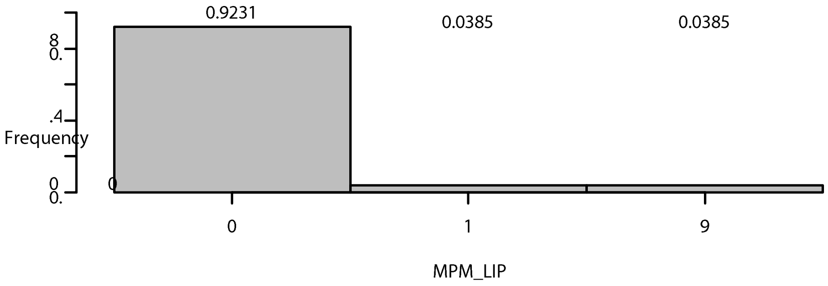


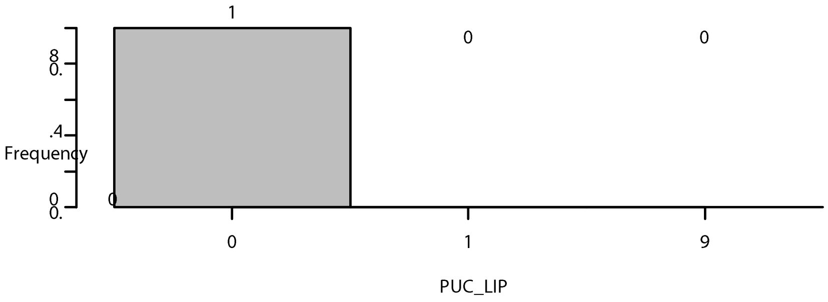


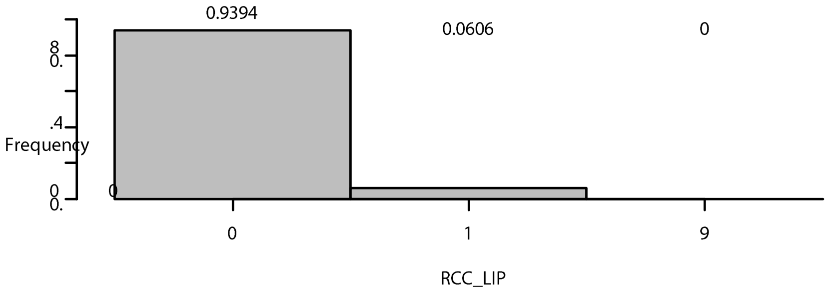


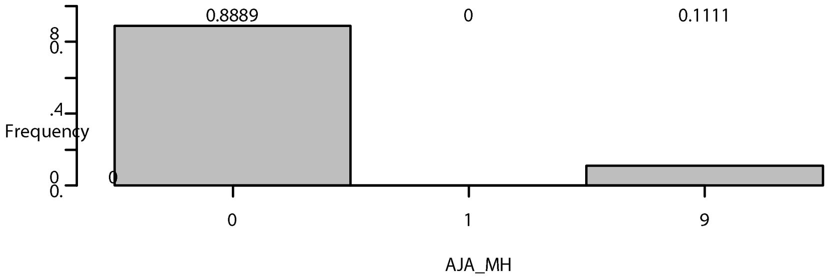

0.8333
0
0.1667
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

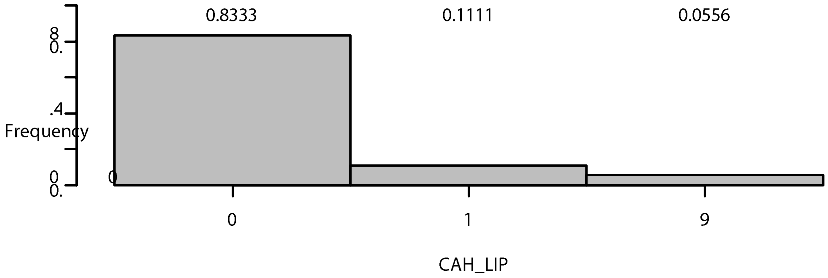

0.9385
0.0462
0.0154
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

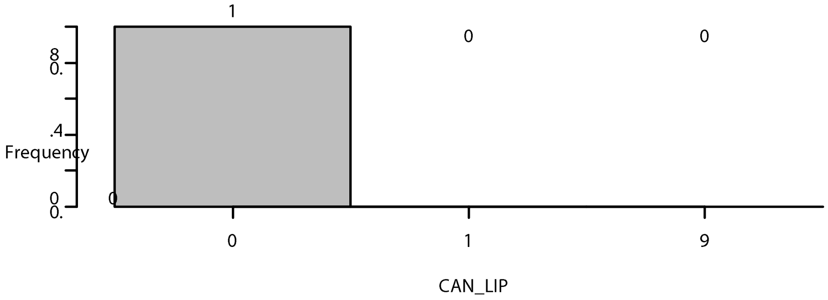

0.9231
0.0385
0.0385
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

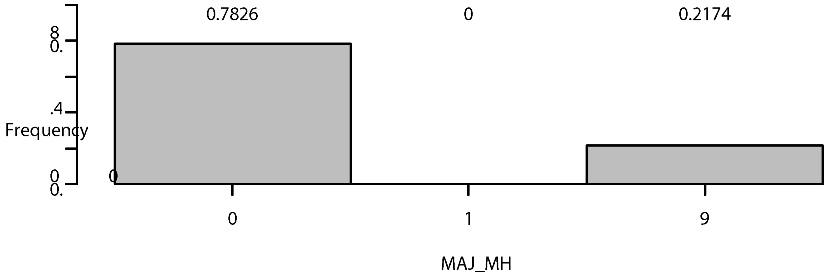

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

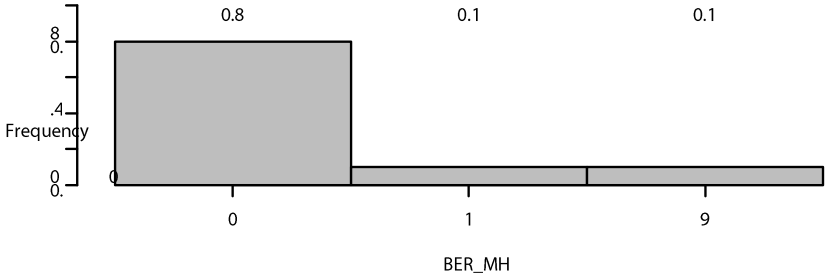

0.9394
0.0606
0
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

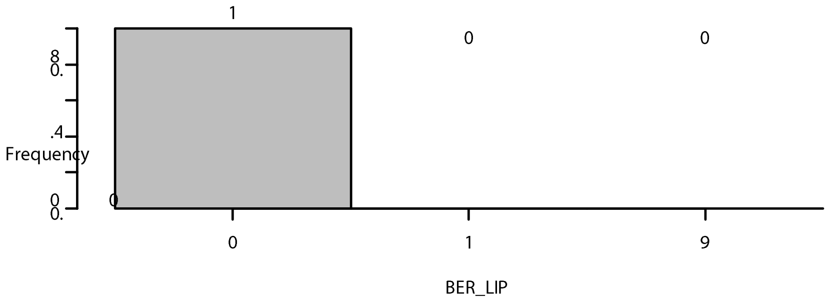

0.8889
0
0.1111
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

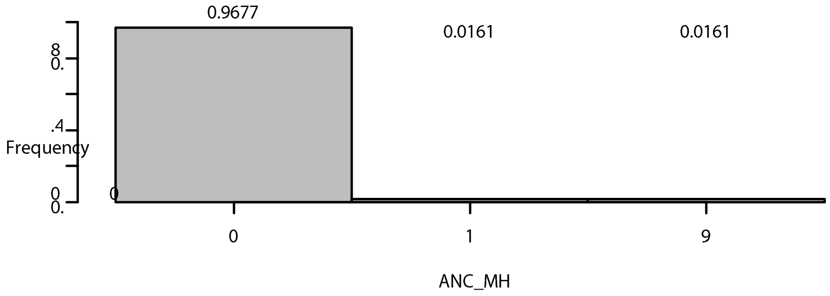

0.8333
0.1111
0.0556
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

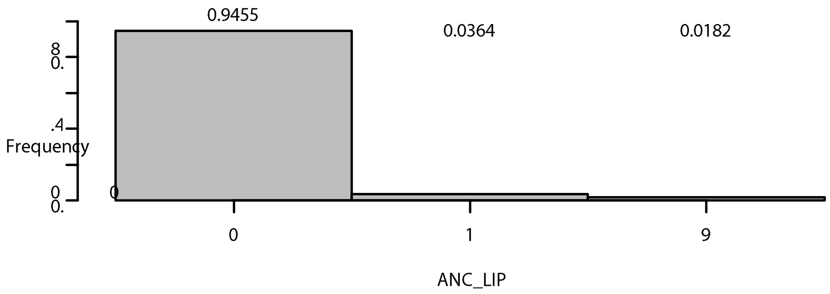

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.7826
0
0.2174
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

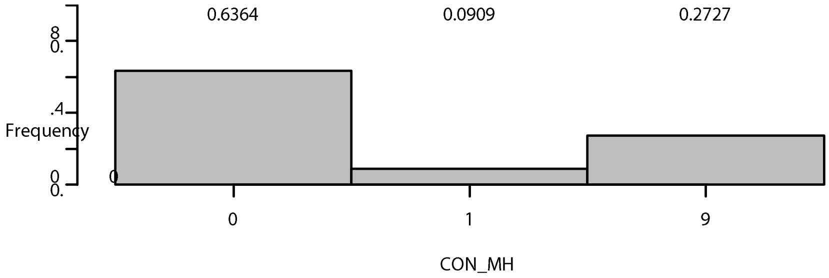

0.8
0.1
0.1
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

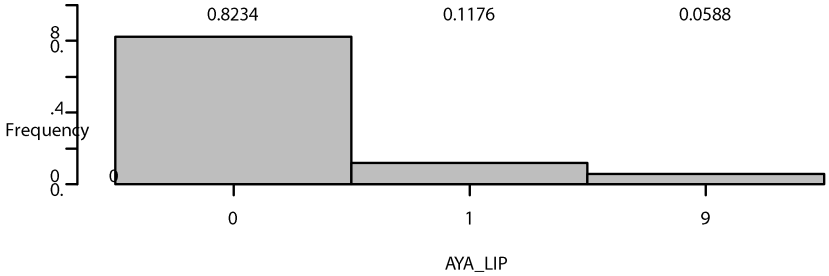

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

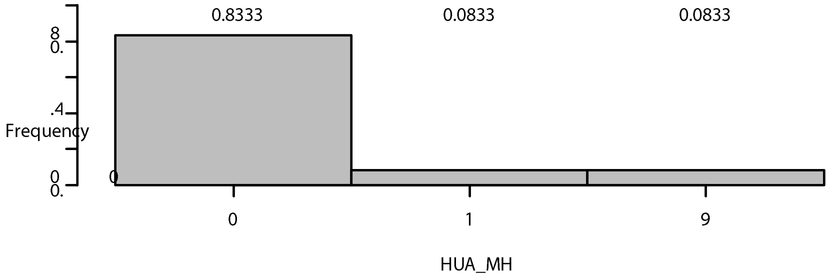

0.9677
0.0161
0.0161
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

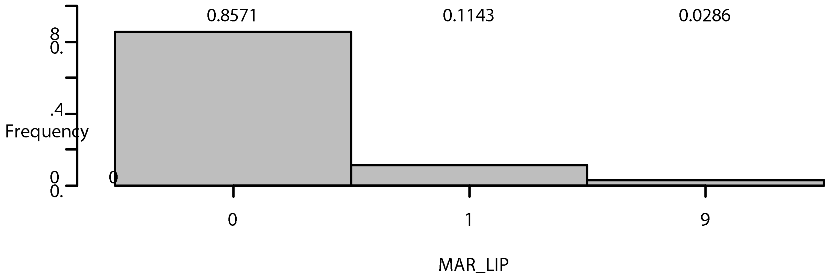

0.9455
0.0364
0.0182
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

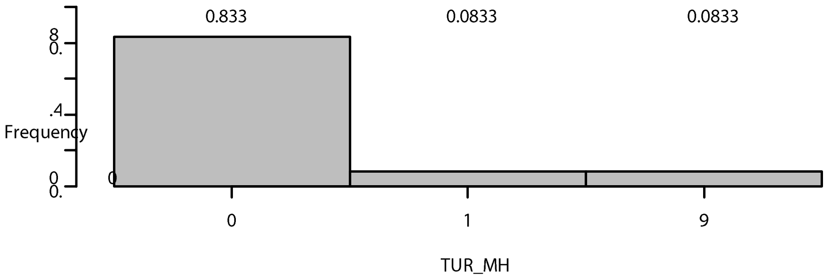
Trait 26 Pterygo-alar bridge

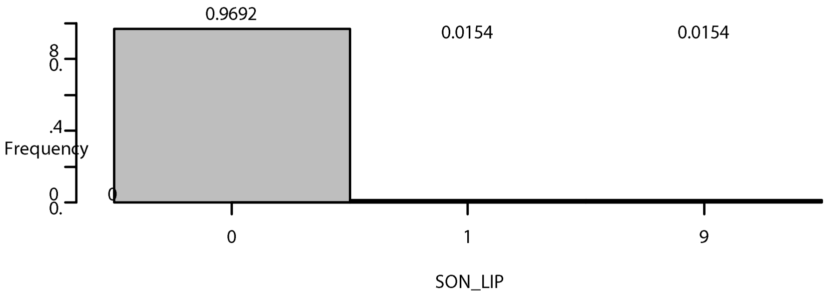


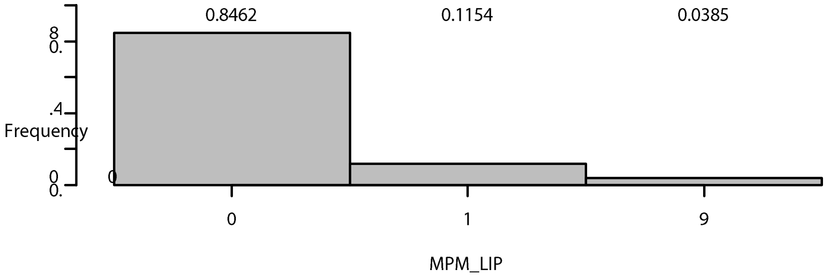


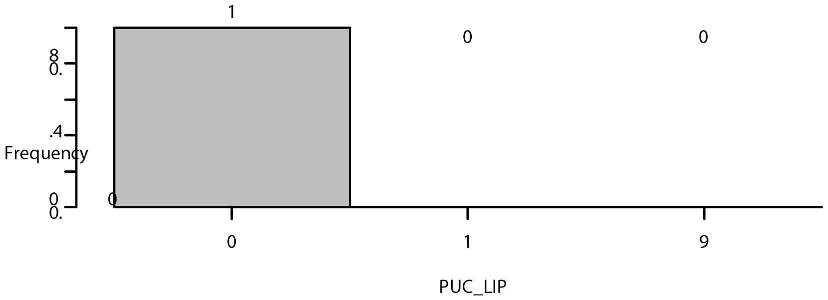


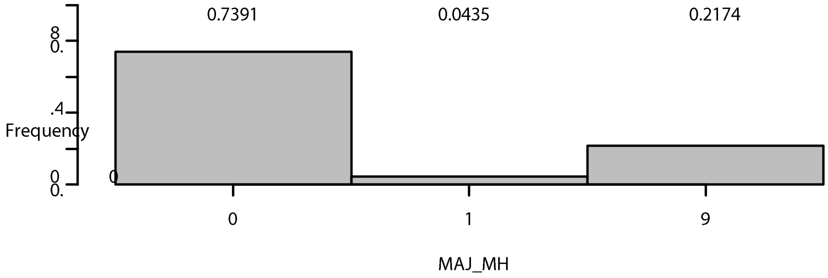


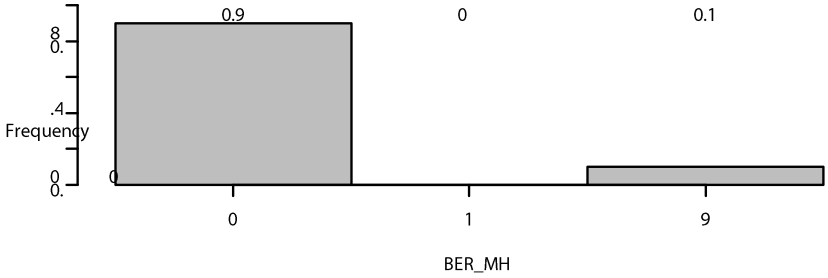

0.833
0.0833
0.0833
0.8
.4
Frequency
0.0
0
0
1
9
TUR_MH

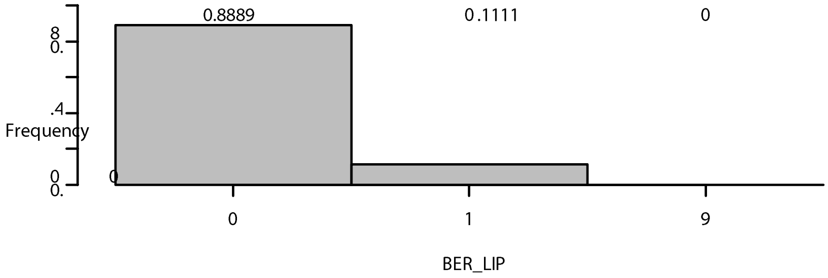

0.9692
0.0154
0.0154
0.8
.4
Frequency
0.0
0
0
1
9
SON_LIP

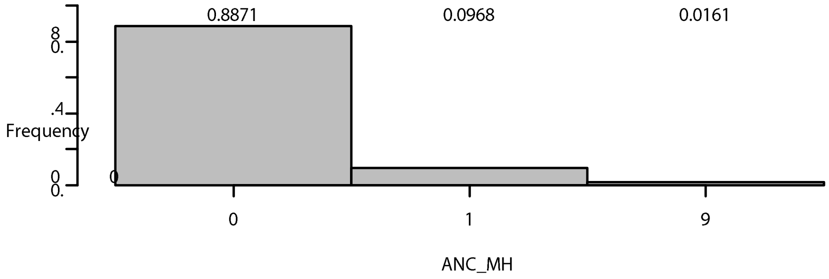

0.8462
0.1154
0.0385
0.8
.4
Frequency
0.0
0
0
1
9
MPM_LIP

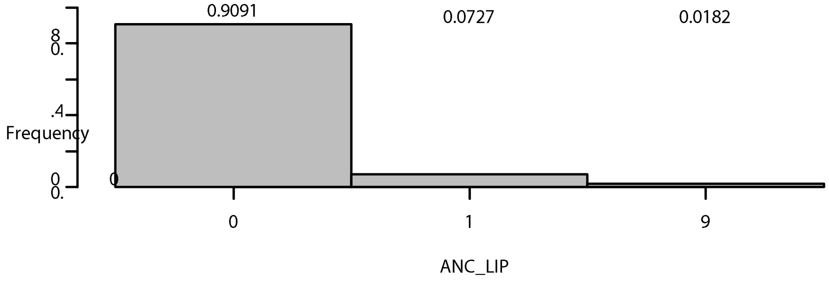

1
0
0
0.8
.4
Frequency
0.0
0
0
1
9
PUC_LIP


0.7391
0.0435
0.2174
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

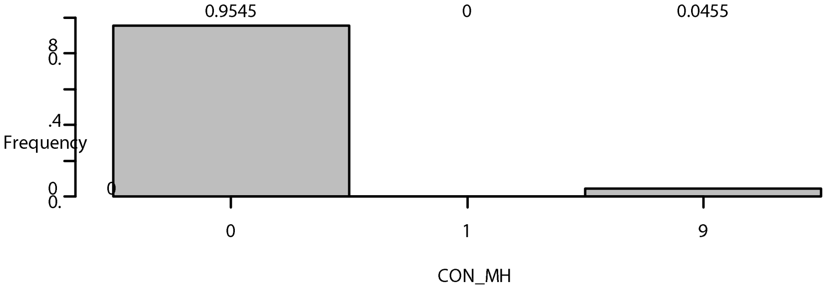

0.9
0
0.1
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

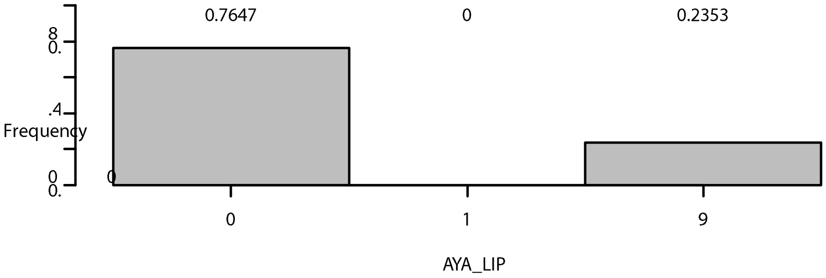

0.8889
0 .1111
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

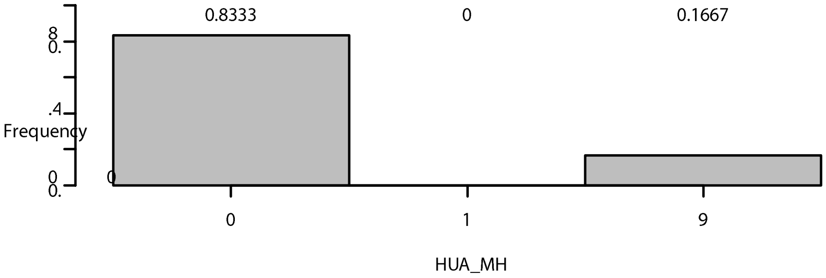

0.8871
0.0968
0.0161
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

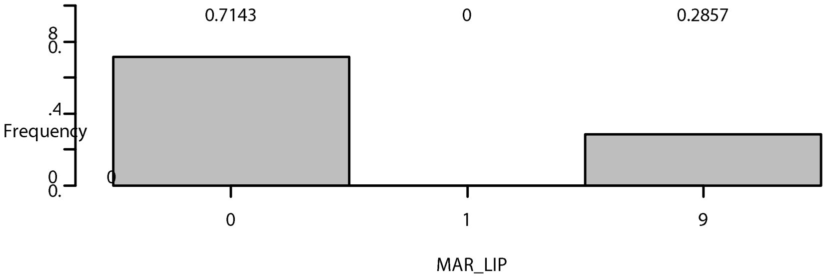

0.9091
0.0727
0.0182
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

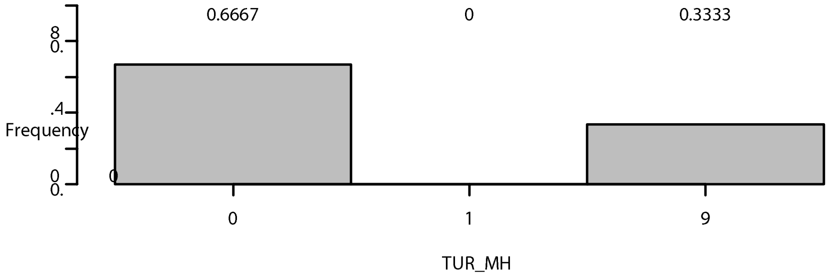
Trait 30 Double condylar facet

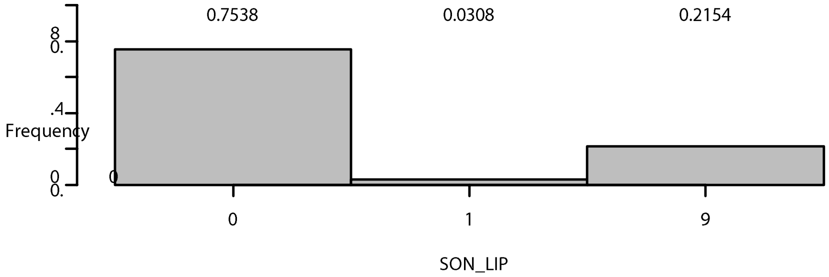


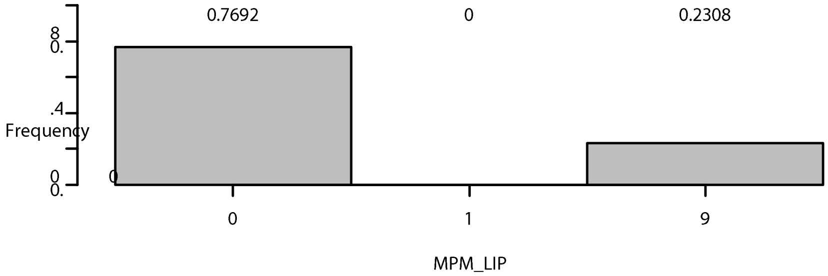


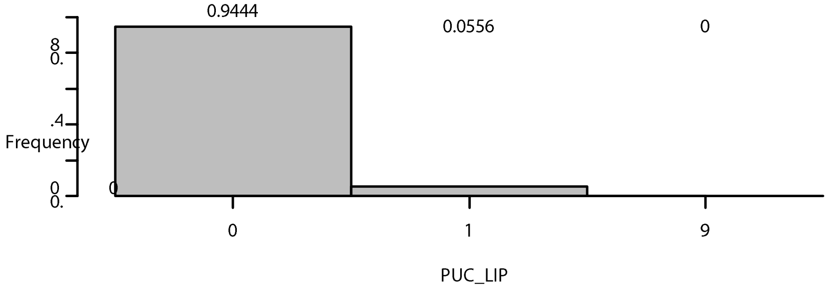


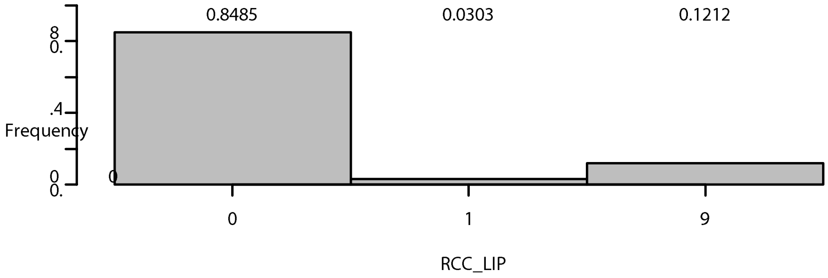


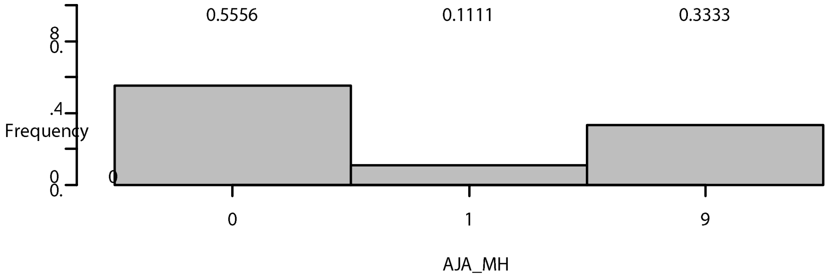

0.6667
0
0.3333
0.8
0.4
Frequency
0.0
0
0
1
9
TUR_MH

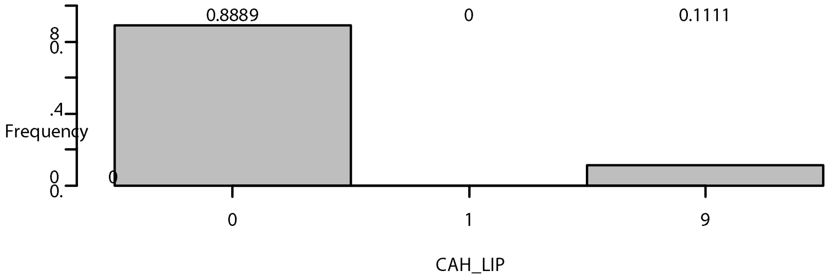

0.7538
0.0308
0.2154
0.8
0.4
Frequency
0.0
0
0
1
9
SON_LIP

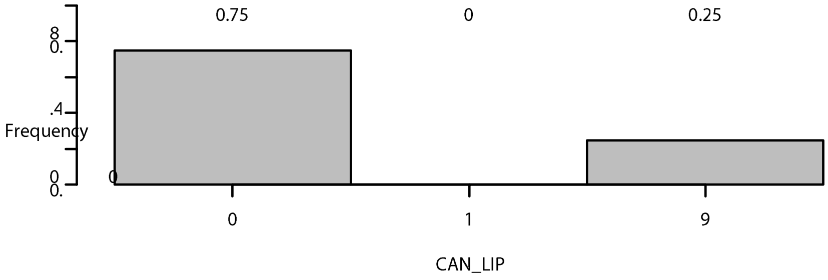

0.7692
0
0.2308
0.8
0.4
Frequency
0.0
0
0
1
9
MPM_LIP

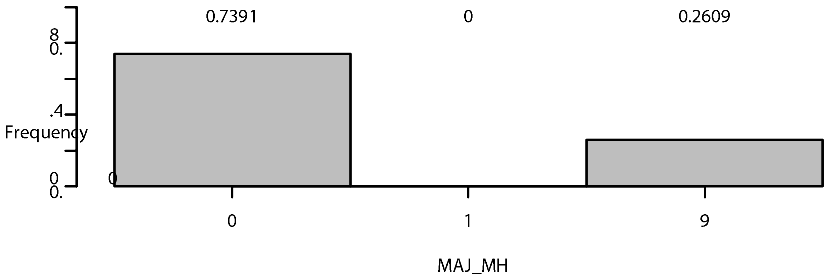

0.9444
0.0556
0
0.8
0.4
Frequency
0.0
0
0
1
9
PUC_LIP

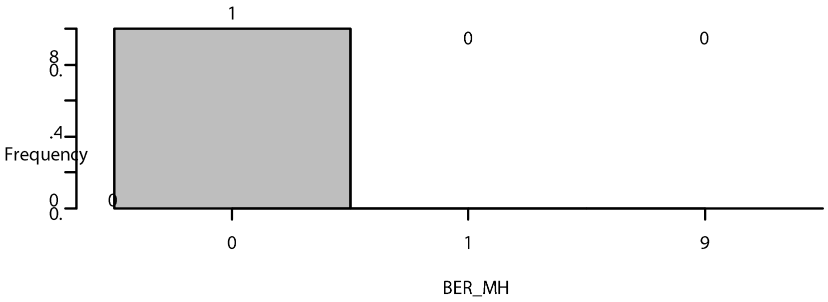

0.8485
0.0303
0.1212
0.8
0.4
Frequency
0.0
0
0
1
9
RCC_LIP

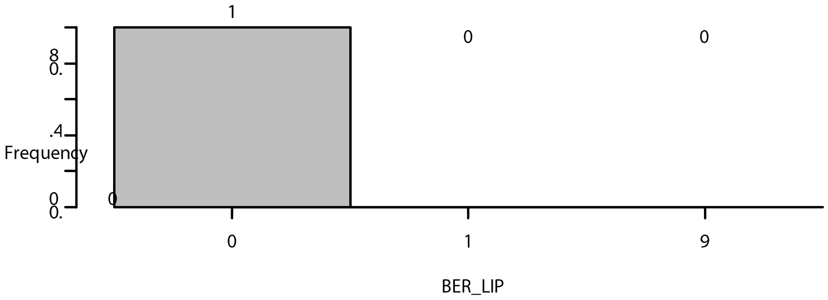

0.5556
0.1111
0.3333
0.8
0.4
Frequency
0.0
0
0
1
9
AJA_MH

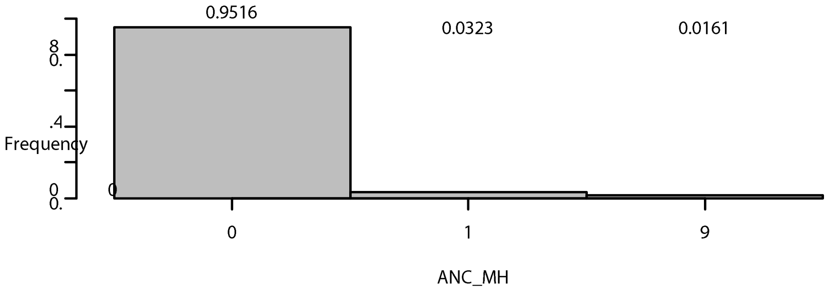

0.8889
0
0.1111
0.8
0.4
Frequency
0.0
0
0
1
9
CAH_LIP

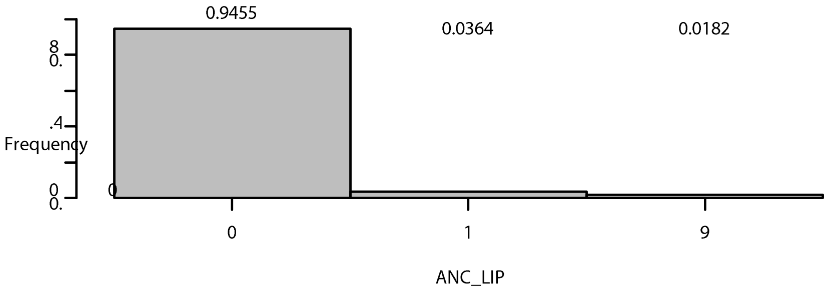

0.75
0
0.25
0.8
0.4
Frequency
0.0
0
0
1
9
CAN_LIP


0.7391
0
0.2609
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH

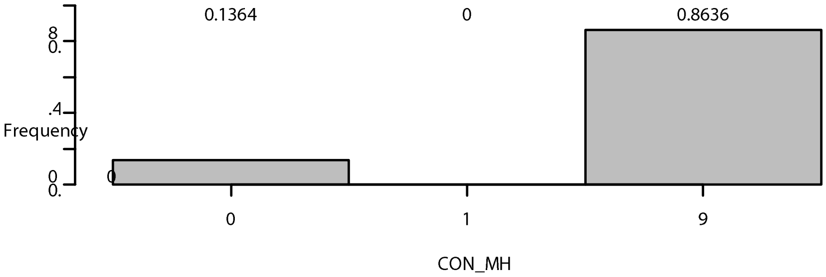

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH

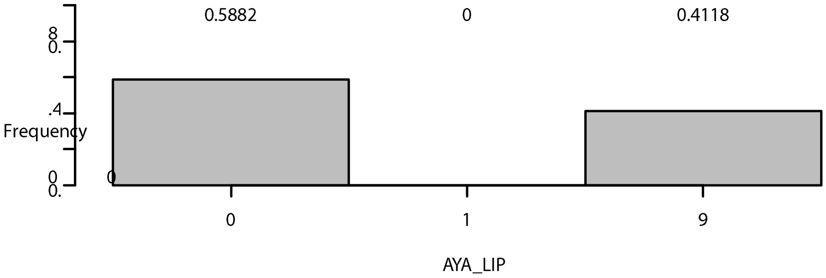

1
0
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP

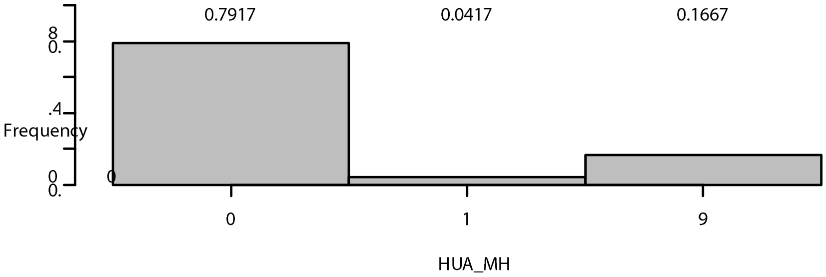

0.9516
0.0323
0.0161
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH

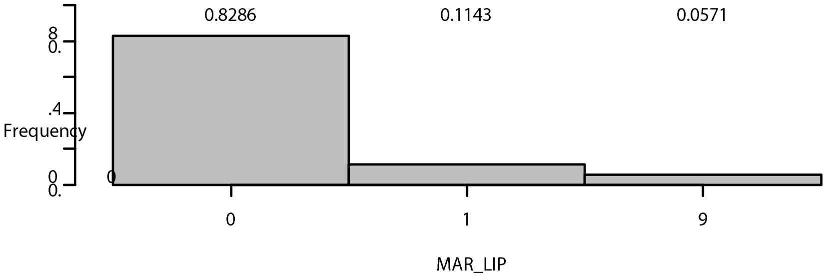

0.9455
0.0364
0.0182
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

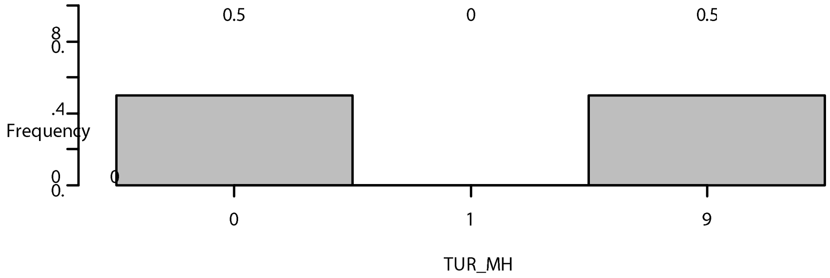
Trait 31 Bridging of the jugular foramen

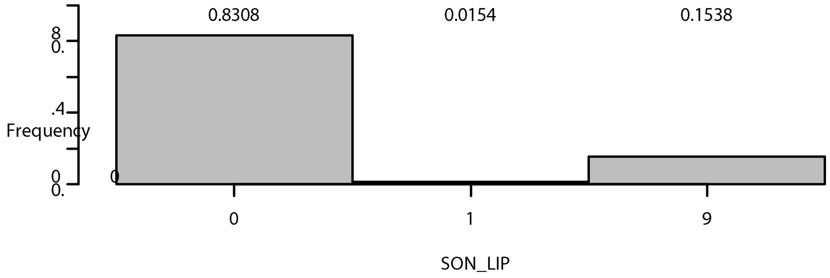


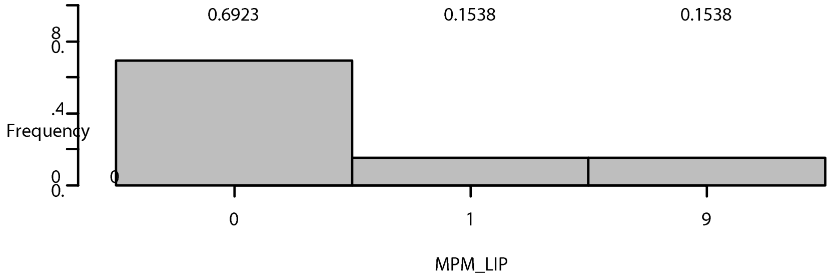


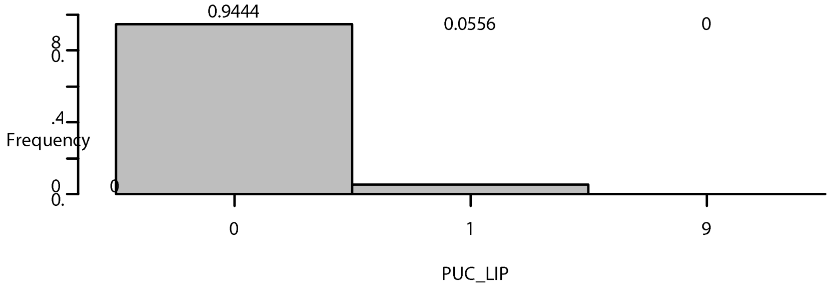


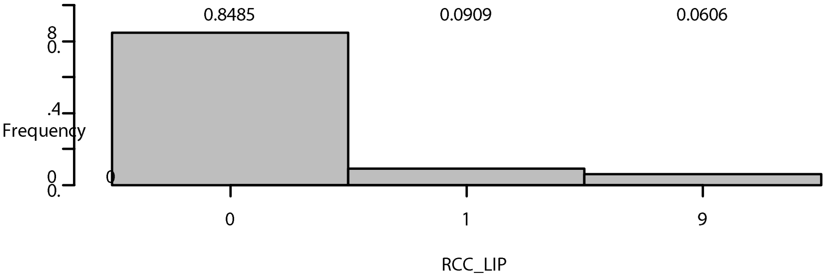


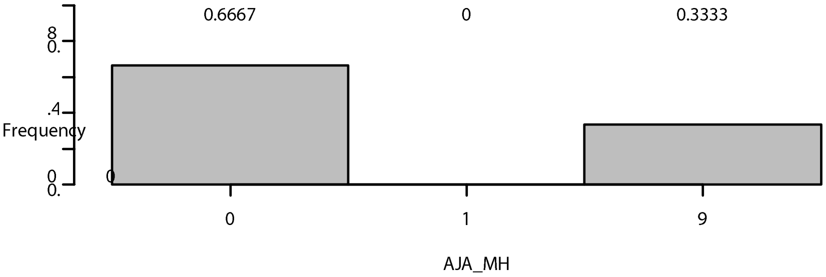

0.5
0
0.5
8
0.
.4
Frequency
0
0.
0
0
1
9
TUR_MH

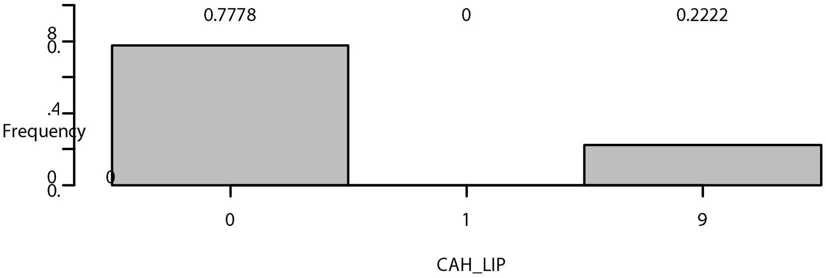

0.8308
0.0154
0.1538
8
0.
.4
Frequency
0
0.
0
0
1
9
SON_LIP

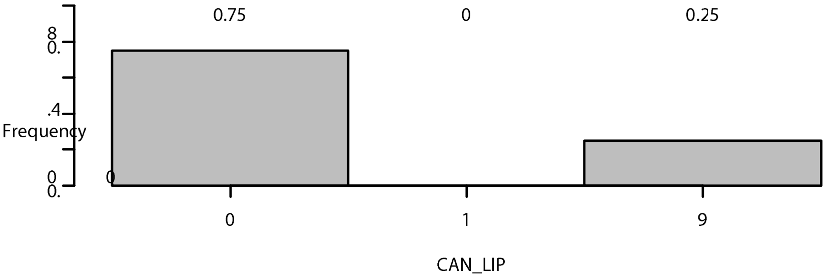

0.6923
0.1538
0.1538
8
0.
.4
Frequency
0
0.
0
0
1
9
MPM_LIP

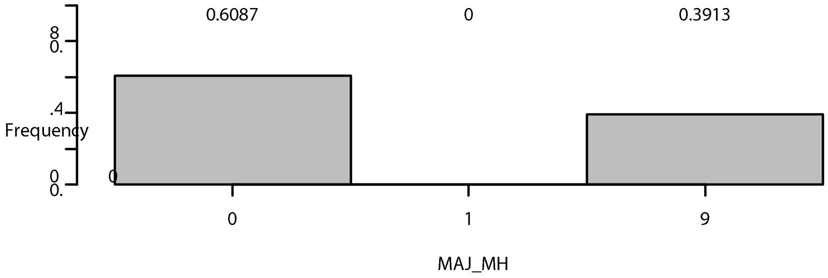

0.9444
0.0556
0
8
0.
.4
Frequency
0
0.
0
0
1
9
PUC_LIP

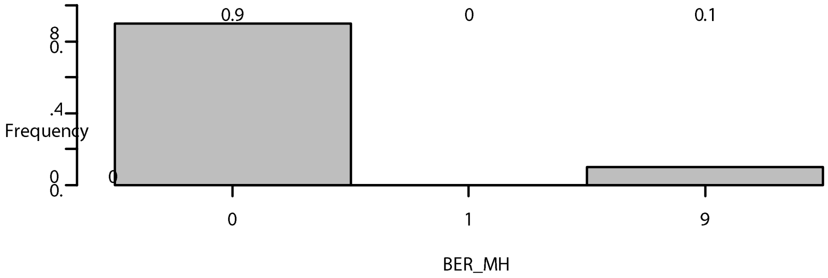

0.8485
0.0909
0.0606
Frequency
0.8
.4
0.0
0
0
1
9
RCC_LIP

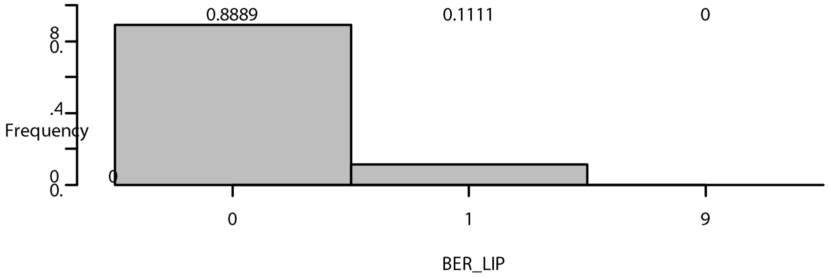

0.6667
0
0.3333
Frequency
0.8
.4
0.0
0
0
1
9
AJA_MH

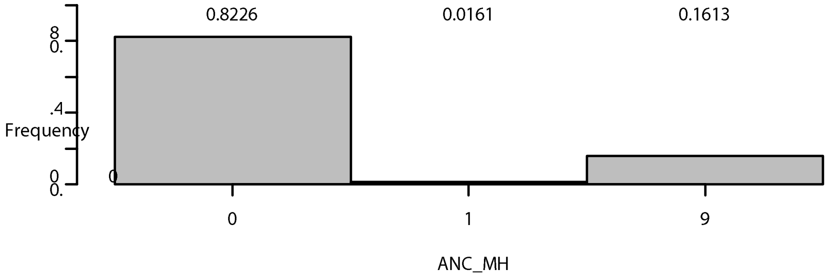

0.7778
0
0.2222
Frequency
0.8
.4
0.0
0
0
1
9
CAH_LIP

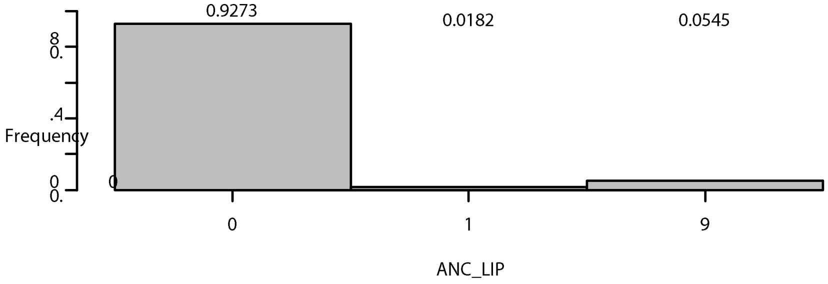

0.75
0
0.25
Frequency
0.8
.4
0.0
0
0
1
9
CAN_LIP


0.6087
0
0.3913
0.8
.4
0.0
Frequency
0
0
1
9
MAJ_MH

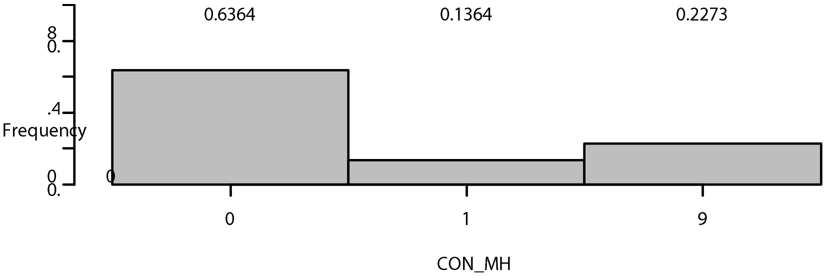

0.9
0
0.1
0.8
.4
0.0
Frequency
0
0
1
9
BER_MH

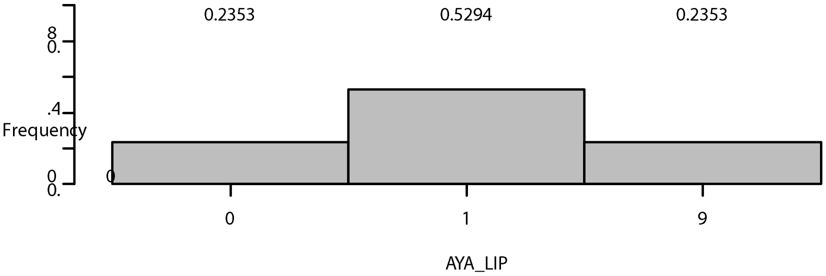

0.8889
0.1111
0
0.8
.4
0.0
Frequency
0
0
1
9
BER_LIP

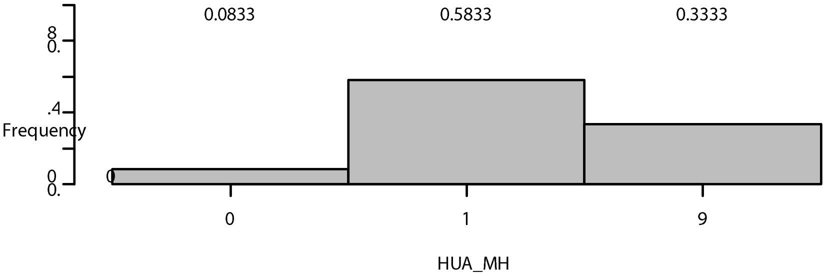

0.8226
0.0161
0.1613
0.8
.4
0.0
Frequency
0
0
1
9
ANC_MH

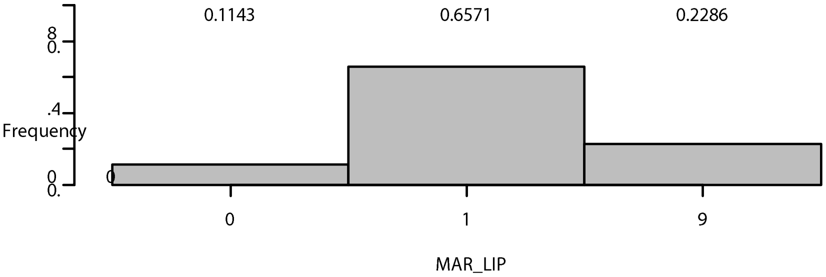

0.9273
0.0182
0.0545
0.8
.4
0.0
Frequency
0
0
1
9
ANC_LIP

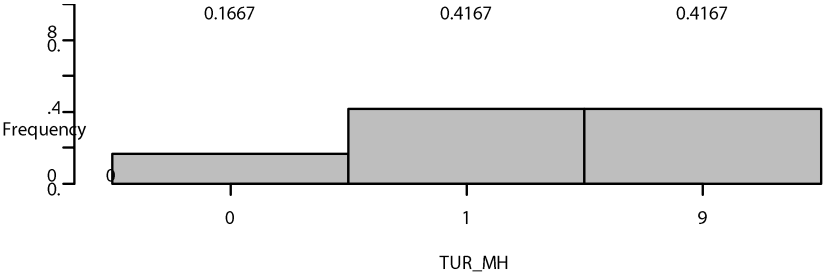
Trait 33 Palatine torus

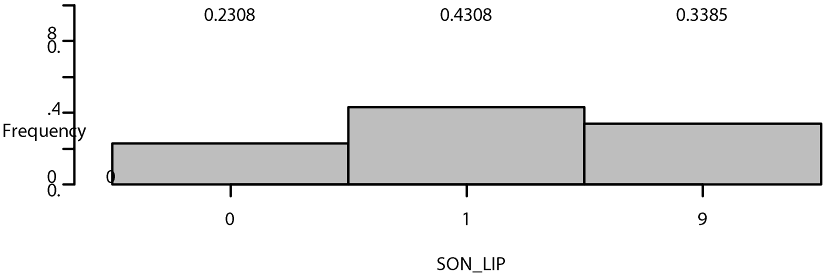


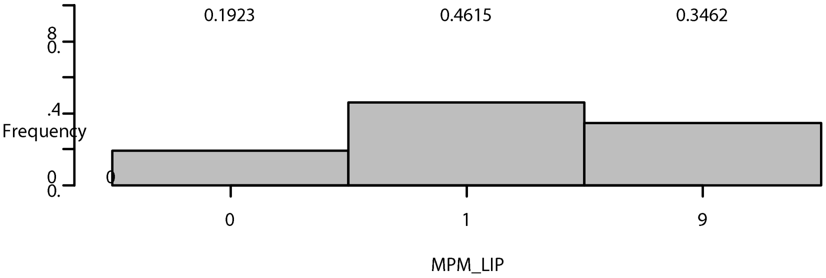


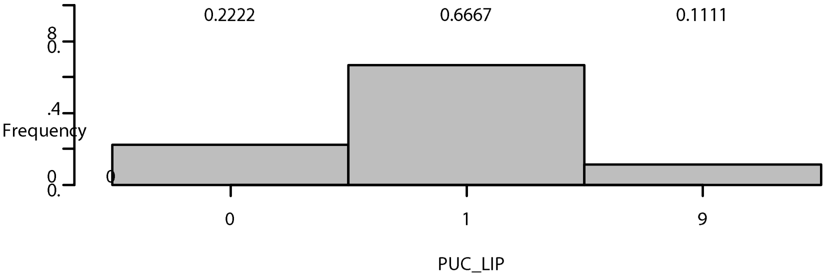


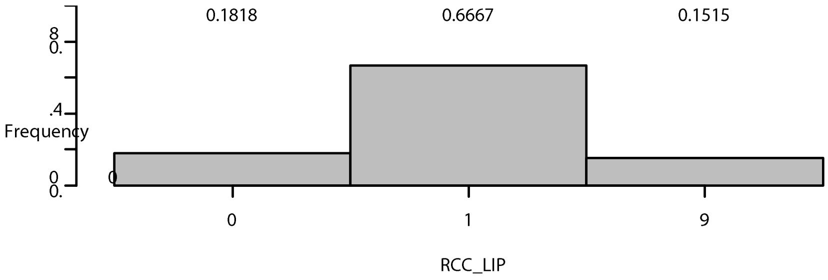


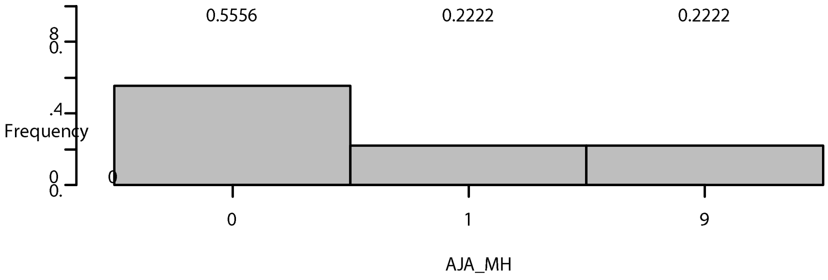

0.1667
0.4167
0.4167
0.8
.4
Frequency
0.0
0
0
1
9
TUR_MH

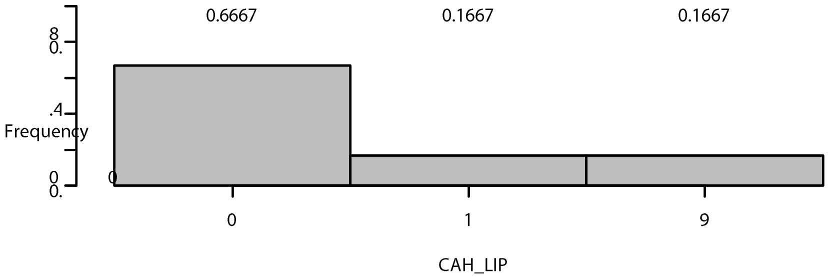

0.2308
0.4308
0.3385
0.8
.4
Frequency
0.0
0
0
1
9
SON_LIP

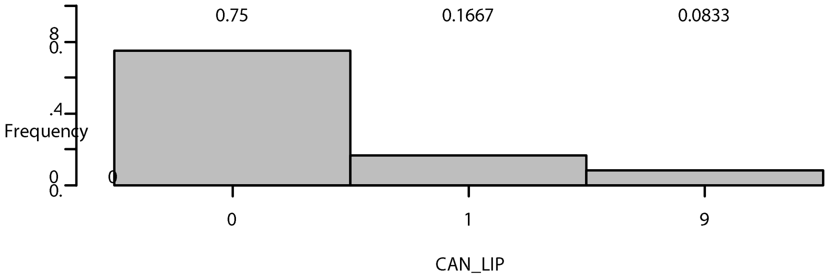

0.1923
0.4615
0.3462
0.8
.4
Frequency
0.0
0
0
1
9
MPM_LIP

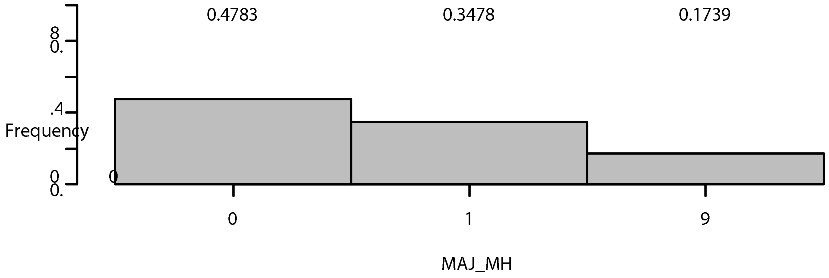

0.2222
0.6667
0.1111
0.8
.4
Frequency
0.0
0
0
1
9
PUC_LIP

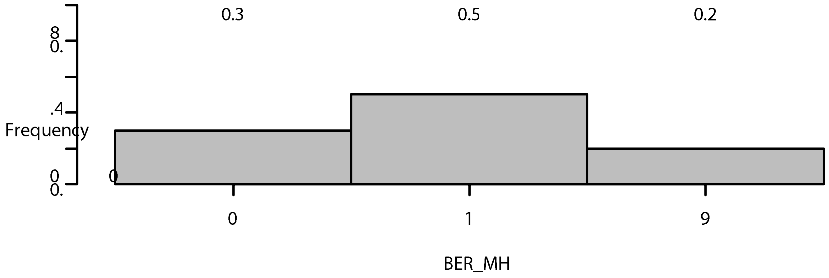

0.1818
0.6667
0.1515
8
0.
.4
Frequency
0
0.
0
0
1
9
RCC_LIP

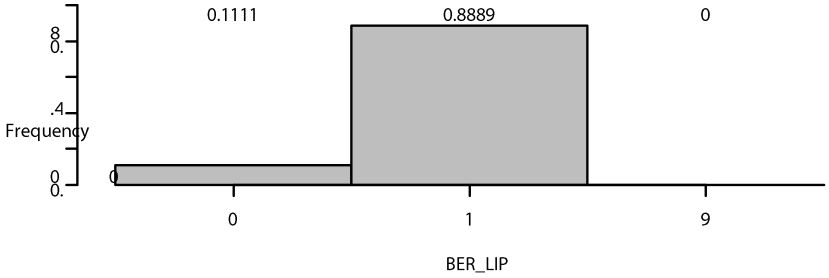

0.5556
0.2222
0.2222
8
0.
.4
Frequency
0
0.
0
0
1
9
AJA_MH

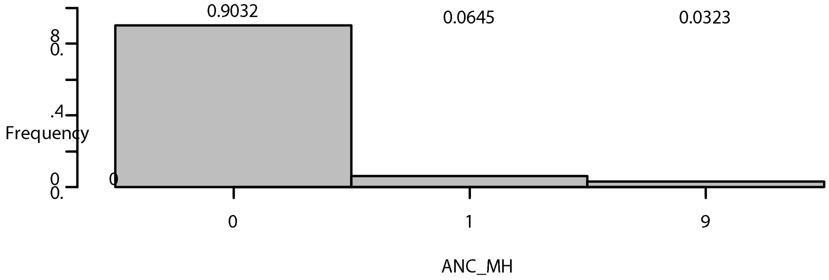

0.6667
0.1667
0.1667
8
0.
.4
Frequency
0
0.
0
0
1
9
CAH_LIP

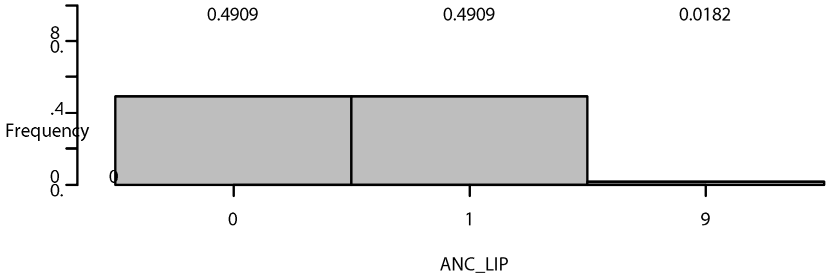

0.75
0.1667
0.0833
8
0.
.4
Frequency
0
0.
0
0
1
9
CAN_LIP


0.4783
0.3478
0.1739
8
0.
.4
Frequency
0
0.
0
0
1
9
MAJ_MH


0.3
0.5
0.2
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_MH


0.1111
0.8889
0
8
0.
.4
Frequency
0
0.
0
0
1
9
BER_LIP


0.9032
0.0645
0.0323
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_MH


0.4909
0.4909
0.0182
8
0.
.4
Frequency
0
0.
0
0
1
9
ANC_LIP

VITA

Christine M. Pink was born in Ann Arbor, MI, to the parents Frank and Linda Pink. She attended Plymouth-Canton High School where she was introduced to the subject of anthropology. After graduation she went on to Michigan State University (MSU) where she had the opportunity to study abroad in England for an intensive human identification course. She eventually worked as a lab assistant at the MSU Forensic Anthropology Lab under the mentorship of Dr. Norman Sauer and earned her Bachelor's of Science degree in 2001. After graduating from MSU, Christine worked for the Department of Public Safety in Canton Township, MI as a police and fire/rescue dispatcher until 2003. She returned to the study of physical anthropology at Wayne State University where she earned her MA in 2005. After receiving her Master's degree she started her studies towards a Doctoral degree in physical anthropology at the University of Tennessee in Knoxville, TN. At the University of Tennessee Christine accepted a graduate teaching associate position teaching introductory courses in physical anthropology. She also worked closely with faculty both at the University of Tennessee and Vanderbilt University to develop a bioarchaeological research project in the Peruvian Andes region. Christine collaborated on the Proyecto de Investigación Arqueológico Regional Ancash (PIARA) in Hualcayan, Peru and the Proyecto Bioarqueológico Andahuaylas based in Andahuaylas, Peru. Through these collaborations and many others she completed her dissertation research concerning regional population movement in the Peruvian central Andes associated with the rise and fall of the Wari Empire from AD 600-1400. Christine graduated from the University of Tennessee with a PhD in physical anthropology in May 2013. Since March 2012 Christine has been employed as a forensic anthropologist with the Joint POW/MIA Accounting Command-Central Identification Laboratory at the Joint Base Pearl Harbor-Hickam, Hawaii.